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JULIANA STRIEDER PHILIPPSEN

Avaliação de estoques pesqueiros do reservatório de Itaipu por meio das abordagens uni-específica e ecossistêmica

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Tese apresentada ao Programa de Pós-Graduação em Ecologia de Ambientes Aquáticos Continentais do Departamento de Biologia, Centro de Ciências Biológicas da Universidade Estadual de Maringá, como requisito parcial para obtenção do título de Doutor em Ciências Ambientais.
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Já dizia Frei Luiz de Xiquexique
Quão chique é ter
Um rio pra nadar a correr
Quão chique é ter
Um rio pra pescar e pra beber
Não deixe o rio morrer
Se não que será de mim
Que só tenho esse rio pra viver
Que será de mim
Que será de José Serafim
Qual será o destino do menino

Que nasceu e cresceu aprendendo
a pescar surubim
Não deixe morrer
Não deixe o rio morrer
Se não morre o ribeirinho
De fome, de sede, de sei lá o quê
Se não morre o ribeirinho
De fome, de sede, de sei lá o quê.

Boato Ribeirinho (Allexandre Aguiar)

“Counting fish is just like counting trees except they are invisible and they keep moving”
John Shepherd

“Essentially, all models are wrong, but some are useful”
George P. Box (1987)

Avaliação de estoques pesqueiros do reservatório de Itaipu por meio das abordagens uni-específica e ecossistêmica

RESUMO

Os principais estoques pesqueiros do reservatório de Itaipu foram avaliados por meio de métodos pobres em dados e por meio de uma abordagem ecossistêmica. Métodos pobres em dados utilizam somente dados de captura; ainda estão sendo investigados e aplicações em situações reais ainda são escassas. A comparação entre dois métodos limitados em dados (CMSY e COM-SIR) demonstrou que é possível chegar a conclusões divergentes em relação ao *status* dos estoques, informações que são muito úteis para embasar a gestão pesqueira. Os dois métodos baseiam-se em pressupostos, que muitas vezes não correspondem à realidade, portanto, é necessário ter cautela ao tomar decisões baseadas nestes tipos de métodos, e quando possível, utilizar abordagens baseadas em outros tipos de dados (e.g. tamanho) para complementar estas avaliações. Indicadores baseados no tamanho evidenciaram uma elevada captura de indivíduos jovens, com exceção de *Prochilodus lineatus* e *Hypophthalmus edentatus*. Os resultados obtidos com o método COM-SIR evidenciaram alta probabilidade de sobrepesca para os estoques de *P. lineatus*, *Plagioscion squamosissimus* e *Zungaro jahu*. Indicadores ecológicos evidenciaram que não há expressivos impactos da pesca no ecossistema de Itaipu. As espécies-chave identificadas no reservatório de Itaipu (*Salminus brasiliensis*, *Z. jahu*, *Serrasalmus* spp., e *Hoplias* spp.), são também importantes para a pesca local, evidenciando a necessidade em manejar com cautela estas espécies, devido não só a sua importância para a pesca, como também ao papel ecológico que desempenham. Simulações demostraram que aumentos no esforço, não resultaram em aumentos expressivos nas capturas, indicando que a pressão pesqueira não deve aumentar em relação à pressão exercida em 2011.

Palavras-chave: Avaliação de estoques. Ecopath with Ecosim. Pesca de água doce. Pobres em dados. Teia trófica.

Stock assessment of Itaipu reservoir fishery through single-species and ecosystem approaches

ABSTRACT

The most important stocks of Itaipu reservoir were assessed through data-poor methods and ecosystem modeling. Data-poor methods are being tested, and applications in real situations still are scarce. The comparison of two data-poor methods (CMSY and COM-SIR) showed different conclusions about stock status, information which is very useful in fisheries management. Both methods rely on assumptions that do not always correspond to reality, thus it is necessary caution when management is based on this type of method, and when possible to adopt methods with different types of data (e.g. length), to complement the assessment. Length-based indicators showed a high proportion of juveniles in the landings, except for *Prochilodus lineatus* and *Hypophthalmus edentatus*. The results obtained with COM-SIR indicated high probability of overfishing for the stocks of *P. lineatus*, *Plagioscion squamosissimus* and *Zungaro jahu*. Ecological indicators showed that there are no expressive impacts due to fishing on the ecosystem. Keystone species identified in Itaipu reservoir (*Salminus brasiliensis*, *Z. jahu*, *Serrasalmus* spp., and *Hoplias* spp.), are also important for the local fishery, highlighting the necessity in managing them carefully, not only due their importance to the fishery but also for the ecological role they play. Simulations evidenced that increases in fishing effort will not result in expressively increases in catches, thus it is suggested that fishing effort do not increase in relation to effort observed in 2011.

Keywords: Data-poor. Ecopath with Ecosim. Food web. Freshwater fisheries. Stock assessment.

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SUMÁRIO

1 INTRODUÇÃO GERAL

1.2 GESTÃO DE ESTOQUES PESQUEIROS

Todos os tipos de pescarias, para que sejam sustentáveis e delas possa se obter o maior rendimento com o menor custo, devem ser geridas (Cochrane *et al*., 2011). O Código de Conduta para a Pesca Responsável (FAO, 1995) estabelece que a gestão deve promover a manutenção da qualidade ambiental e da biodiversidade, como também a disponibilidade dos recursos pesqueiros em quantidades suficientes para as gerações presentes e futuras, num contexto de segurança alimentar, de mitigação da pobreza e de desenvolvimento sustentável. Abordagens comumente usadas para a avaliação e a gestão de pescarias artesanais, especialmente em países em desenvolvimento, têm se mostrado menos efetivas do que o necessário para garantir a sustentabilidade e o suprimento de pescado (FAO, 2003; Cochrane, 2000).

Um dos pilares de uma gestão pesqueira eficiente é a produção de conhecimento sobre a dinâmica dos estoques alvo e de seus ecossistemas. Para tanto, são necessárias informações sobre o que e quanto está sendo capturado (dados de desembarque) e também sobre a biologia e ecologia das principais espécies alvo. Entretanto, 90% das pescarias de pequena escala operam em países em desenvolvimento, onde não há muito investimento na obtenção de dados biológicos e ecológicos e programas de monitoramento de desembarques são raros (FAO, 2016a; Peixer e Petrere Junior, 2009).

Historicamente, a avaliação de estoques pesqueiros tem sido realizada utilizando modelos uni-específicos, e as ações de manejo são tomadas unicamente em relação às populações dos estoques alvo da pesca. Nos últimos anos, novas abordagens passaram a incluir dois pontos fundamentais: a valorização do conhecimento do pescador sobre os recursos que ele explora e o conhecimento e proteção do ecossistema (incluindo espécies não-alvo da pesca).

Especificamente, o conhecimento do pescador tem sido cada vez mais útil principalmente em situações dado-deficientes (*data-poor fisheries*), isto é, situações em que dados científicos formais para a gestão dos recursos não são disponíveis (O'Donnell *et al*., 2010). Este conhecimento local dos pescadores tem sido adotado para obter informações sobre a biologia e ecologia das espécies alvo (Leite e Gasalla, 2013; Heyman e Granados-Dieseldorff, 2012); avaliações temporais sobre captura e tamanho das espécies explotadas (Sáenz-Arroyo *et al*., 2005; Damasio *et al*., 2015; Philippsen *et al*. 2016); e também para construir modelos ecossistêmicos (Ainsworth e Pitcher, 2005; Bevilacqua *et al*., 2016). Cabe ressaltar aqui que, durante a elaboração desta tese, sua autora e colaboradores publicaram o trabalho "Fishers' and scientific histories: an example of consensus from an inland fishery" (Marine and Freshwater Research, 2016. http://dx.doi.org/10.1071/MF16053), no qual foi abordado o conhecimento local dos pescadores de Itaipu como instrumento para a gestão. Este trabalho não está incluído formalmente nesta tese.

Considerando a abordagem tradicional uni-específica para avaliação de estoques pesqueiros, a ausência de dados disponíveis alavancou o desenvolvimento de métodos que requisitassem menor quantidade de dados. Modelos baseados em dados de captura (*catch-only models*) têm sido desenvolvidos e testados nos últimos anos (Rosenberg *et al*., 2014; Froese *et al*., 2016). Estes métodos consideram modelos de dinâmica populacional mais simples, como por exemplo, o modelo de produção excedente de Schaefer (1954), e adotam uma abordagem Bayesiana, que permite a inclusão de informações *a priori* para os parâmetros de interesse, produzindo estimativas de parâmetros importantes para a tomada de decisão, como por exemplo, o rendimento máximo sustentável (MSY), e assim extrair informações relevantes quanto ao nível de capturas que mantenha o estoque ao longo do tempo (Medley *et al*., 2009; Martell e Froese, 2012). Embora exista forte argumentação em relação ao uso de dados de captura para a avaliação de estoques pesqueiros (Hilborn e Branch, 2013; Pauly, 2013), este tipo de dado é muitas vezes a única informação disponível, principalmente em países em desenvolvimento (Vasconcellos e Cochrane, 2005), e pode ser extremamente útil para a modelagem em sistemas considerados limitados em dados, característica também associada à pesca continental (Welcomme *et al*., 2010).

Dados de comprimento também têm sido analisados a fim de obter informações sobre o *status* dos estoques explorados. Froese (2004) apresenta indicadores simples, baseados na proporção de indivíduos maduros, com comprimento ótimo e indivíduos maiores e mais velhos nos desembarques. A relação entre parâmetros de história de vida, a curva de crescimento de von Bertalanffy é a base para outro método recém-desenvolvido, que demostra a ligação entre a composição de comprimentos esperada de um estoque explotado e a biomassa desovante (Hordyk *et al*. 2015). Dados de comprimento são relativamente fáceis de serem obtidos e, portanto métodos baseados neste tipo de dados podem ser muito úteis em pescarias pobres em dados (Prince *et al*. 2015).

A atividade pesqueira é sustentável se os ecossistemas aquáticos, incluindo suas funções e serviços, persistirem em longo prazo (Arlinghaus *et al*., 2002). Assim, a preocupação com os impactos diretos, indiretos e cumulativos da pesca comercial no ecossistema não pode ser negligenciada (Fluharty, 2000; Zhou *et al*., 2010), e a gestão da pesca que foca apenas na maximização da captura de uma espécie alvo, ignorando as relações ecológicas entre os componentes do ecossistema, tende a ser limitada (Pikitch *et al*., 2004).

Nesse sentido, cada vez mais tem sido discutida a abordagem ecossistêmica da gestão de recursos naturais, que envolve diferentes dimensões (institucional, humana e ecológica). Assim, quando se dá ênfase à perspectiva pesqueira ou a uma visão holística do ecossistema, denomina-se de gestão da pesca baseada no ecossistema ("*ecosystem-based fisheries management*" – EBFM) (FAO, 2003; Pikitch *et al*., 2004). O objetivo geral de uma EBFM é manter os ecossistemas saudáveis, como também a pesca que eles suportam (Cury *et al*., 2005). Esta abordagem vem sendo usada para complementar, e não substituir, as avaliações baseadas em modelos uni-específicos (Coll *et al*., 2009; Gascuel *et al*., 2016).

1.3 A PESCA CONTINENTAL E A PESCA NO RESERVATÓRIO DE ITAIPU

A pesca continental funciona, de maneira geral, como uma atividade de pequena escala, ou artesanal, que é de fundamental importância para populações locais (Junk, 2007). Ela caracteriza-se por operar em uma grande variedade de ambientes e pela diversidade de aparatos de pesca que são utilizados (De Graaf *et al*., 2015). Em um contexto global, a produção pesqueira em águas interiores é uma importante fonte de proteína para milhões de pessoas (FAO, 2016a; FAO 2016b).

A maior parte dos ecossistemas de água doce em países industrializados está impactada e a pesca severamente degradada ou modificada (Cowx e Gerdeaux, 2004). A construção de barragens configura como um dos principais impactos em águas continentais, e a expectativa é de que a construção de reservatórios hidroelétricos aumente nos próximos anos (Winemiller *et al*. 2016). A construção de barragens afeta negativamente o rendimento pesqueiro e provoca mudanças na composição das espécies exploradas (Hoeinghaus *et al*., 2009; Hallwass *et al*., 2013; Philippsen *et al*., 2016). O ambiente lótico que abriga espécies adaptadas a estas condições é transformado em um ambiente lêntico que não apresenta as condições ideais para estas espécies. Além disso, as barragens interrompem a rota migratória de espécies que realizam grandes migrações para se reproduzir (Agostinho *et al*. 2008). Estas espécies possuem alto valor econômico para a pesca local, e são substituídas por espécies sedentárias, de menor tamanho e valor comercial, após a formação dos reservatórios (Hoeinghaus *et al*. 2009; Philippsen *et al*. 2016).

A presente tese apresenta duas abordagens para a avaliação da pesca de pequena escala, desenvolvida em um dos principais reservatórios hidroelétricos do Brasil, o reservatório de Itaipu. A pesca desenvolvida neste reservatório começou a ser monitorada cinco anos após sua formação, e produziu uma série temporal de dados de captura e tamanho dos indivíduos pescados, provavelmente única no contexto nacional. Nesse sentido, este conjunto de dados fornece uma excelente oportunidade para aplicar as abordagens citadas anteriormente, gerando informações que podem subsidiar a gestão da pesca local, como também produzir conhecimento científico a cerca dos métodos empregados.

A estrutura desta tese está organizada em três segmentos:

1 Comparação de dois métodos baseados em capturas (CMSY e COM-SIR), e discute os pressupostos e técnicas que cada um utiliza, e como eles podem afetar os resultados do modelo, quanto à classificação do estado de explotação dos estoques pesqueiros (Figura 1A).

2 O método COM-SIR (Vasconcellos e Cochrane, 2005; Rosenberg *et al*., 2014) e um método baseado em comprimentos (*length-based method*: LBM; Froese, 2004) foram adotados para inferir o estado de explotação dos principais estoques do reservatório de Itaipu. Os resultados obtidos podem subsidiar medidas de gestão local (Figura 1B).

3 Abordagem ecossistêmica, através do emprego do software Ecopath with Ecosim, para avaliar os efeitos da pesca no ecossistema do reservatório de Itaipu, utilizando também indicadores ecológicos como o nível trófico médio das capturas. Além disso, foram estimados o rendimento máximo sustentável (MSY), e a mortalidade que produz o MSY, com o modelo ecossistêmico que leva em consideração as relações tróficas para estimar valores de MSY e F_{MSY}. Simulações foram realizadas com cenários de aumento e diminuição do esforço pesqueiro, e também foram utilizados os valores de F_{MSY}, a fim de investigar os efeitos da pesca realizada em nível de F_{MSY} nos indicadores ecológicos e na captura e biomassa das espécies alvo (Figura 1C).

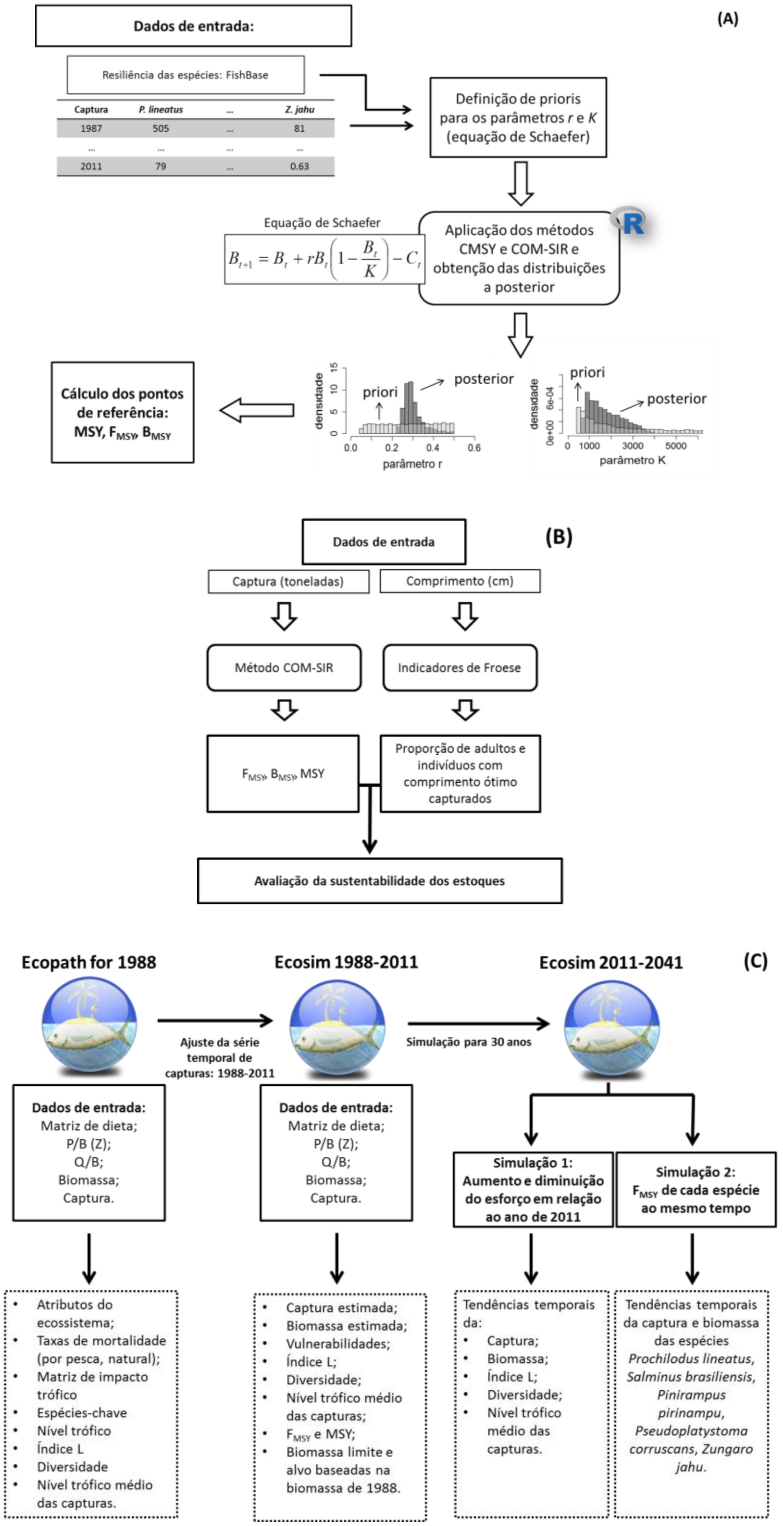

Figura 1. Diagrama das análises realizadas em cada segmento.

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2 COMPARING STOCK STATUS FROM TWO DATA-LIMITED METHODS IN A TROPICAL INLAND FISHERY

Abstract

We compared estimates of stock status indicators (maximum sustainable yield: MSY, fishing mortality that produces MSY: F_{MSY}, and biomass that produces MSY: B_{MSY} obtained with two data-poor methods that used only catch data (catch-maximum sustainable yield: CMSY, and catch-only model with sampling importance resampling: COM-SIR). Five species were analyzed with different resilience categories: *Prochilodus lineatus*, *Salminus brasiliensis*, *Pinirampus pirinampu*, *Pseudoplatystoma corruscans* and *Zungaro jahu*. Although both methods relied on the same biomass dynamic model (Schaefer model), they differed greatly in regard of some assumptions, resulting in quite different stock status for the species analyzed. COM-SIR showed lower estimates for all parameters and indicators than CMSY, except for one stock (*P. pirinampu*) and for F_{MSY}. The lower estimates of F_{MSY} from CMSY were due a linear reduction on the intrinsic rate of population increase (*r*), when final biomass is below B_{MSY}, a way the method accounted for the effects of depensation in low biomass levels. The outputs from COM-SIR exhibited wider credibility intervals for the biomass estimates than CMSY, as well as higher biomass estimates for the last year of the time series. These results seem to be due the prior for the final relative biomass, assumed in the CMSY method, which caused a great impact on the biomass trends.

Keywords Bayesian Schaefer model; catch-only models; fisheries management; inland fisheries; small-scale fisheries.

2.1 INTRODUCTION

The majority of small-scale fisheries (SSFs) are in developing countries, where the financial resources to acquire data may not exist or the economic value of the fishery may be considered too low to justify the investment on data collection (Cochrane et al., 2011; FAO, 2012). Although the economic value of SSFs is negligible comparing to industrial fisheries, SSFs play a vital social role as income and food source for millions of people (Béné et al., 2007; Kurien and Willmann, 2009). It is recognized that most small and unmanaged fisheries are in strong need of attention (Hilborn and Ovando, 2014) because there is evidence that they might be in worse condition than assessed ones (Costello et al. 2012).

In recent years, models based on catch data alone have been developed for assessments of stock status of data-poor fisheries (Martell and Froese, 2013; Rosenberg et al., 2014; Thorson and Cope, 2015; Froese et al., 2016). In addition, simulations studies have been carried out with the aim to understand differences in performance among methods (Carruthers et al., 2014; Rosenberg et al., 2014; Wetzel and Punt, 2015). Some of these models adopt a Bayesian approach that allows for the incorporation of information through prior distributions of the parameters, which contributes to the estimation of key management parameters (Punt and Hilborn, 1997; Bentley, 2015). There are, however, few examples of real application of those data-poor methods in the assessment of SSFs in general, and in developing countries in particular.

In this study, we applied two data-poor methods i.e. that use catch data alone in combination with prior information, to assess the main stocks exploited by an inland SSF developed in one of the main hydroelectric reservoir in Brazil, and discuss their strength and weaknesses highlighted by our real data application. The methods are the Monte Carlo Catch-MSY (CMSY; Froese et al., 2016), and COM-SIR, a catch-only model fitted using the Bayesian sampling-importance-resampling algorithm (Vasconcellos and Cochrane, 2005; Rosenberg et al. 2014). Both COM-SIR and the early version of CMSY were tested with simulated data, and a coherent next step suggested would be the application of these methods to real data to verify their limitations and abilities (Rosenberg et al., 2014). We compared the management quantities and stock status obtained from both methods and discussed the similarities and differences.

2.2 METHODS

2.2.1 Monte Carlo method (CMSY)

The CMSY method estimates maximum sustainable yield (MSY) and indicators of stock status (B_{MSY}, the biomass that produces MSY, and F_{MSY}, fishing mortality that produces MSY) from catch data and information on resilience (Froese et al., 2016). The method is based on a Schaefer production model and uses a Monte Carlo approach to seek a set of viable pairs of the two model parameters, *r* (the maximum intrinsic rate of population increase) and *K* (the unexploited stock size). The pairs are considered viable if, given the observed catches, they maintain the population: (i) above extinction, (i) without exceeding *K*; (iii) within prior biomass ranges in final years, defined by ad-hoc rules (see Table S1 in Supplementary material/Section 1). This method requires prior distributions for *r* and *K* (Table 1), and prior biomass ranges for the beginning and the end of the times series. This method accounts for depensation at severely depleted stock sizes, and provides estimates of *r*, *K*, biomass, and exploitation rate (Froese et al., 2016). The depensation is accounted by including a term $\left(4 {B_t}/{K}\right)$ in the Schaefer model that assumes a linear decline of surplus production, which is a function of recruitment, somatic growth and natural mortality (equation 2 in Supp. Material). A detailed description of the method is provided in Supp. material/Section 1.

2.2.2 Catch-only model – sampling importance resampling model (COM-SIR)

The COM-SIR method is also based on the Schaefer production model. It considers that the harvest rate can also be modeled as a logistic function based on the assumption that changes in effort of unmanaged fisheries follow a path dictated by economic returns. The model predicts the catch over time from a coupled effort-biomass dynamics model. By incorporating prior information and fitting to observed catches, the model estimates *r* (intrinsic rate of population increase) and *K* (the unexploited stock size), from which management quantities, such as MSY, F_{MSY}, and B_{MSY}, can be computed, as well as the harvest dynamics parameters: *x*: rate of increase in effort, and *a*: the bioeconomic equilibrium point. This catch-only model assumes that catch data contains information on both fishing effort and stock biomass dynamics, given the priors on *r, K, x* and *a* (Vasconcellos and Cochrane, 2005). The estimation is done using the sampling-importance-resampling algorithm (SIR; McAllister et al., 1994; Gelman et al., 2004), implemented in R (R Development Core Team 2013). The COM-SIR method needs as input catch data and information on the resilience of the species, from which prior and posterior distributions for *r* and *K* are obtained (see Table 1). The method assumes that the initial biomass is equal to the carrying capacity of the stock. A detailed description of this method is found in Supp. Material/Section 1.

Table 1. Prior distributions for the methods investigated. U: uniform distribution. In parentheses is the resilience: VL: very low, L: low, M: medium

	CMSY method			
	r	*K*		
P. lineatus (M)	U(ln(0.2), ln(1))	U(ln(505), ln(1010))		
S. brasiliensis (M)	U(ln(0.2), ln(1))	U(ln(14.5), ln(291))		
P. pirinampu (L)	U(ln(0.05), ln(0.5))	U(ln(106), ln(4250))		
P. corruscans (L)	U(ln(0.05), ln(0.5))	U(ln(123), ln(4940))		
Z. jahu (VL)	U(ln(0.015), ln(0.1))	U(ln(417), ln(2220))		
	COM-SIR method			
	r	*K*	*x*	*a*
P. lineatus	U(0.2, 1)	U(ln(505.031), ln(50503.2))	U(10^{-6}, 1)	U(0, 1)
S. brasiliensis	U(0.2, 1)	U(ln(15.52), ln(1552))	U(10^{-6}, 1)	U(0, 1)
P. pirinampu	U(0.05, 0.5)	U(ln(60.46), ln(6046.04))	U(10^{-6}, 1)	U(0, 1)
P. corruscans	U(0.05, 0.5)	U(ln(61.726), ln(6172.6))	U(10^{-6}, 1)	U(0, 1)
Z. jahu	U(0.015, 0.1)	U(ln(95.7), ln(9573.3))	U(10^{-6}, 1)	U(0, 1)

For both methods the prior distributions of *r* and *K* are assumed to be uniform. For *r* the bounds depend on the resilience category assumed for each species, obtained from FishBase (Froese and Pauly, 2016; see Table S2 in Supp. Material/Section 1). In the CMSY method bounds for *K* are set by ad hoc rules (see Table S3 in Supp. Material), and in the COM-SIR method, the lower and upper bounds for *K* are set as the maximum observed catch and 100 times this value, respectively (Table 1). The time step for the models is assumed to be annual. The initial depletion was assumed to be a value between 0.2 and 0.6, based on ad-hoc rules described in table S1, for all species analyzed (required for the CMSY method), and the prior final relative biomass ranged between 0.01 and 0.3, depending on the stock.

2.2.3 Times series of catch from an inland fishery: application example

The data is from a small-scale fishery developed in Itaipu reservoir, one of the main hydropower dams in South America (Agostinho et al., 2007). There are almost 700 fishers in the region (Okada et al., 2012). The catch data come from the fishing monitoring program carried out by a partnership between the Itaipu Binacional and Research Nucleus in Limnology, Ichthyology and Aquaculture (Nupélia/Universidade Estadual de Maringá) (Okada et al., 2012). The time series of catches ranged from 1987 to 2011. Five stocks were assessed: two species that are among those with the largest catches (*Prochilodus lineatus* and *Pinirampu pirinampus*), and three species of migratory fish with high commercial value (*Salminus brasiliensis*, *Pseudoplatystoma corruscans*, and *Zungaro jahu*). It is noteworthy that *P. lineatus* is among the most exploited stocks in impounded southeastern Brazilian rivers and reservoirs (Silvano and Begossi, 2001; Agostinho et al., 2008), and another species from the same genus (*P. nigricans*) is important in fisheries developed in the occidental Amazonian rivers in Brazil (Hallwass et al., 2013).

2.3 RESULTS

The estimated *r* was higher and had a narrower credibility intervals for CMSY than for COM-SIR for two species, *P. lineatus* and *S. brasiliensis* (Fig.1, Table 2). The posterior distributions for *r* obtained with CMSY were very similar to their respective prior distributions for *P. pirinampu, P. corruscans* and *Z. jahu*. The posterior distribution for *K* from COM-SIR were narrower than for CMSY, although the prior distribution was much wider for COM-SIR (Fig. 2).

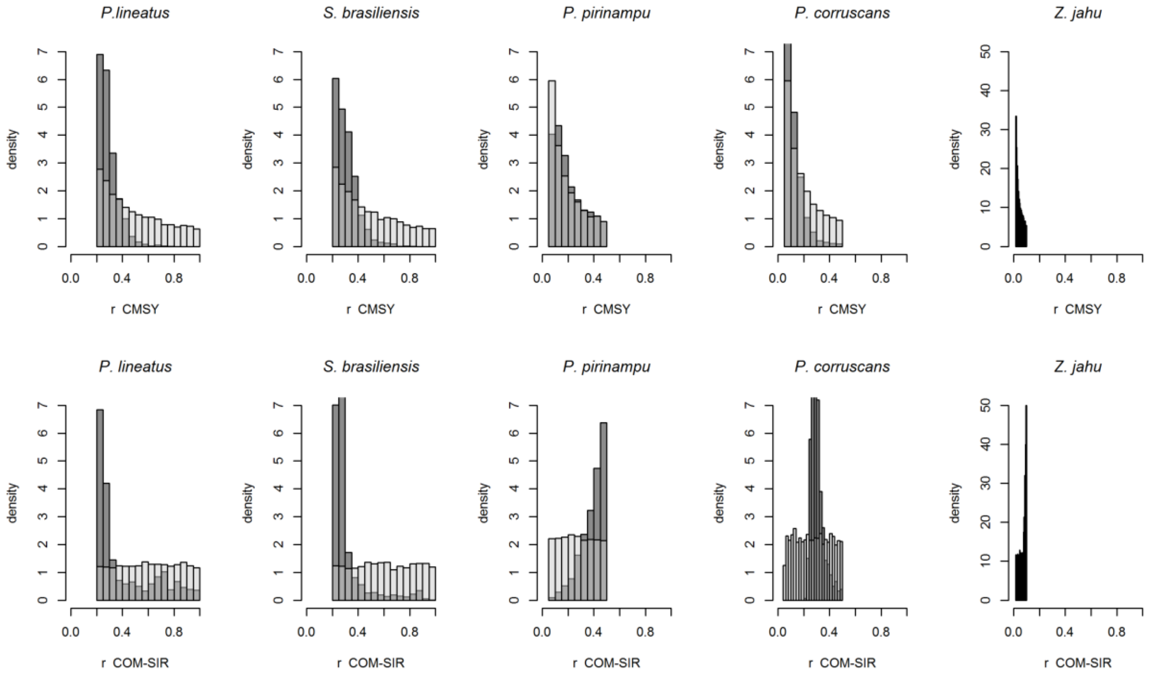

Figure 1. Prior (light grey) and posterior (dark grey) distributions for the estimated *r* parameters from CMSY and COM-SIR methods.

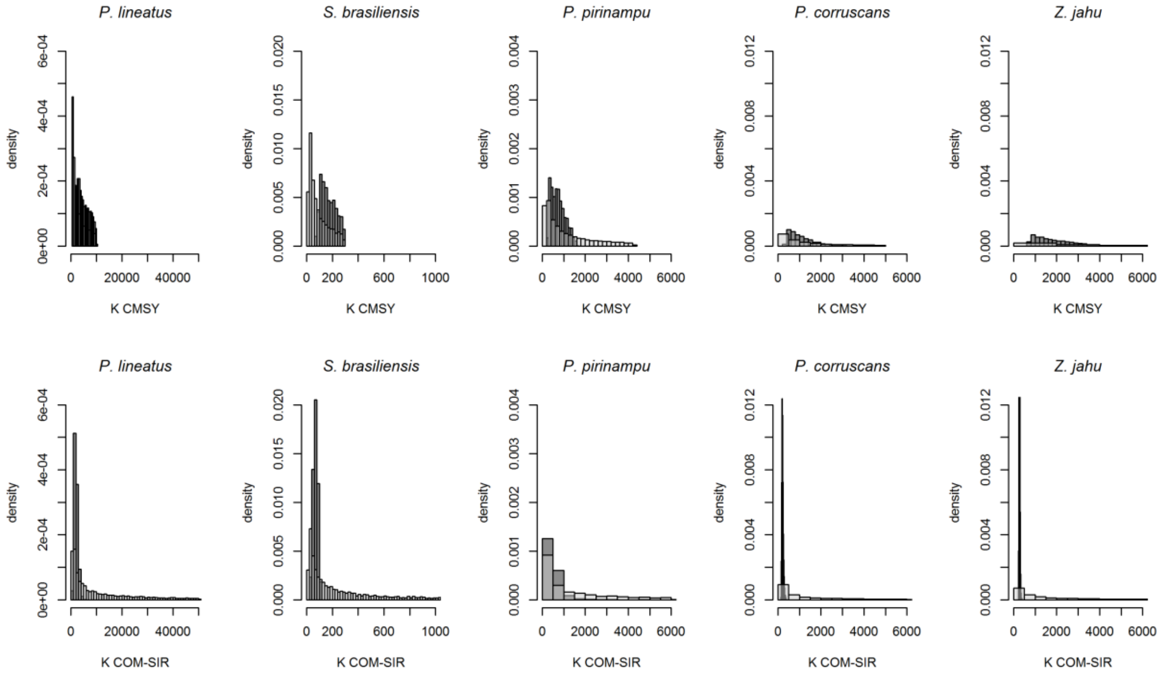

Figure 2. Prior (light grey) and posterior (dark grey) distributions for the estimated *K* parameters from CMSY and COM-SIR methods.

The estimated values for MSY and B_{MSY} obtained with CMSY method were higher than the COM-SIR (Table 2). In the contrary, the higher values for F_{MSY} were obtained with COM-SIR. Regarding the credibility intervals, estimates from COM-SIR method were narrower than CMSY.

Table 2. Estimated parameters and reference points from the CMSY and COM-SIR models. For CMSY: to estimate *r*, all viable *r* values are assigned to 25-100 bins of equal width in log-space. The 75th percentile of the mid-values of occupied bins is taken as the most probable estimate of *r*. *K* is determined from a linear regression fitted to log(*K*) as a function of log(*r*), for *r*-*K* pairs where *r* is larger than median of mid-values of occupied bins, with log(4MSY) as intercept and with a fixed slope of -1, based on the rearranged Schaefer model (MSY=*rK*/4 → log(*K*)=log(4MSY) + (-1)log(*r*)). MSY was estimated as the mean value from the *r*-*K* pairs above median of mids. For COM-SIR: median values and 95% credibility intervals. Mean and maximum catches are in tonnes.

		P. lineatus	*S. brasiliensis*	*P. pirinampu*	*P. corruscans*	*Z. jahu*
Mean catch		130.4	4.3	38.2	13.2	15.5
Maximum catch		505	15.5	60.5	62	96
CMSY	*r*	0.492 (0.325-0.745)	0.563 (0.384-0.825)	0.282 (0.163-0.487)	0.27 (0.155-0.469)	0.062 (0.039-0.097)
	K	3490 (1710-7150)	112 (55.2-226)	475 (251-899)	553 (210-1460)	1450 (585-3580)
	MSY	429 (325-745)	16 (7.57-32.6)	33.5 (28-40)	37.3 (16-88)	22.4 (9.13-55)
	B_{MSY}	1750 (853-3580)	55.8 (27.6-113)	237 (125-450)	276 (105-730)	723 (293-1790)
	F_{MSY}	0.108 (0.07-0.16)	0.084 (0.057-0.123)	0.125 (0.072-0.216)	0.038 (0.022-0.067)	0.006 (0.004-0.01)
COM-SIR	*r*	0.279 (0.21-0.86)	0.262 (0.220-0.691)	0.412 (0.209-0.493)	0.290 (0.25-0.385)	0.088 (0.057-0.099)
	K	1936 (1072-3396)	68.5 (41-98)	436 (292-1133)	205 (164-269)	271 (243-311)
	MSY	161 (114-255)	4.76 (3.82-6.68)	43.3 (31.5-87.2)	15 (13-19)	5.8 (4-7.2)
	B_{MSY}	968 (536-1698)	34 (20.5-48.8)	218 (146-567)	102 (82-135)	135 (121-155)
	F_{MSY}	0.139 (0.106-0.432)	0.131 (0.110-0.346)	0.206 (0.104-0.246)	0.145 (0.125-0.192)	0.044 (0.028-0.049)

Exploitation rates differed only at the end of the time series (Fig.3). On the contrary, predicted biomass trajectories differed greatly between the methods investigated, with COM-SIR overestimating biomass in comparison with CMSY, except for *Z. jahu* after 1995 (Fig. 4).

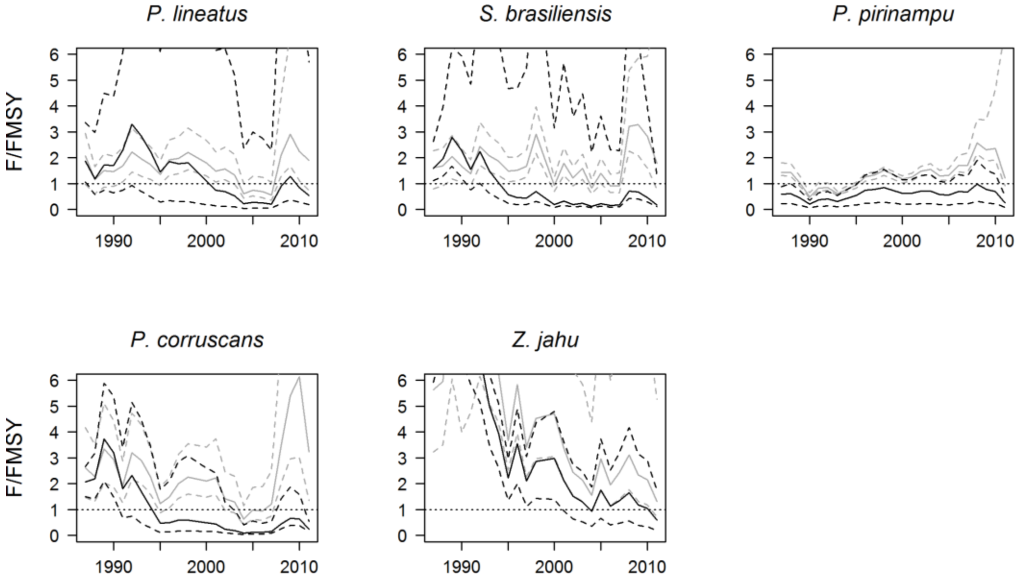

Figure 3. Exploitation rate according to CMSY (grey) and COM-SIR (black) methods.

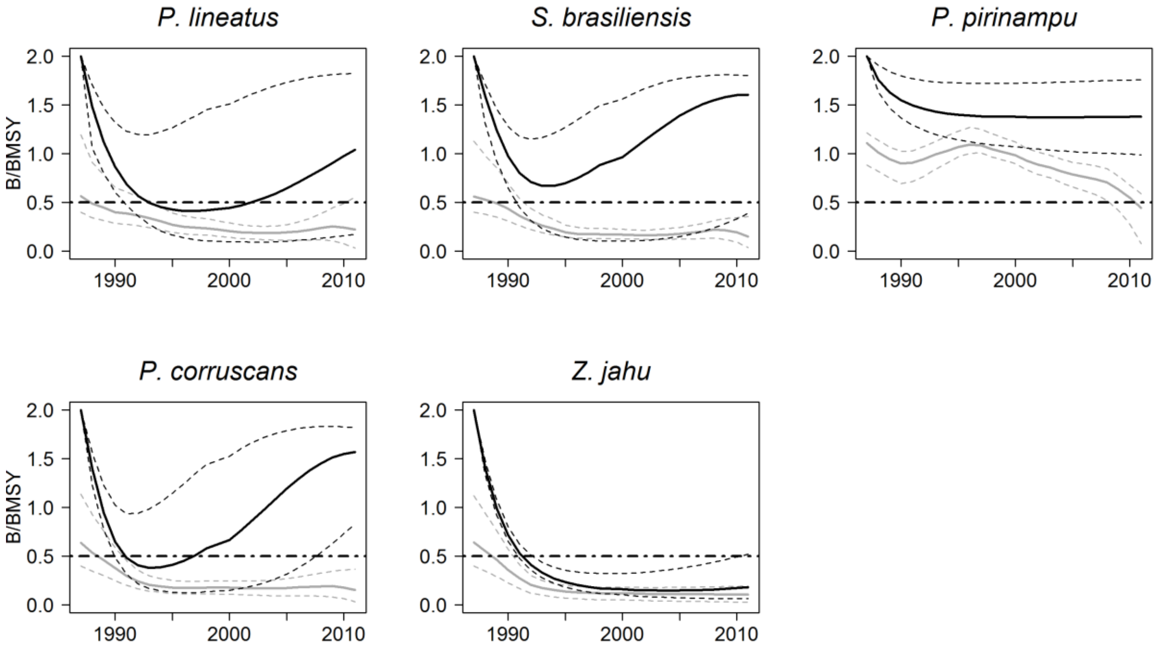

Figure 4. Biomass over B_{MSY} from CMSY (grey lines) and COM-SIR (dark lines). Solid and

dotted-dash lines represent median and 95% credibility intervals, respectively. The dotdashed line represents the limit to classify the stock as overfished ($B_{current}/B_{MSY}$ < 50%).

Stock status obtained with the methods investigated showed disagreement regarding biomass levels and fishing mortality (Figs. 3 and 4). The only stock that exhibited the same status was *Z. jahu*, but only for biomass level (Fig. 4).

The diagnostics showed that no vector of parameters was assigned more than one percent of the posterior probability, during the resampling procedure of COM-SIR. Also, the ERU diagnostics showed that the degree of proximity between the importance function, and the posterior distribution were good (Table S4 in the Supp. material).

2.4 DISCUSSION

The methods employed in this study differed greatly in the estimated parameters and in the classification of stock status. In general, larger estimates of *r* and *K* were obtained from CMSY than from COM-SIR, except for F_{MSY}. Also, CMSY provided more pessimistic conclusions regarding stock status than COM-SIR. The CMSY method searches for the most probable *r* estimate in the tip region of the triangle formed by the viable *r*-*K* pairs (Froese et al., 2016). The authors of CMSY argue that this way of calculating *r* is based on the description of the parameter that defines it as a maximum rate of increase of the population. Thus, the method seeks for *r* values among the highest ones (see Section 1 in Supp. Material for details on how *r* is obtained). This way to obtain the most probable *r* is argued to reduce the bias caused by the triangular shape of the cloud of *r*-*K* pairs (Froese et al., 2016). On the contrary, the estimated *r* from COM-SIR is calculated simply as the median value of the posterior distribution obtained.

Determining prior distributions is not an easy task, and inappropriate choices for priors can lead to incorrect inferences (Punt and Hilborn, 1997). The CMSY method assumed the logarithm of *r* as a uniform distribution, thus values among the *r* prior range had different weights. This could lead to prioris too informative, as in the case of three species analyzed (*P. pirinampu*, *P. corruscans*, and *Z. jahu*), which the posterior distributions were very similar to the priors. Thereby, the probability that the observed catch would have occurred given the model was true, was too small (the data became uninformative with such informative prior). On the other hand, there is also the possibility that the data wasn't informative at all. However, if we look to the posterior distributions for *r* obtained from the COM-SIR method, there is evidence that the data contained information. Another interesting result was that the mode of all the posterior distributions for *r* was at their extreme, except for *P. corruscans* in COM-SIR results. This may occur when the likelihood favours values close to where the prior assigns zero probability (values outside prior range), which is not desirable (Punt and Hilborn, 1997). A sensitivity analysis would permit to investigate if this was the case, as also to assess if the results are sensitive to the choice of priors, because if this would be true, the data probably is not informative (Punt and Hilborn, 2001).

The CMSY method also differs from COM-SIR, by providing prior distributions of relative biomass at the beginning and the end of the time series, depending on the assumed depletion level. The COM-SIR method assumes a model for the harvest dynamic that will restrict the possible trajectories for the biomass. The CMSY uses ad-hoc rules to set up prior distributions for the depletion on the final year. The biomass trajectories are variables derived from the input parameters and the catches. It is recommended that the assignment of prior probabilities to derived quantities such as the biomass (or depletion) in the final year, at the same time that prior distributions are assigned to the parameters from which those quantities are a function of, be avoided because that might lead to an instance of what is known as the "Borel's paradox": (i) use of priors under different parameterizations of the same model can result in different marginal posteriors for the same model quantities, and (ii) the possibility to specify priors with contradictory assumptions about model input parameters (Punt and Hilborn, 1997; McAllister and Kirkwood, 1998). In this way, further testing of the impact in defining prior distributions for relative biomass on the results should be done. Also, assuming a prior for relative biomass in the final year, constrained the possible outcomes from the CMSY method, since all stocks analyzed were classified as low relative biomass in the final year, by the default rules. The analysis without this assumption, produced different results, with higher levels of biomass in the last years (see Fig. S5 in Supp. Material), and consequently, different stock status regarding biomass levels.

Reference points (RP) used in fishery management, such as MSY, B_{MSY} and F_{MSY} are calculated based on estimated *r* and *K*, from surplus production models, as CMSY and COM-SIR. Thus, it is not surprising that they were higher for the method that estimated higher *r* and *K*. The exception was for F_{MSY}, which was lower for CMSY than COM-SIR, for all stocks analyzed. This happened because when biomass in the last year was below half B_{MSY}, F_{MSY} is linearly reduced in the CMSY method (Froese et al. 2016). Another difference between methods is that

CMSY estimates MSY only from the viable *r*-*K* pairs where *r* values were higher than the median, in contrast with COM-SIR which used all the posterior distribution of *r* to estimate MSY, thus contributing for the difference we observed in results.

The CMSY method accounts for depensation at severely depleted stock sizes, by incorporating the term $4\,{}^{B_t}\!/_{K}$, in the biomass dynamic equation (see equation 2 in section 1 in Supp. material), therefore it assumes a linear decline of recruitment below half of the biomass that is capable of producing MSY (Froese et al. 2016). When final biomass is below half B_{MSY}, F_{MSY} estimates are linearly reduced, producing lower values when compared to COM-SIR. Besides, the procedure adopted by the CMSY method is highly based on ad hoc rules, differing from COM-SIR.

The models applied in our study have assumptions that do not always correspond to reality, although they are necessary, mainly in data-poor situations. An example is the assumption of initial biomass being equal to carrying capacity in the COM-SIR method. In our study, it is known that this is not true, since fishing activity was performed even before reservoir construction (Agostinho et al., 1999). This assumption is strong and is absent in CMSY method, which assume initial relative biomass (B_t /K) based on the start year of the time series. Punt (1991) showed that setting initial biomass equals to K, resulted in less biased estimates, than setting B_t/K in a production model that assumes observation errors, which is the case of COM-SIR.

Both methods analyzed set prior ranges for some parameters of interest from its own data set, as for example for *K* priors which were defined based on maximum observed catch. Thus, data was used to construct the prior ranges for some parameters and also to update the priors and obtain the posterior distributions. This double use of data could bias the posterior distributions of the parameter and is advised to be avoided (Minte-Vera et al., 2005). Another assumption made in the COM-SIR method that is not true, in the case of Itaipu fishery, is in relation to “no subsidies or constant subsidies”, because this would modify the expected harvest dynamics as some of the cost of fishing would be taken up by the subsidies and the fishers would take longer to decrease their effort when the biomass is decreasing. It is known that during the time period where catch data was obtained, a bank credit line became available from the Brazilian government, which allowed fishers to improve their equipment (boats and engine). Therefore, in data-poor situations, fishery scientists face the trade-offs between assumptions that have to be made to overcome the absence of data.

Stock status according to both methods showed divergent results. If management would be based on COM-SIR estimates, fishing mortality could be maintained in the level of 2011, since it was below F_{MSY}, and biomass was above $0.5B_{MSY}$, except for one stock (*Z. jahu*). On the contrary, the management advice based on CMSY results would be to reduce fishing mortality for all stocks, because fishing mortality was above F_{MSY} and biomass below $0.5B_{MSY}$. The only stock with the same stock status, regardless the method employed was *Z. jahu*. The catch data for this species showed considerable contrast, indicating that the data was very informative. Other interesting evidence that validates the results obtained with COM-SIR was the similarity between the tendency of Bt/B_{MSY} and the depletion index estimated for curimba, with an integrated model framework (Stock Synthesis 3.0 model; Santana, unpublished data). This is a good evidence that COM-SIR method, even being simple in model structure and assumptions, provided a similar tendency compared to the complex model that was based on an age-structured model, accounted for an environmental process (local hydrological variability), and incorporated multiple data sources (fishery dependent and independent data) (Santana, unpublished data).

Considering that catch-only methods are based on the most simple models from fishery science and taking into account the discussion about using catch data to infer stock status (Pauly et al., 2013), it would be safe to combine catch-only analyses with other techniques that rely on different types of data, as size indicators, for example (Froese, 2004; Hordyk et al., 2015). So, if results from different methods and data types show convergence, we will have more confidence in the performance of data-poor methods.

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APÊNDICE A – Comparing stock status with two data-poor methods in a tropical inland fishery

Section 1 – detailed description of CMSY and COM-SIR methods

Monte Carlo method (CMSY)

The CMSY method is a new version of the Catch-MSY (Martell and Froese, 2013), that estimates maximum sustainable yield (MSY), biomass, and exploitation rate from catch data and information on resilience (Froese et al., 2016). The CMSY method differs from the previous version (Martell and Froese, 2013), by searching for the most probable *r* not in the center but rather in the tip of the triangle formed by the viable *r*-*K* pairs. This is done due the definition of *r*, which states it as the maximum rate of increase for the examined population, which should be found among the highest viable *r* values. The method searches between probable ranges of maximum intrinsic rate of population growth (*r*), and of unexploited population size to detect viable *r*-*K* pairs via a Monte Carlo approach. Also, biomass ranges for the beginning and the end of the times series are defined by ad-hoc rules, based on observed catches (Table S1).

Table S1. Rules for setting ranges of initial and final biomass in the CMSY method, and the respective default prior biomass ranges relative to *K* (Table from Froese et al., 2016).

Time period	Rules	Range
Initial biomass	If start year of time series of catch was before 1960: high initial biomass is assumed	0.5 – 0.9 K
	If start year was after 1960: medium initial biomass is assumed	0.2 – 0.6 K
Final biomass	If $\frac{catch\ last\ year}{mean\ catch\ last\ 5\ years} > 0.7$: high final prior biomass	0.5 – 0.9 K
	If $0.3 > \frac{catch\ last\ year}{mean\ catch\ last\ 5\ years} < 0.7$: medium final prior biomass	0.2 – 0.6 K
	If $\frac{catch\ last\ year}{mean\ catch\ last\ 5\ years} < 0.3$: low final prior biomass	0.01 – 0.4 K

For the setting of the intermediate biomass range, the years with minimum and maximum catch are identified. In the cases where minimum or maximum catch fall within 3 years of the beginning or the end of the time series are ignored, as it is deemed to make little sense to set intermediate prior biomass so close to start or end biomass. Instead, the next closest values were used for minimum and maximum catch. The following rules for the intermediate prior biomass range are applied in priority of sequence (Froese et al., 2016).

1. If overall contrast in catch data is low (overall min catch / overall max catch > 0.6), the intermediate year is set to the mid of the time series and biomass is assumed to be the same as the initial prior biomass.
2. If the minimum catch occurs after the maximum catch, the year before the minimum catch is used to set the intermediate prior biomass.
    a. If initial prior biomass is high and the minimum catch occurs in the first half of the time series and the difference between min and max catch is moderate (min catch / max catch > 0.3) then the intermediate prior biomass range is set to medium.
    b. Else the intermediate prior biomass range is set to low (0.01 – 0.4K).

3. If the minimum catch occurs before the maximum catch, the year before the maximum catch is used as intermediate year.

    a. If initial prior biomass is high and the maximum catch occurs in the first half of the time series then the intermediate prior biomass range is set to high.

    b. If there is a steep increase in catches ((max catch - min catch) / max catch / (max year – min year) > 0.04), a developing or recovering fishery is assumed and the intermediate prior biomass range is set to high.

    c. Else the intermediate prior biomass range is set to medium.

The bounds for *r* prior distribution were dependent on the resilience category assumed for each species (see Table 1 in the main text, and Table S2). The resilience category for each stock was set according to FishBase (Froese and Pauly, 2016). The prior distribution for *r* was set as a Uniform distribution on a logarithm scale: $\log(r) \sim Uniform(\ln(\text{lower bound}), \ln(\text{upper bound}))$.

Table S2. Resilience categories from FishBase and corresponding prior distributions for *r* (Table from Froese et al., 2016).

Resilience category	**Bounds for the prior probability for *r***
Very low	(0.015, 0.1)
Low	(0.05, 0.5)
Medium	(0.2, 1)
High	(0.6, 1.5)

The prior range for *K* was derived based on three assumptions: (i) unexploited stock size (*K*) is larger than the largest catch in the time series, because it is highly unlike that a fishery finds and catches, in a single year, all individuals of a previously unexploited stock (Vasconcellos and Cochrane, 2005). Thus, maximum catch in the time series was used to set the lower bound of K; (ii) the maximum sustainable catch expressed as a fraction of the available biomass (F_{MSY}) depends on the productivity of the stock. This relationship was accounted for by dividing maximum catch by the upper and lower bounds of r and using these values as the benchmarks for the lower and upper bounds of K; (iii) maximum catch will constitute a larger fraction of K in substantially depleted rather than lightly depleted stocks. These considerations are summarized in Table S3. The prior distribution for K was set as the logarithm of the Uniform distribution: $\log(K) \sim Uniform(\ln(\text{lower bound}), \ln(\text{upper bound}))$ (Froese et al., 2016).

Table S3. Ranges for prior distribution for K. maxCatch is the maximum observed catch in the time series (Table from Froese et al., 2016).

Prior biomass at the end of the time series	Start K (minimum, maximum)
Stocks with low prior biomass	(maxCatch/upper range for r, 4*maxCatch /lower range for r)
Stocks with high prior biomass	(2*maxCatch /upper range for r, 12*maxCatch /lower range for r)

To reduce the influence of extreme catches, catch data were smoothed by a 3-year moving average (Froese et al., 2016).

To find for viable r-K pairs, a random r-K pair is selected from within the prior ranges for r and K, and then a starting biomass is selected from the prior biomass range for the first year, and the Schaefer biomass dynamics (equation 1) is used to calculate the predicted biomass for the next years:

$$B_{t+1} = B_t + r\left(1 - \frac{B_t}{K}\right)B_t - C_t \qquad \text{(Equation 1)}$$

where B_{t+1} is the exploited biomass in the subsequent year $t+1$, B_t is the current biomass, and C_t is the catch in year t.

To account for depensation or reduced recruitment at severely depleted stock sizes, a linear decline of surplus production, which is a function of recruitment, somatic growth and natural mortality (Schnute and Richards, 2002), is incorporated if biomass fall below ¼*K* (equation 2):

$$B_{t+1} = B_t + 4\frac{B_t}{K}r\left(1 - \frac{B_t}{K}\right)B_t - C_t \qquad \text{given} \quad \frac{B_t}{K} < 0.25 \qquad \text{(Equation 2)}$$

The term $4\,{}^{B_t}\!/_{K}$ assumes a linear decline of recruitment below half of the biomass that is capable of producing MSY (B_{MSY}) (Froese et al., 2016).

An *r*-*K* pair is discarded if any of the following conditions applies: (i) the predicted biomass is smaller than 0.01*K* (the stock crashes); (ii) the predicted biomass falls outside the prior biomass range of the intermediate year; (iii) the predicted biomass fall outside the prior biomass range of the final year. If none of these conditions apply, the *r*-*K* pair and the estimated biomass for the time series are stored for analysis (Froese et al., 2016).

The CMSY method seeks the most probable *r* value near the tip of the triangle of viable pairs. To do so, all viable *r* values are assigned to 25-100 bins of equal width in log-space. The 75th percentile of the mid-values of occupied bins is taken as the most probable estimate of *r*. This procedure gives equal weight to all occupied bins and reduces the bias caused by the triangular (instead of ellipsoid) shape of the cloud of viable *r*-*K* pairs. The credibility intervals are obtained as 51.25th and 98.75th percentiles of the mid-values of occupied bins. The most probable value of K is determined from a linear regression fitted to log(K) as a function of log(r), for r-K pairs where r is larger than median of mid-values of occupied bins, with log(4MSY) as intercept and with a fixed slope of -1, based on the rearranged Schaefer model (equation 3) (Froese et al., 2016).

$$MSY = \frac{rK}{4} \rightarrow \log(K) = \log(4MSY) + (-1)\log(r) \qquad \text{(equation 3)}$$

Credibility intervals for K are obtained by adding the standard deviation of the residuals of the regression line to the predicted K value at the lower credibility interval of r, and subtracting it from the K values predicted for the upper credibility interval of r. MSY was obtained as geometric mean of the MSY values calculated for each r-K pairs, where r is larger than the median. Viable biomass trajectories were restricted to those associated with an r-K pair that fell within the confidence limits of the CMSY estimates of r and K. The median of the predicted values for each year was used as the most probable biomass and the 95th percentiles were used as credibility intervals (Froese et al., 2016).

Catch-only model – sampling importance resampling model (COM-SIR)

The COM-SIR method estimates catch over time with a coupled equation of effort and biomass, allowing an estimation of r (intrinsic population growth rate) and K (carrying capacity) parameters that are used to calculate indicators for stock assessments, such as MSY, F_{MSY}, and B_{MSY}. The catch-only model assumes that catch data contains information on both fishing effort and stock biomass dynamics (Vasconcellos and Cochrane, 2005). A Schaefer biomass dynamics model (Equation 4) and a harvest rate dynamics model (Equation 5) were combined to predict catches over time (Equation 6), allowing inference about stock status, production and exploitation rate (Vasconcellos and Cochrane, 2005).

The Schaefer biomass dynamic model is:

$$B_{t+1} = B_t + rB_t\left(1 - \frac{B_t}{K}\right) - C_t \qquad \text{(equation 4)}$$

The annual harvest rate evolves over time according to a logistic model (Medley et al., 2009; Rosenberg et al. 2014):

$$P_{t+1} = P_t\left[1 + x\left(\frac{B_t}{aK} - 1\right)\right] \qquad \text{(equation 5)}$$

where P_t is the proportion of biomass caught at time t, a ($0 < a < 1$) is the bioeconomic equilibrium as a proportion of K, assuming no subsidies or constant subsidies in the fishery, and x is the rate of effort change. The initial harvest rate is given by $P_0 = C_0 / B_0$. The initial catch, C_0, is assumed to be equal to the first observed catch in the time series and $B_0 = K$.

Catches are predicted by the following equation:

$$\hat{C}_{t+1} = P_{t+1}\left[B_t + rB_t\left(1 - \frac{B_t}{K}\right) - \hat{C}_t\right] \qquad \text{(equation 6)}$$

where $\hat{C}_{t+1}$ is the predicted catch in year $t+1$, P_{t+1} is the harvest rate or proportion of the biomass caught in year $t+1$, K is the carrying capacity or the biomass where population growth is null and r is the intrinsic rate of population growth. The four parameters to be estimated are r, K, x, and a.

The parameters were estimated using a Bayesian approach with a sampling importance resampling algorithm (SIR; McAllister et al., 1994; Gelman et al., 2004), implemented in R (R Development Core Team 2013). The observed catch was assumed to follow a lognormal likelihood function (Casella and Berger, 2002) with expected values equal to the predicted catch by the model:

$$L(\phi|w) = \prod_{t=1}^{n} \frac{1}{\sigma C_t \sqrt{2\pi}} \exp\left[-\frac{1}{2\sigma^2}\left(\ln C_t - \mu\right)^2\right]$$

where $\mu = \ln E(C_t) - \frac{\sigma^2}{2}$, *n* is the sample size, C_t is the observed catch in year *t*, $E(C_t)$ is the predicted catch for year *t* given by Equation 6, and σ^2 is the variability parameter assumed known and equal to 0.4 (Vasconcellos and Cochrane, 2005).

The prior probability distributions assumed for the parameters a, x, r, and K follow Rosenberg et al. (2014) (see Table 1 in the main text).

The bounds for the prior distribution of *r* parameter were dependent on the resilience category assumed for each species (see Table 1 in the main text, and Table S2 above). The resilience category for each stock was set according to FishBase (Froese and Pauly, 2016). The lower and upper bounds for the prior distribution of *K* were set based on the maximum observed catch, and 100 times the maximum observed catch, respectively.

The importance function was equal to the joint prior function, and thus the importance ratio was equal to the likelihood. We considered a total of 5,000,000 parameter vectors randomly sampled from the joint prior distribution. From them, 5,000 samples were taken with replacement and probability proportional to the importance ratio. To verify if the sample of parameters was drawn from an importance function similar to the posterior distribution, we considered: (i) the maximum single density (MSD) lower than 1%, which means that the resampling was done until no vector was assigned more than one percent of the posterior probability (Punt and Hilborn, 1997); and (ii) the entropy of the importance weights relative to uniformity (ERU), describes the degree of proximity between the importance function and the posterior distribution; when ERU is close to 1, it is an indicate that they are close (Kinas, 1996). The R code to run the model was written by C.V. Minte-Vera, and it is available from Rosenberg et al. (2014). To assess the fit of the model, we performed a posterior predictive check (Gelman, 2006). To do so, we simulated catch data from a log-normal distribution, with mean equal to the estimated catch from the COM-SIR method, and variance equal the variance assumed in the COM-SIR method (0.4). After the simulation, we graphically displayed the simulated data, along with the observed catch. If the posterior predictive interval of 95% contained the observed catch, we concluded that the fit of the model was adequate.

Section 2 – Diagnostics from COM-SIR method, model fit, and posterior predictive checking

Table S4. Diagnostic values for the species analyzed. MSD: maximum single density; ERU: entropy of the importance weights relative to uniformity.

Species	MSD	ERU
Prochilodus lineatus	0.32	0.92
Salminus brasiliensis	0.22	0.96
Pinirampus pirinampu	0.08	0.95
Pseudoplatystoma corruscans	0.37	0.95
Zungaro jahu	0.20	0.96

Model fit and the posterior predictive checking

The median predicted catches from COM-SIR method showed good agreement with the observed catches, except for *P. pirinampu* (Figure S1).

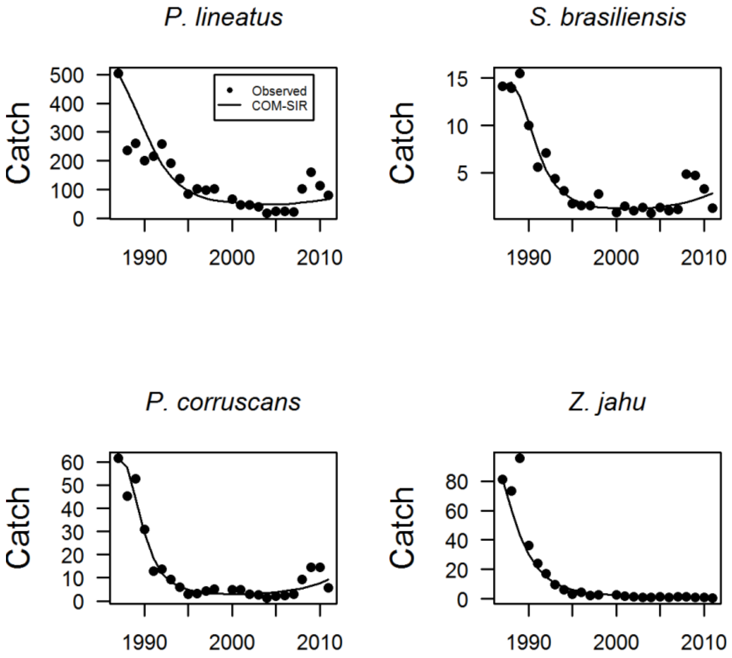
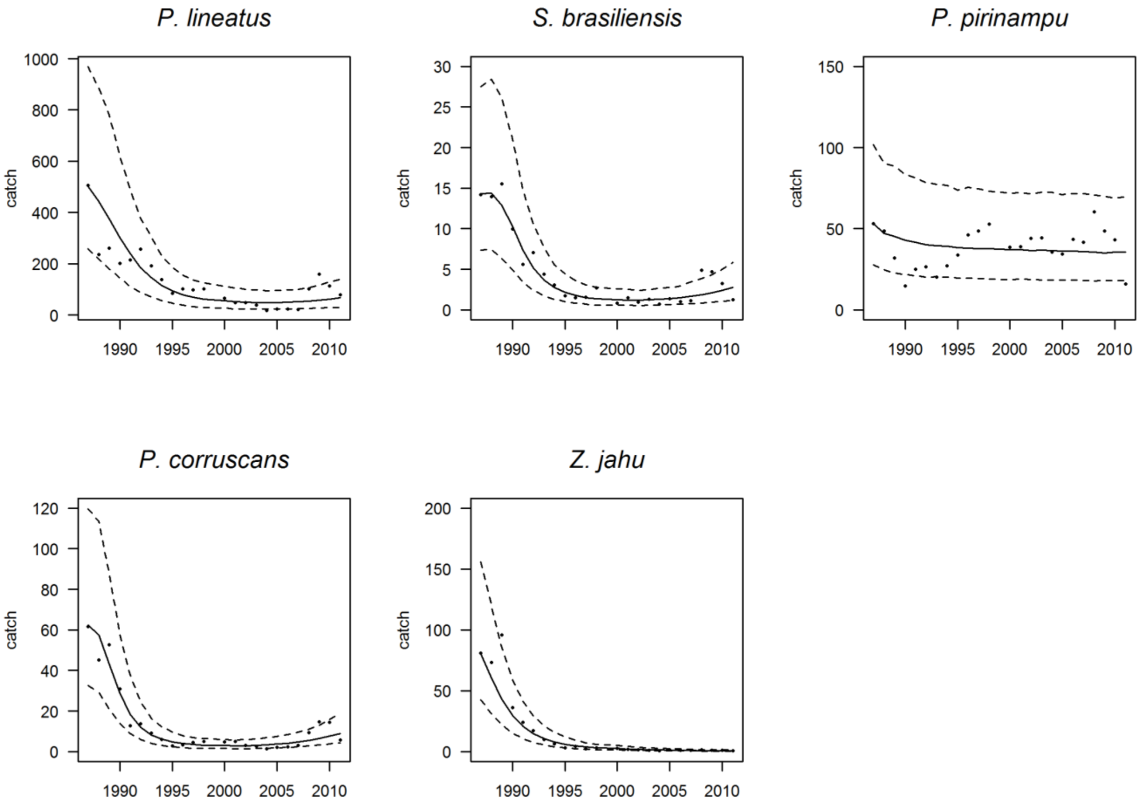


Figure S1. Observed and predicted (median) catches (in tonnes) for the species analyzed. Note that y-axes are different.

The posterior predictive analysis showed that the credibility intervals of the simulated data contained the observed catches for the majority of the stocks analyzed (Figure S2). For *P. lineatus*, *S. brasiliensis* and *P. corruscans*, observed catches in 2009 were outside the 95% credibility interval, and between 2004 and 2007, observed catch was at the lower credibility interval. The posterior predictive checking for *P. pirinampu* showed wide credibility intervals, and two observations outside the credibility intervals.



P. lineatus

S. brasiliensis

P. pirinampu

P. corruscans

Z. jahu

Figure S2. Posterior predictive distributions of the catch data from the COM-SIR method. The solid and dashed lines represent the median and the 95 credibility intervals, respectively. Dots represent the observed catch. Note that y-axes are different.

Prior and posterior distributions for x and a parameters from COM-SIR.

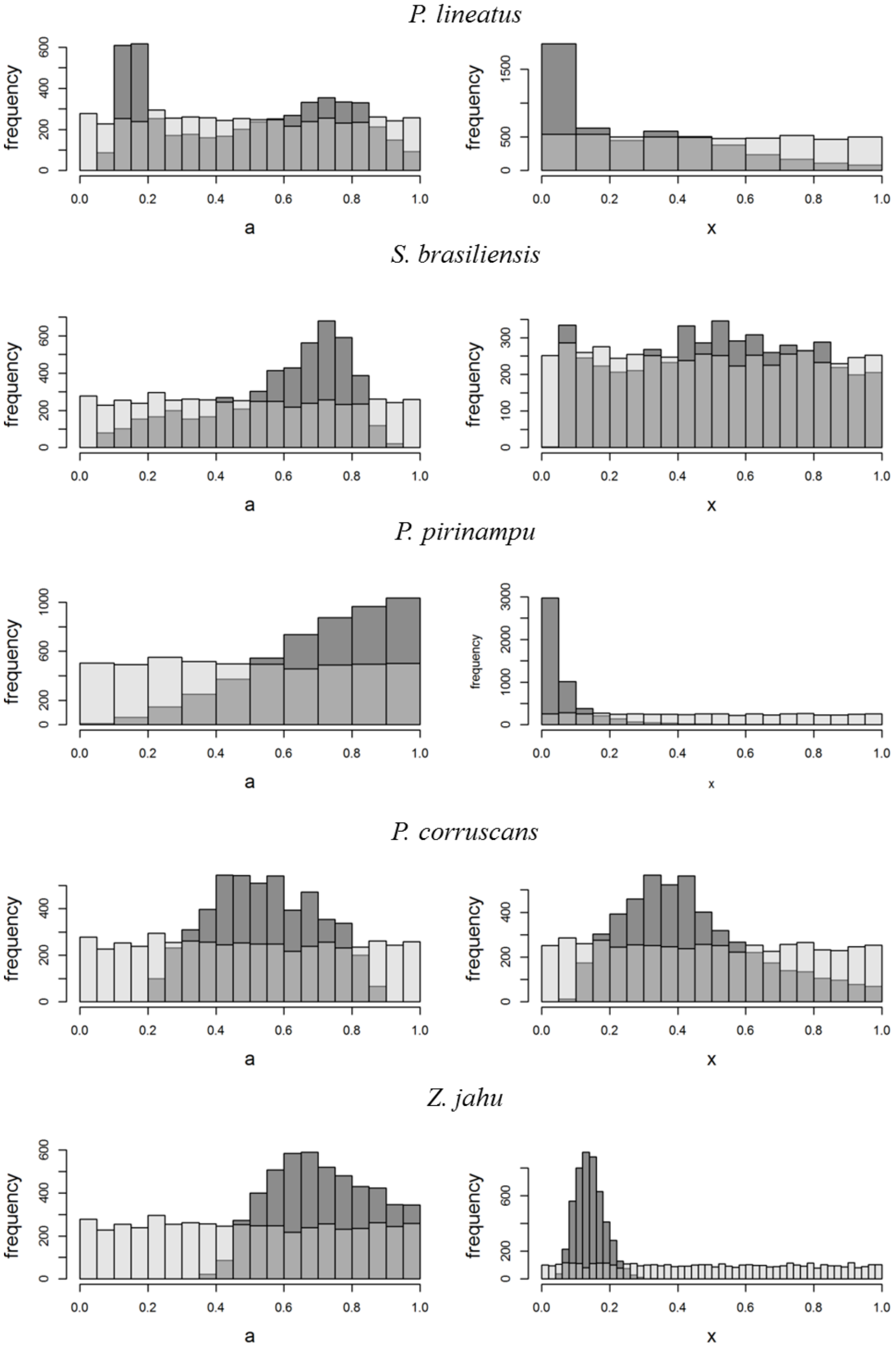


Figure S3. Prior (light grey) and posterior (dark grey) distributions for the parameters: bioeconomic equilibrium (a), and intrinsic rate of increase in effort (x).

Section 3 – Catch and estimated MSY

This section shows the results obtained regarding catch and MSY from both methods for the entire times series of catches available. Catches and the respective MSY for each species are shown in Figure S4.

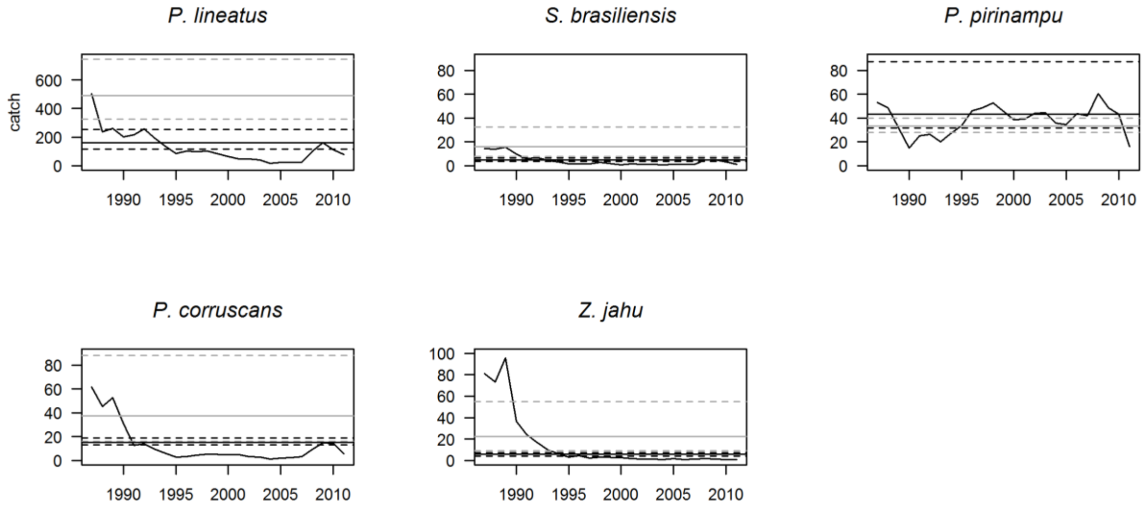


Figure S4. Observed catches and estimated MSY from CMSY (grey solid line) and COM-SIR (black solid line). Dashed lines represent the 95 credibility intervals.

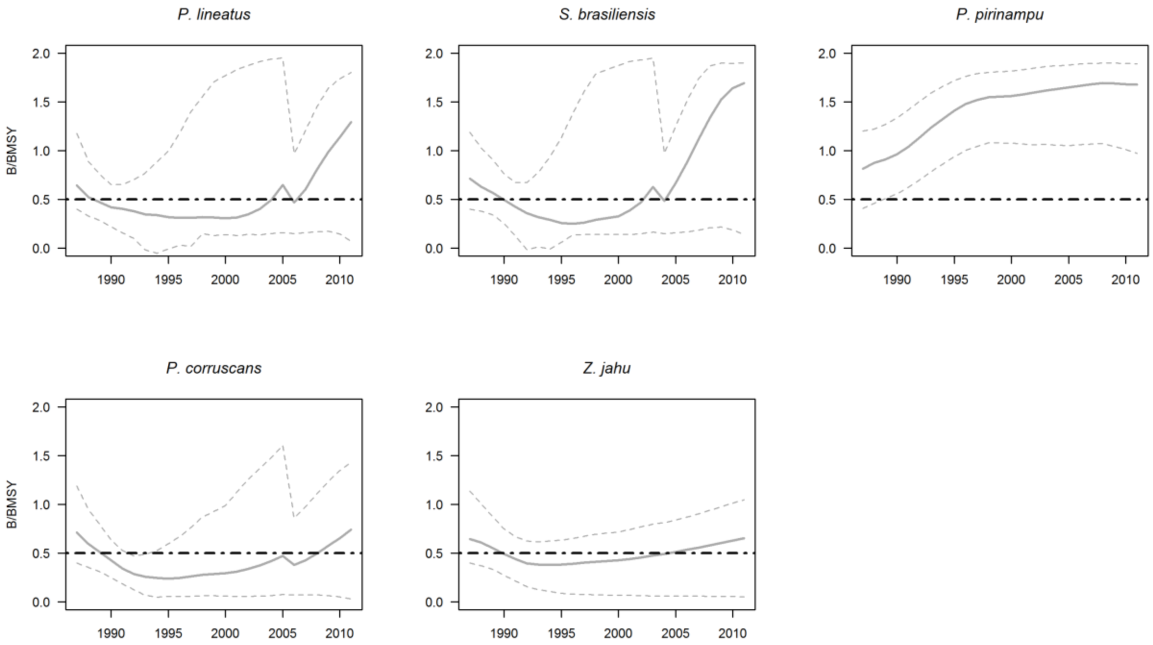


Figure S5. Estimated biomass obtained from the CMSY method without the prior relative biomass for the final year. The dotdashed line represents half B_t/B_{MSY}.

ANEXO A – Código do método CMSY (retirado de Froese *et al.*, 2016)

```
##-------------------------------------------------------------------------------------------
## CMSY and BSM analysis
## Written by Rainer Froese, Gianpaolo Coro and Henning Winker
## Version of November 2016
## Note that time series excluding 2004 - 2010 will give an error in dataframe; set write.output <-
F to avoid that error
##-------------------------------------------------------------------------------------------
library(R2jags)  # Interface with JAGS
library(coda)
library("parallel")
library("foreach")
library("doParallel")
library("gplots")

#-----------------------------------------
# Some general settings
#-----------------------------------------
# set.seed(999) # use for comparing results between runs
rm(list=ls(all=TRUE)) # clear previous variables etc
options(digits=3) # displays all numbers with three significant digits as default
graphics.off() # close graphics windows from previous sessions
FullSchaefer <- F    # initialize variable; automatically set to TRUE if enough abundance data are
available
n.chains     <- ifelse(detectCores() > 2,3,2) # set 3 chains in JAGS if more than 2 cores are
available
ncores_for_computation=detectCores() # cores to be used for parallel processing of CMSY
cl           <- makeCluster(ncores_for_computation)
registerDoParallel(cl, cores = ncores_for_computation)

#-----------------------------------------
# Required settings, File names
#-----------------------------------------
catch_file  <-  "Stocks_Catch_Itaipu.csv" #  name of file containing "stock", "yr", "ct", and
optional "bt"
id_file     <-  "Stocks_ID_Itaipu.csv"  #  name of file containing stock-specific info and settings
for the analysis

outfile     <- paste("Out_",format(Sys.Date(),format="%B%d%Y_"),id_file,sep="") # default
name for output file
outfile.txt <- paste(outfile,".txt", sep="")

#----------------------------------------
# Select stock to be analyzed
#----------------------------------------
```

```
stocks      <-NA
# If the input files contain more than one stock, specify below the stock to be analyzed
# If the line below is commented out (#), all stocks in the input file will be analyzed
 #stocks <-  "ILLECOI_AL" #
c("SEPIOFF_CY","MICRPOU_IS","EPINGUA_IS","CHAMGAL_SA","CORYHIP_SA","ILLE
COI_SA")
stocks <- "pintado"
#----------------------------------------
# General settings for the analysis
#----------------------------------------
dataUncert   <- 0.1  # set observation error as uncertainty in catch - default is SD=0.1
sigmaR       <- 0.1 # overall process error for CMSY; SD=0.1 is the default
n            <- 10000 # initial number of r-k pairs
n.new        <- n # initialize n.new
ni           <- 3 # iterations for r-k-startbiomass combinations, to test different variability patterns;
no improvement seen above 3
nab          <- 2 # default=5; minimum number of years with abundance data to run BSM
mgraphs      <- T # set to TRUE to produce additional graphs for management
save.plots   <- T # set to TRUE to save graphs to JPEG files
close.plots  <- F # set to TRUE to close on-screen plots after they are saved, to avoid "too many
open devices" error in batch-processing
write.output <- T # set to TRUE if table with results in output file is wanted; expects years 2004-
2010 to be available
force.cmsy   <- F # set to TRUE if CMSY results are to be preferred over BSM results
select.yr    <- NA # option to display F, B, F/Fmsy and B/Bmsy for a certain year; default NA

#---------------------------------------------
#  FUNCTIONS
#---------------------------------------------
# Monte Carlo filtering with Schaefer Function
#---------------------------------------------
SchaeferParallelSearch<-function(ni, nyr,sigR,duncert,ct,int.yr,intbio, startbt, ki,i, ri,int.yr.i,
nstartbt, yr, end.yr, endbio, npoints, pt){
  ptm<-proc.time()
  # create vectors for viable r, k and bt
  inmemorytable <- vector()
  # parallelised for the points in the r-k space
  inmemorytable <- foreach (i = 1 :
npoints, .combine='rbind', .packages='foreach', .inorder=TRUE) %dopar%{
  nsbt = length(startbt)
  VP   <- FALSE
   for(nj in 1:nsbt) {
    # create empty vector for annual biomasses
    bt <- vector()
    j<-startbt[nj]
    # set initial biomass, including 0.1 process error to stay within bounds
```

```
  bt[1]=j*ki[i]*exp(rnorm(1,0, 0.1*sigR))  ## set biomass in first year
  # repeat test of r-k-startbt combination to allow for different random error
  for(re in 1:ni)   {
   #loop through years in catch time series
   for (t in 1:nyr)  {  # for all years in the time series
    xt=rnorm(1,0, sigR) # set new process error for every year
    zlog.sd = sqrt(log(1+(duncert)^2))
    zt=rlnorm(1,meanlog = 0, sdlog = zlog.sd) # model the catch error as a log normal distribution.
    # calculate biomass as function of previous year's biomass plus surplus production minus catch
    bt[t+1] <- ifelse(bt[t]/ki[i] >= 0.25,
             bt[t]+ri[i]*bt[t]*(1-bt[t]/ki[i])*exp(xt)-ct[t]*zt,
              bt[t]+(4*bt[t]/ki[i])*ri[i]*bt[t]*(1-bt[t]/ki[i])*exp(xt)-ct[t]*zt) # assuming reduced r at B/k < 0.25

    # if biomass < 0.01 k, discard r-k-startbt combination
    if(bt[t+1] < 0.01*ki[i]) {
     break
    } # stop looping through years, go to next upper level
    # intermediate year check
    if ((t+1)==int.yr.i && (bt[t+1]>(intbio[2]*ki[i]) || bt[t+1]<(intbio[1]*ki[i]))) {
     break
    }
   } # end of loop of years
    # if loop was broken or last biomass falls outside of expected ranges
    # do not store results, go directly to next startbt
    if(t < nyr || bt[yr==end.yr] > (endbio[2]*ki[i]) || bt[yr==end.yr] < (endbio[1]*ki[i]) ) {
      next
     } else {
      #each vector will be finally appended to the others found by the threads - this is done by the .combine='rbind' option
      inmemorytablerow<-c(i,j,ri[i],ki[i],bt[1:(nyr+1)]/ki[i])
      if (length(inmemorytablerow)==(4+nyr+1)){
       if (VP==FALSE)
        {
        inmemorytable<-inmemorytablerow
        }
       else
        {
          inmemorytable<-rbind(inmemorytable,inmemorytablerow)
        }
       VP<-TRUE
       }
     }
   } # end of repetition for random error
```

```
    } # end of j-loop of initial biomasses
  # instruction necessary to make the foreach loop see the variable:
  if (length(inmemorytable)==0)
     {inmemorytable<-vector(length=4+nyr+1)*NA}
    else
     {inmemorytable}
  }#end loop on points

  #create the output matrix
  mdat        <- matrix(data=NA, nrow = npoints*nstartbt, ncol = 2+nyr+1)
  npointsmem = dim(inmemorytable)[1]
  npointscols = dim(inmemorytable)[2]
  #reconstruction of the processing matrix after the parallel search
  if (npointsmem>0 && npointscols>0){
   for (idxr in 1:npointsmem){
        i = inmemorytable[idxr,1]
        if (!is.na(i)){
          j = inmemorytable[idxr,2]
          mdatindex<-((i-1)*nstartbt)+which(startbt==j)
          mdat[mdatindex,1]           <- inmemorytable[idxr,3]
          mdat[mdatindex,2]           <- inmemorytable[idxr,4]
          mdat[mdatindex,3:(2+nyr+1)] <- inmemorytable[idxr,5:(4+nyr+1)]
          if(pt==T) points(x=ri[i], y=ki[i], pch=".", cex=4, col="gray")
        }
    }
  }
  ptm<-proc.time()-ptm
  mdat <- na.omit(mdat)
  return(mdat)
}

SchaeferMC <- function(ri, ki, startbio, int.yr, intbio, endbio, sigR, pt, duncert, startbins, ni) {

  # create vector for initial biomasses
  startbt     <- seq(from =startbio[1], to=startbio[2], by = (startbio[2]-startbio[1])/startbins)
  nstartbt    <- length(startbt)
  npoints     <- length(ri)
  # get index of intermediate year
  int.yr.i     <- which(yr==int.yr)

  #loop through r-k pairs with parallel search
  mdat<-SchaeferParallelSearch(ni, nyr,sigR,duncert,ct,int.yr,intbio, startbt, ki, i, ri, int.yr.i,
nstartbt, yr, end.yr, endbio, npoints,pt)

  cat("\n")
  return(list(mdat))
```

```
} # end of SchaeferMC function

#----------------------------------------------
# Function for moving average
#----------------------------------------------
ma    <- function(x){
  x.1    <-   filter(x,rep(1/3,3),sides=1)
  x.1[1] <- x[1]
  x.1[2] <- (x[1]+x[2])/2
  return(x.1)
}
#--------------------------------------------
# END OF FUNCTIONS
#--------------------------------------------

#----------------------------------------
# Start output to screen
#----------------------------------------
cat("------------------------------------------\n")
cat("CMSY Analysis,", date(),"\n")
cat("------------------------------------------\n")

#----------------------------------------
# Read data and assign to vectors
#----------------------------------------
# create headers for data table file
if(write.output==T){
  outheaders = data.frame("Group","Region",
"Subregion","Name","SciName","Stock","start.yr","end.yr","btype",
                          "MaxCatch","LastCatch","MSY_BSM","lcl","ucl","r_BSM","lcl","ucl",

"k_BSM","lcl","ucl","q_BSM","lcl","ucl","rel_B_BSM","lcl","ucl","rel_F_BSM",
                          "r_CMSY","lcl","ucl","k_CMSY","lcl","ucl","MSY_CMSY","lcl","ucl",
                          "rel_B_CMSY","2.5th","97.5th","rel_F_CMSY",
                          "F_msy","lcl","ucl","curF_msy","lcl","ucl",
                          "MSY","lcl","ucl","Bmsy","lcl","ucl",
                          "B","lcl","ucl","B_Bmsy","lcl","ucl",
                          "F","lcl","ucl","F_Fmsy","lcl","ucl",
                          "sel_B","sel_B_Bmsy","sel_F","sel_F_Fmsy",

"c00","c01","c02","c03","c04","c05","c06","c07","c08","c09","c10","c11","c12","c13","c14","c1
5",

"F.Fmsy00","F.Fmsy01","F.Fmsy02","F.Fmsy03","F.Fmsy04","F.Fmsy05","F.Fmsy06","F.Fmsy0
7","F.Fmsy08","F.Fmsy09","F.Fmsy10","F.Fmsy11","F.Fmsy12","F.Fmsy13","F.Fmsy14","F.Fms
y15",
```

```
"B00","B01","B02","B03","B04","B05","B06","B07","B08","B09","B10","B11","B12","B13","
B14","B15")

   write.table(outheaders,file=outfile, append = T, sep=",",row.names=F,col.names=F)
}

cat("Parallel processing will use",ncores_for_computation,"cores\n")
# Read data
cdat         <- read.csv(catch_file, header=T, dec=".", stringsAsFactors = FALSE)
cinfo        <- read.csv(id_file, header=T, dec=".", stringsAsFactors = FALSE)
cat("Files", catch_file, ",", id_file, "read successfully","\n")

#---------------------------------
# Analyze stock(s)
#---------------------------------
if(is.na(stocks[1])==TRUE){
   stocks         <- as.character(cinfo$Stock) # Analyze stocks in sequence of ID file
  # stocks         <- sort(as.character(cinfo$Stock)) # Analyze stocks in alphabetic order
  # stocks         <- as.character(cinfo$Stock[cinfo$Subregion=="Sardinia"]) # Analyze stocks in
Region
}

# analyze one stock after the other
for(stock in stocks) {
  cat("Processing",stock,",", as.character(cinfo$ScientificName[cinfo$Stock==stock]),"\n")
  # assign data from cinfo to vectors
  res          <- as.character(cinfo$Resilience[cinfo$Stock==stock])
  start.yr     <- as.numeric(cinfo$StartYear[cinfo$Stock==stock])
  end.yr       <- as.numeric(cinfo$EndYear[cinfo$Stock==stock])
  r.low        <- as.numeric(cinfo$r.low[cinfo$Stock==stock])
  r.hi         <- as.numeric(cinfo$r.hi[cinfo$Stock==stock])
  user.log.r   <- ifelse(is.na(r.low)==F & is.na(r.hi)==F,TRUE,FALSE)
  stb.low      <- as.numeric(cinfo$stb.low[cinfo$Stock==stock])
  stb.hi       <- as.numeric(cinfo$stb.hi[cinfo$Stock==stock])
  int.yr       <- as.numeric(cinfo$int.yr[cinfo$Stock==stock])
  intb.low     <- as.numeric(cinfo$intb.low[cinfo$Stock==stock])
  intb.hi      <- as.numeric(cinfo$intb.hi[cinfo$Stock==stock])
  endb.low     <- as.numeric(cinfo$endb.low[cinfo$Stock==stock])
  endb.hi      <- as.numeric(cinfo$endb.hi[cinfo$Stock==stock])
  btype        <- as.character(cinfo$btype[cinfo$Stock==stock])
  force.cmsy   <- ifelse(force.cmsy==T,T,cinfo$force.cmsy[cinfo$Stock==stock])
  comment      <- as.character(cinfo$Comment[cinfo$Stock==stock])
  # set global defaults for uncertainty
  duncert      <- dataUncert
  sigR         <- sigmaR
```

```
  # check for common errors
  if (length(btype)==0){
    cat("ERROR: Could not find the stock in the ID input file - check that the stock names match in ID and Catch files and that commas are used (not semi-colon)")
    return (NA) }
  if(start.yr < cdat$yr[cdat$Stock==stock][1]){
    cat("ERROR: start year in ID file before first year in catch file\n")
    return (NA)}

  # extract data on stock
  yr          <- as.numeric(cdat$yr[cdat$Stock==stock & cdat$yr >= start.yr & cdat$yr <= end.yr])

  if (length(yr)==0){
    cat("ERROR: Could not find the stock in the Catch input files - Please check that the code is written correctly")
    return (NA)
  }

  ct.raw          <- as.numeric(cdat$ct[cdat$Stock==stock & cdat$yr >= start.yr & cdat$yr <= end.yr])/1000  ## assumes that catch is given in tonnes, transforms to '000 tonnes
  if(btype=="biomass" | btype=="CPUE" ) {
    bt <- as.numeric(cdat$bt[cdat$Stock==stock & cdat$yr >= start.yr & cdat$yr <= end.yr])/1000  ## assumes that biomass is in tonnes, transforms to '000 tonnes
  } else {bt <- NA}

  if(is.na(mean(ct.raw))){
  cat("ERROR: Missing value in Catch data; fill or interpolate\n")
  }
  nyr         <- length(yr) # number of years in the time series

  # change catch to 3 years moving average where value is average of past 3 years
  ct             <- ma(ct.raw)

  # initialize vectors for viable r, k, bt, and all in a matrix
  mdat.all    <- matrix(data=vector(),ncol=2+nyr+1)

  # initialize other vectors anew for each stock
  current.attempts <- NA

  # use start.yr if larger than select year
  if(is.na(select.yr)==F) {
    sel.yr <- ifelse(start.yr > select.yr,start.yr,select.yr)
  } else sel.yr <- NA

  #--------------------------------------------------
```

```
  # Determine initial ranges for parameters and biomass
  #----------------------------------------------------
  # initial range of r from input file
  if(is.na(r.low)==F & is.na(r.hi)==F) {
    start.r <- c(r.low,r.hi)
  } else {
    # initial range of r based on resilience
    if(res == "High") {
      start.r <- c(0.6,1.5)} else if(res == "Medium") {
        start.r <- c(0.2, 1)}    else if(res == "Low") {  #Juliana: changed range of medium res, this
way is equal to COM-SIR
          start.r <- c(0.05,0.5)}  else { # i.e. res== "Very low"
            start.r <- c(0.015,0.1)}
  }

  # get index of years with lowest and highest catch between start+3 and end-3 years
  min.yr.i     <- which.min(ct[4:(length(ct)-3)])+3
  max.yr.i     <- which.max(ct[4:(length(ct)-3)])+3
  min.ct       <- ct[min.yr.i]
  max.ct       <- ct[max.yr.i]

  # use initial biomass range from input file if stated
  if(is.na(stb.low)==F & is.na(stb.hi)==F) {
    startbio <- c(stb.low,stb.hi)
  } else {
    # if start year < 1960 assume high biomass
    if(start.yr < 1960) {startbio <- c(0.5,0.9)} else {
      # else use medium prior biomass range
      startbio <- c(0.2,0.6)} }

  # use year and biomass range for intermediate biomass from input file
  if(is.na(intb.low)==F & is.na(intb.hi)==F) {
    int.yr   <- int.yr
    intbio   <- c(intb.low,intb.hi)

    # if contrast in catch is low, use initial range again in mid-year
  } else if(min(ct)/max(ct) > 0.6) {
    int.yr    <- as.integer(mean(c(start.yr, end.yr)))
    intbio    <- startbio

    # else if year of minimum catch is after max catch then use min catch
  } else if(min.yr.i > max.yr.i) {
    int.yr    <- yr[min.yr.i-1]
    if(startbio[1]>=0.5 &  (int.yr-start.yr) < (end.yr-int.yr) &
         (min.ct/max.ct) > 0.3) intbio <- c(0.2,0.6) else intbio <- c(0.01,0.4)
```

```
    # else use max catch
  } else {
    # assume that biomass range in year before maximum catch was high or medium
    int.yr    <- yr[max.yr.i-1]
    intbio    <- if((startbio[1]>=0.5 & (int.yr-start.yr) < (end.yr-int.yr))| # if initial biomass is high, assume same for intermediate
                      # ((min.ct/max.ct < 0.3 & (max.yr.i - min.yr.i) < 25))) c(0.5,0.9) else c(0.2,0.6) }
                      (((max.ct-min.ct)/max.ct)/(max.yr.i-min.yr.i) > 0.04)) c(0.5,0.9) else c(0.2,0.6) } # if incease is steep, assume high, else medium
  # end of intbio setting

  # final biomass range from input file
  if(is.na(endb.low)==F & is.na(endb.hi)==F) {
    endbio   <- c(endb.low,endb.hi)
  } else {
    # else use mean final catch/max catch to estimate final biomass
    rawct.ratio=ct.raw[nyr]/max(ct)
    endbio  <- if(ct[nyr]/max(ct) > 0.8) {c(0.4,0.8)} else if(rawct.ratio < 0.5) {c(0.01,0.4)} else {c(0.2,0.6)}

    # if default endbio is low (0.01-0.4), check whether the upper bound should be lower than 0.4 for depleted stocks
    if(endbio[2]==0.4){
      if(rawct.ratio< 0.05) {endbio[2] <- 0.1} else
        if(rawct.ratio< 0.15) {endbio[2] <- 0.2} else
          if(rawct.ratio< 0.35) {endbio[2] <- 0.3} else {endbio[2] <- 0.4}
    }
  } # end of final biomass setting

  # initial prior range of k values, assuming min k will be larger than max catch / prior for r
  if(mean(endbio) <= 0.5) {
    start.k <- c(max(ct)/start.r[2],4*max(ct)/start.r[1])} else {
      start.k <- c(2*max(ct)/start.r[2],12*max(ct)/start.r[1])}
  # start.k <- c(start.k[1],3000)
  cat("startbio=",startbio,ifelse(is.na(stb.low)==T,"default","expert"),
      ", intbio=",int.yr,intbio,ifelse(is.na(intb.low)==T,"default","expert"),
      ", endbio=",endbio,ifelse(is.na(endb.low)==T,"default","expert"),"\n")

  #----------------------------------------------------------------
  # Uniform sampling of the r-k space
  #----------------------------------------------------------------
  # get random set of r and k from log space distribution
  ri1 = exp(runif(n, log(start.r[1]), log(start.r[2])))
  ki1 = exp(runif(n, log(start.k[1]), log(start.k[2])))

  #---------------------------------------------------------------
```

```
  # Plot data and progress
  #-----------------------------------------------------------
  # check for operating system, open separate window for graphs if Windows
  if(grepl("win",tolower(Sys.info()['sysname']))) {windows(14,9)}
  par(mfrow=c(2,3))
  # plot catch
  plot(x=yr, y=ct.raw,
       ylim=c(0,max(ifelse(substr(id_file,1,3)=="Sim",
                         1.1*true.MSY,0),1.2*max(ct.raw))),
       type ="l", bty="l", main=paste("A: ",stock,"catch"), xlab="Year", ylab="Catch", lwd=2)
  lines(x=yr,y=ct,col="blue", lwd=1)
  points(x=yr[max.yr.i], y=max.ct, col="red", lwd=2)
  points(x=yr[min.yr.i], y=min.ct, col="red", lwd=2)

  # plot r-k graph
  plot(x=ri1, y=ki1, xlim = start.r, ylim = start.k, log="xy", xlab="r", ylab="k",
       main="B: Finding viable r-k", pch=".", cex=3, bty="l", col="gray95")

  #--------------------------------------------------------------
  # 1 - Call CMSY-SchaeferMC function to preliminary explore the r-k space
  #--------------------------------------------------------------
  cat("First Monte Carlo filtering of r-k space with ",n," points...\n")
  MCA <-  SchaeferMC(ri=ri1, ki=ki1, startbio=startbio, int.yr=int.yr, intbio=intbio,
endbio=endbio, sigR=sigR,
                    pt=T, duncert=dataUncert, startbins=10, ni=ni)
  mdat.all <- rbind(mdat.all,MCA[[1]])
  rv.all   <- mdat.all[,1]
  kv.all   <- mdat.all[,2]
  btv.all  <- mdat.all[,3:(2+nyr+1)]
  # count viable trajectories and r-k pairs
  n.viable.b   <- length(mdat.all[,1])
  n.viable.pt <- length(unique(mdat.all[,1]))
  cat("Found ",n.viable.b," viable trajectories for", n.viable.pt," r-k pairs\n")

  #----------------------------------------------------------------
  # 2 - if the lower bound of k is too high, reduce it by half and rerun
  #----------------------------------------------------------------
  if(length(kv.all[kv.all < 1.1*start.k[1] & rv.all < mean(start.r)]) > 10) {
    cat("Reducing lower bound of k, resampling area with",n,"additional points...\n")
    start.k <- c(0.5*start.k[1],start.k[2])
    ri1 = exp(runif(n, log(start.r[1]), log(start.r[2])))
    ki1 = exp(runif(n, log(start.k[1]), log(start.k[2])))
    MCA <-  SchaeferMC(ri=ri1, ki=ki1, startbio=startbio, int.yr=int.yr, intbio=intbio,
endbio=endbio, sigR=sigR,
                      pt=T, duncert=dataUncert, startbins=10, ni=ni)
    mdat.all <- rbind(mdat.all,MCA[[1]])
```

```
    rv.all   <- mdat.all[,1]
    kv.all   <- mdat.all[,2]
    btv.all  <- mdat.all[,3:(2+nyr+1)]
    n.viable.b   <- length(mdat.all[,1])
    n.viable.pt <- length(unique(mdat.all[,1]))
    cat("Found altogether",n.viable.b," viable trajectories for", n.viable.pt," r-k pairs\n")
  }

  #--------------------------------------------------------------
  # 3 - if few points were found then resample and shrink the log k space
  #--------------------------------------------------------------
  if (n.viable.b <= 1000){
    log.start.k.new  <- log(start.k)
    max.attempts     <- 3
    current.attempts <- 1
    startbins        <- 10
    while (n.viable.b <= 1000 && current.attempts <= max.attempts){
      if(n.viable.pt > 0) {
        log.start.k.new[1] <- mean(c(log(start.k[1]), min(log(kv.all))))
        log.start.k.new[2] <- mean(c(log.start.k.new[2], max(log(kv.all)))) }
      n.new <- n*current.attempts #add more points
      ri1 = exp(runif(n.new, log(start.r[1]), log(start.r[2])))
      ki1 = exp(runif(n.new, log.start.k.new[1], log.start.k.new[2]))
      cat("Shrinking k space: repeating Monte Carlo in the interval
[",exp(log.start.k.new[1]),",",exp(log.start.k.new[2]),"]\n")
      cat("Attempt ",current.attempts," of ",max.attempts," with ",n.new," additional points...","\n")
      if(current.attempts==2 & n.viable.b < 50){
        duncert   <- 2*dataUncert
        sigR      <- 2*sigmaR
        startbins <- 20
        cat("Doubling startbins, catch and process error, and number of variability patterns \n")
      }
      MCA <-  SchaeferMC(ri=ri1, ki=ki1, startbio=startbio, int.yr=int.yr, intbio=intbio,
endbio=endbio, sigR=sigR,
                         pt=T, duncert=duncert, startbins=startbins, ni=2*ni)
      mdat.all <- rbind(mdat.all,MCA[[1]])
      rv.all   <- mdat.all[,1]
      kv.all   <- mdat.all[,2]
      btv.all  <- mdat.all[,3:(2+nyr+1)]
      n.viable.b   <- length(mdat.all[,1])
      n.viable.pt <- length(unique(mdat.all[,1]))
      cat("Found altogether",n.viable.b," viable trajectories for", n.viable.pt," r-k pairs\n")
      current.attempts=current.attempts+1 #increment the number of attempts
    }
    if(n.viable.b < 5) {
      cat("Only",n.viable.pt,"viable r-k pairs found, check data and settings \n")
```

```
      next
    }
  }

  #----------------------------------------------------------------
  # 4 - if tip of viable r-k pairs is 'thin', do extra sampling there
  #----------------------------------------------------------------
  if(length(rv.all[rv.all > 0.9*start.r[2]]) < 5) {
    l.sample.r       <- quantile(rv.all,0.6)
    add.points       <-
ifelse(is.na(current.attempts)==T,n,ifelse(current.attempts==2,2*n,ifelse(length(rv.all)>500,3*n,6
*n)))
    cat("Final sampling in the tip area above r =",l.sample.r,"with",add.points,"additional
points...\n")
    log.start.k.new <- c(log(0.8*min(kv.all)),log(max(kv.all[rv.all > l.sample.r])))

    ri1 = exp(runif(add.points, log(l.sample.r), log(start.r[2])))
    ki1 = exp(runif(add.points, log.start.k.new[1], log.start.k.new[2]))
    MCA <-  SchaeferMC(ri=ri1, ki=ki1, startbio=startbio, int.yr=int.yr, intbio=intbio,
endbio=endbio, sigR=sigR,
                       pt=T, duncert=duncert, startbins=10, ni=ni)
    mdat.all <- rbind(mdat.all,MCA[[1]])
    rv.all   <- mdat.all[,1]
    kv.all   <- mdat.all[,2]
    btv.all  <- mdat.all[,3:(2+nyr+1)]
    n.viable.b   <- length(mdat.all[,1])
    n.viable.pt <- length(unique(mdat.all[,1]))
    cat("Found altogether",n.viable.b," viable trajectories for", n.viable.pt," r-k pairs\n")
  }

  # ----------------------------------------------------------------
  # Bayesian analysis of catch & biomass (or CPUE) with Schaefer model
  # ----------------------------------------------------------------
  FullSchaefer <- F
  if(btype != "None" & length(bt[is.na(bt)==F])>=nab) {
    FullSchaefer <- T

    # set inits for r-k in lower right corner of log r-k space
    init.r      <- start.r[1]+0.8*(start.r[2]-start.r[1])
    init.k      <- start.k[1]+0.1*(start.k[2]-start.k[1])

    # vector with no penalty (=0) if predicted biomass is within viable range, else a penalty of 10 is
set
    pen.bk = pen.F = rep(0,length(ct))

    #><>><>
```

```
  # Add biomass priors
  b.yrs = c(1,length(start.yr:int.yr),length(start.yr:end.yr))
  b.prior =
rbind(matrix(c(startbio[1],startbio[2],intbio[1],intbio[2],endbio[1],endbio[2]),2,3),rep(0,3)) # last
row includes the 0 pen
  #><>><>

  cat("Running MCMC analysis....\n")
  if(btype == "biomass" ) {
    # Data to be passed on to JAGS
    jags.data        <- c('ct','bt','nyr', 'start.r','startbio','start.k',
                         'init.r','init.k', 'pen.bk','pen.F','b.yrs','b.prior')
    # Parameters to be returned by JAGS
    jags.save.params <- c('r','k','P') #

    # JAGS model
    Model = "model{
        # to avoid crash due to 0 values
        eps<- 0.01
        penm[1] <- 0 # no penalty for first biomass
        Pmean[1] <- log(alpha)
        P[1] ~ dlnorm(Pmean[1],itau2)

        for (t in 2:nyr) {
    Pmean[t] <- ifelse(P[t-1] > 0.25,
    log(max(P[t-1] + r*P[t-1]*(1-P[t-1]) - ct[t-1]/k,eps)),  # Process equation
    log(max(P[t-1] + 4*P[t-1]*r*P[t-1]*(1-P[t-1]) - ct[t-1]/k,eps))) # assuming reduced r at B/k <
0.25
    P[t] ~ dlnorm(Pmean[t],itau2) # Introduce process error
    penm[t]  <- ifelse(P[t]<(eps+0.001),log(k*P[t])-log(k*(eps+0.001)),ifelse(P[t]>1,log(k*P[t])-
log(k*(0.99)),0)) # penalty if Pmean is outside viable biomass

  }

    # ><> Biomass priors/penalties are enforced as follows
    for (i in 1:3) {
    penb[i]  <- ifelse(P[b.yrs[i]]<b.prior[1,i],log(k*P[b.yrs[i]])-
log(k*b.prior[1,i]),ifelse(P[b.yrs[i]]>b.prior[2,i],log(k*P[b.yrs[i]])-log(k*b.prior[2,i]),0))
    b.prior[3,i] ~ dnorm(penb[i],100)
    }

    for (t in 1:nyr){
    Fpen[t]   <- ifelse(ct[t]>(0.9*k*P[t]),ct[t]-(0.9*k*P[t]),0) #><> Penalty term on F > 1, i.e.
ct>B
    pen.F[t]  ~ dnorm(Fpen[t],1000)
    pen.bk[t] ~ dnorm(penm[t],10000)
```

```
      Bm[t] <- log(P[t]*k);
      bt[t]    ~ dlnorm(Bm[t],isigma2);
      }

            # priors
            # search in the alpha space from the center of the range. Allow high variability
            log.alpha               <- log((startbio[1]+startbio[2])/2)
            sd.log.alpha            <- (log.alpha-log(startbio[1]))/5
            tau.log.alpha           <- pow(sd.log.alpha,-2)
            alpha                   ~  dlnorm(log.alpha,tau.log.alpha)

            # search in the k space from 20% of the range
            log.km              <- log(start.k[1]+0.2*(start.k[2]-start.k[1]))
            sd.log.k            <- (log.km-log(start.k[1]))/4
            tau.log.k           <- pow(sd.log.k,-2)
            k                   ~  dlnorm(log.km,tau.log.k)

            # define process (tau) and observation (sigma) variances as inversegamma priors
            itau2 ~ dgamma(2,0.01)
            tau2  <- 1/itau2
            tau   <- pow(tau2,0.5)

            isigma2 ~ dgamma(2,0.01)
            sigma2 <- 1/isigma2
            sigma <- pow(sigma2,0.5)

  log.rm              <- mean(log(start.r))
  sigma.log.r           <- abs(log.rm - log(start.r[1]))/2
  tau.log.r           <- pow(sigma.log.r,-2)
  r                   ~  dlnorm(log.rm,tau.log.r)
  } " # end of JAGS model for btype=="biomass"

  # ------------------------------------------------------------------
  # Schaefer model for Catch & CPUE
  # ------------------------------------------------------------------
  } else {
    # get prior for q from stable catch/biomass period, min 5 years; get range of years from input
file
    q.start    <- cinfo$q.start[cinfo$Stock==stock]
    q.end      <- cinfo$q.end[cinfo$Stock==stock]
    if(is.na(q.start)==F & is.na(q.end)==F) {
      mean.last.ct      <-mean(ct[yr >= q.start & yr <= q.end], na.rm=T) # get mean catch of
indicated years
      mean.last.cpue    <-mean(bt[yr >= q.start & yr <= q.end], na.rm=T) # get mean of CPUE of
indicated years
    } else {
```

```
   # get prior range for q from mean catch and mean CPUE in recent years
   lyr           <- ifelse(mean(start.r)>=0.5,5,10)  # determine number of last years to use, 5 for
normal and 10 for slow growing fish
   mean.last.ct      <-mean(ct[(nyr-lyr):nyr],na.rm=T) # get mean catch of last years
   mean.last.cpue    <-mean(bt[(nyr-lyr):nyr],na.rm=T) # get mean of CPUE of last years

  }
  gm.start.r      <- exp(mean(log(start.r))) # get geometric mean of prior r range
  if(mean(endbio) >= 0.5) {  # if biomass is high
   q.1          <- mean.last.cpue*0.25*gm.start.r/mean.last.ct
   q.2          <- mean.last.cpue*0.5*start.r[2]/mean.last.ct
  } else {
   q.1          <- mean.last.cpue*0.5*gm.start.r/mean.last.ct
   q.2          <- mean.last.cpue*start.r[2]/mean.last.ct
  }
  q.prior        <- c(q.1,q.2)
  init.q         <- mean(q.prior)

  # Data to be passed on to JAGS
  jags.data        <- c('ct','bt','nyr', 'start.r', 'start.k', 'startbio', 'q.prior',
                    'init.q','init.r','init.k','pen.bk','pen.F','b.yrs','b.prior')
  # Parameters to be returned by JAGS
  jags.save.params <- c('r','k','q', 'P')

  # JAGS model
  Model = "model{
  # to reduce chance of non-convergence, Pmean[t] values are forced >= eps
  eps<-0.01
  penm[1] <- 0 # no penalty for first biomass
  Pmean[1] <- log(alpha)
  P[1] ~ dlnorm(Pmean[1],itau2)

  for (t in 2:nyr) {
   Pmean[t] <- ifelse(P[t-1] > 0.25,
   log(max(P[t-1] + r*P[t-1]*(1-P[t-1]) - ct[t-1]/k,eps)),  # Process equation
   log(max(P[t-1] + 4*P[t-1]*r*P[t-1]*(1-P[t-1]) - ct[t-1]/k,eps))) # assuming reduced r at B/k <
0.25
   P[t] ~ dlnorm(Pmean[t],itau2) # Introduce process error
   penm[t]  <- ifelse(P[t]<(eps+0.001),log(q*k*P[t])-
log(q*k*(eps+0.001)),ifelse(P[t]>1,log(q*k*P[t])-log(q*k*(0.99)),0)) # penalty if Pmean is
outside viable biomass
  }

  # ><> Biomass priors/penalties are enforced as follows
  for (i in 1:3) {
   penb[i]  <- ifelse(P[b.yrs[i]]<b.prior[1,i],log(q*k*P[b.yrs[i]])-
```

```
log(q*k*b.prior[1,i]),ifelse(P[b.yrs[i]]>b.prior[2,i],log(q*k*P[b.yrs[i]])-log(q*k*b.prior[2,i]),0))
     b.prior[3,i] ~ dnorm(penb[i],100)
    }

    for (t in 1:nyr){
      Fpen[t]   <- ifelse(ct[t]>(0.9*k*P[t]),ct[t]-(0.9*k*P[t]),0) #><> Penalty term on F > 1, i.e.
ct>B
      pen.F[t]  ~ dnorm(Fpen[t],1000)
      pen.bk[t] ~ dnorm(penm[t],10000)
      cpuem[t]  <- log(q*P[t]*k);
      bt[t]     ~ dlnorm(cpuem[t],isigma2);
    }

  # priors
  log.alpha               <- log((startbio[1]+startbio[2])/2) # needed for fit of first biomass
  sd.log.alpha             <- (log.alpha-log(startbio[1]))/4
  tau.log.alpha            <- pow(sd.log.alpha,-2)
  alpha                   ~  dlnorm(log.alpha,tau.log.alpha)

  # search in the k space starting from 20% of the range
  log.km              <- log(start.k[1]+0.2*(start.k[2]-start.k[1]))
  sd.log.k            <- (log.km-log(start.k[1]))/4
  tau.log.k           <- pow(sd.log.k,-2)
  k                  ~  dlnorm(log.km,tau.log.k)

  # set realistic prior for q
  log.qm              <- mean(log(q.prior))
  sd.log.q            <- (log.qm-log(q.prior[1]))/4
  tau.log.q           <- pow(sd.log.q,-2)
  q                  ~  dlnorm(log.qm,tau.log.q)

  # define process (tau) and observation (sigma) variances as inversegamma prios
  itau2 ~ dgamma(4,0.01)
  tau2  <- 1/itau2
  tau   <- pow(tau2,0.5)

  isigma2 ~ dgamma(2,0.01)
  sigma2 <- 1/isigma2
  sigma <- pow(sigma2,0.5)

  log.rm              <- mean(log(start.r))
  sigma.log.r          <- abs(log.rm - log(start.r[1]))/2
  tau.log.r           <- pow(sigma.log.r,-2)
  r                  ~  dlnorm(log.rm,tau.log.r)
 } "    # end of JAGS model for CPUE
```

```
} # end of else loop for Schaefer with CPUE

# Write JAGS model to file
cat(Model, file="r2jags.bug")

if(btype=="biomass") {
  j.inits     <- function(){list("r"=rnorm(1,mean=init.r,sd=0.2*init.r),
                                 "k"=rnorm(1,mean=init.k,sd=0.1*init.k),
                                 "itau2"=1000,
                                 "isigma2"=1000)}} else {
  j.inits <- function(){list("r"=rnorm(1,mean=init.r,sd=0.2*init.r),
                                  "k"=rnorm(1,mean=init.k,sd=0.1*init.k),
                                  "q"=rnorm(1,mean=init.q,sd=0.2*init.q),
                                  "itau2"=1000,
                                  "isigma2"=1000)}}
# run model
jags_outputs <- jags.parallel(data=jags.data,
                              working.directory=NULL, inits=j.inits,
                              parameters.to.save=jags.save.params,
                              model.file="r2jags.bug", n.chains = n.chains,
                              n.burnin = 30000, n.thin = 10,
                              n.iter = 60000)

# ------------------------------------------------------
# Results from JAGS Schaefer
# ------------------------------------------------------
r_raw            <- as.numeric(mcmc(jags_outputs$BUGSoutput$sims.list$r))
k_raw            <- as.numeric(mcmc(jags_outputs$BUGSoutput$sims.list$k))
# Importance sampling: only accept r-k pairs where r is near the prior range
r_out            <- r_raw[r_raw > 0.5*start.r[1] & r_raw < 1.5 * start.r[2]]
k_out            <- k_raw[r_raw > 0.5*start.r[1] & r_raw < 1.5 * start.r[2]]

mean.log.r.jags  <- mean(log(r_out))
sd.log.r.jags    <- sd(log(r_out))
r.jags           <- exp(mean.log.r.jags)
lcl.r.jags       <- exp(mean.log.r.jags - 1.96*sd.log.r.jags)
ucl.r.jags       <- exp(mean.log.r.jags + 1.96*sd.log.r.jags)
mean.log.k.jags  <- mean(log(k_out))
sd.log.k.jags    <- sd(log(k_out))
k.jags           <- exp(mean.log.k.jags)
lcl.k.jags       <- exp(mean.log.k.jags - 1.96*sd.log.k.jags)
ucl.k.jags       <- exp(mean.log.k.jags + 1.96*sd.log.k.jags)
MSY.posterior     <- r_out*k_out/4 # simpler
mean.log.MSY.jags <- mean(log(MSY.posterior))
sd.log.MSY.jags   <- sd(log(MSY.posterior))
MSY.jags          <- exp(mean.log.MSY.jags)
```

```
lcl.MSY.jags      <- exp(mean.log.MSY.jags - 1.96*sd.log.MSY.jags)
ucl.MSY.jags      <- exp(mean.log.MSY.jags + 1.96*sd.log.MSY.jags)

if(btype=="CPUE") {
  q_out           <- as.numeric(mcmc(jags_outputs$BUGSoutput$sims.list$q))
  mean.log.q      <- mean(log(q_out))
  sd.log.q        <- sd(log(q_out))
  mean.q          <- exp(mean.log.q)
  lcl.q           <- exp(mean.log.q-1.96*sd.log.q)
  ucl.q           <- exp(mean.log.q+1.96*sd.log.q)
  F.bt.cpue       <- mean.q*ct.raw/bt
  Fmsy.cpue       <- r.jags/2
}

# get F from observed biomass
if(btype == "biomass") {
  F.bt       <- ct.raw/bt
  Fmsy.bt    <- r.jags/2
 }

# get relative biomass P=B/k as predicted by BSM, including predictions for years with NA
abundance
all.P    <- jags_outputs$BUGSoutput$sims.list$P # matrix with P distribution by year
quant.P  <- apply(all.P,2,quantile,c(0.025,0.5,0.975),na.rm=T)

# get k, r posterior ><>
all.k  <- jags_outputs$BUGSoutput$sims.list$k # matrix with P distribution by year
all.r  <- jags_outputs$BUGSoutput$sims.list$r # matrix with P distribution by year

# get B/Bmys posterior
all.b_bmsy=NULL
for(t in 1:ncol(all.P)){
  all.b_bmsy  <- cbind(all.b_bmsy,all.P[,t]*2)}

# get F/Fmys posterior ><>
all.F_Fmsy=NULL
for(t in 1:ncol(all.P)){
  all.F_Fmsy<-
cbind(all.F_Fmsy,(ct.raw[t]/(all.P[,t]*all.k))/ifelse(all.P[,t]>0.25,all.r/2,all.r/2*4*all.P[,t]))}

} # end of MCMC Schaefer loop

#------------------------------------
# get results from CMSY
#------------------------------------
# get estimate of most probable r as 75th percentile of mid log.r-classes
```

```
# get unique combinations of r-k
unique.rk         <- unique(mdat.all[,1:2])
# get remaining viable log.r and log.k
log.rs           <- log(unique.rk[,1])
log.ks           <- log(unique.rk[,2])
# get vectors with numbers of r and mid values in classes
# determine number of classes as a function of r-width
r.width         <- (max(unique.rk[,1])-start.r[1])/(start.r[2]-start.r[1])
classes         <- ifelse(r.width>0.8,100,ifelse(r.width>0.5,50,ifelse(r.width>0.3,25,12)))
hist.log.r      <- hist(x=log.rs, breaks=classes, plot=F)
log.r.counts    <- hist.log.r$counts
log.r.mids      <- hist.log.r$mids
# get most probable log.r as 75th percentile of mids with counts > 0
log.r.est       <- as.numeric(quantile(log.r.mids[which(log.r.counts > 0)],0.75))
median.log.r    <- as.numeric(quantile(x=log.r.mids[which(log.r.counts > 0)], 0.50))
lcl.log.r       <- as.numeric(quantile(x=log.r.mids[which(log.r.counts > 0)], 0.5125))
ucl.log.r       <- as.numeric(quantile(x=log.r.mids[which(log.r.counts > 0)], 0.9875))
sd.log.r.est    <- (ucl.log.r - log.r.est) / 1.96
r.est           <- exp(log.r.est)
lcl.r.est       <- exp(log.r.est-1.96*sd.log.r.est)
ucl.r.est       <- exp(log.r.est+1.96*sd.log.r.est)

# get r-k pairs above median of mids
rem             <- which(unique.rk[,1] > exp(median.log.r))
rem.log.r       <- log(unique.rk[,1][rem])
rem.log.k       <- log(unique.rk[,2][rem])
# do linear regression of log k ~ log r with slope fixed to -1 (from Schaefer)
reg             <- lm(rem.log.k ~ 1 + offset(-1*rem.log.r))
int.reg         <- as.numeric(reg[1])
sd.reg      <- sd(resid(reg))
# get estimate of log(k) from y where x = log.r.est
log.k.est       <- int.reg + (-1) * log.r.est
# get estimates of ucl of log.k.est from y + SD where x = ucl.log.r
ucl.log.k      <- int.reg + (-1) * lcl.log.r + sd.reg
# get estimates of sd.log.k.est from upper confidence limit of log.k.est
sd.log.k.est   <- (ucl.log.k - log.k.est) / 1.96
lcl.log.k       <- log.k.est - 1.96*sd.log.k.est
ucl.log.k       <- log.k.est + 1.96*sd.log.k.est

k.est       <- exp(log.k.est)
lcl.k.est   <- exp(lcl.log.k)
ucl.k.est   <- exp(ucl.log.k)

# get MSY from remaining log r-k pairs
log.MSY.est     <- mean(rem.log.r + rem.log.k - log(4))
sd.log.MSY.est  <- sd(rem.log.r + rem.log.k - log(4))
```

```
lcl.log.MSY.est <- log.MSY.est - 1.96*sd.log.MSY.est
ucl.log.MSY.est <- log.MSY.est + 1.96*sd.log.MSY.est
MSY.est         <- exp(log.MSY.est)
lcl.MSY.est     <- exp(lcl.log.MSY.est)
ucl.MSY.est     <- exp(ucl.log.MSY.est)

# get predicted biomass vectors as median and quantiles
# only use biomass trajectories from r-k pairs within the confidence limits
rem.btv.all <- mdat.all[which(mdat.all[,1] > lcl.r.est & mdat.all[,1] < ucl.r.est
                        & mdat.all[,2] > lcl.k.est & mdat.all[,2] < ucl.k.est),3:(2+nyr+1)]
median.btv <- apply(rem.btv.all,2, median)
median.btv.lastyr  <- median.btv[length(median.btv)-1]
nextyr.bt  <- median.btv[length(median.btv)]
lcl.btv    <- apply(rem.btv.all,2, quantile, probs=0.025)
q.btv      <- apply(rem.btv.all,2, quantile, probs=0.25)
ucl.btv    <- apply(rem.btv.all,2, quantile, probs=0.975)
lcl.median.btv.lastyr <- lcl.btv[length(lcl.btv)-1]
ucl.median.btv.lastyr <- ucl.btv[length(lcl.btv)-1]
lcl.nextyr.bt <- lcl.btv[length(lcl.btv)]
ucl.nextyr.bt <- ucl.btv[length(lcl.btv)]

# get F derived from predicted CMSY biomass
F.CMSY      <- ct.raw/(median.btv[1:nyr]*k.est)
Fmsy.CMSY  <- r.est/2 # Fmsy from CMSY

# -------------------------------------------
# Get results for management
# -------------------------------------------
if(FullSchaefer==F | force.cmsy==T) { # if only CMSY is available or shall be used
  MSY   <-MSY.est; lcl.MSY<-lcl.MSY.est; ucl.MSY<-ucl.MSY.est
  Bmsy  <-k.est/2; lcl.Bmsy<-lcl.k.est/2; ucl.Bmsy<-ucl.k.est/2
  Fmsy  <-r.est/2; lcl.Fmsy<-lcl.r.est/2; ucl.Fmsy<-ucl.r.est/2
  B.Bmsy<-2*median.btv[1:nyr];lcl.B.Bmsy<-2*lcl.btv[1:nyr];ucl.B.Bmsy<-2*ucl.btv[1:nyr]
  if(is.na(sel.yr)==F){B.Bmsy.sel<-2*median.btv[yr==sel.yr]}

    } else {
    MSY   <-MSY.jags; lcl.MSY<-lcl.MSY.jags; ucl.MSY<-ucl.MSY.jags
    Bmsy  <-k.jags/2; lcl.Bmsy<-lcl.k.jags/2; ucl.Bmsy<-ucl.k.jags/2
    Fmsy  <-r.jags/2; lcl.Fmsy<-lcl.r.jags/2; ucl.Fmsy<-ucl.r.jags/2
    B.Bmsy<-2*quant.P[2,];lcl.B.Bmsy<-2*quant.P[1,];ucl.B.Bmsy<-2*quant.P[3,]
    if(is.na(sel.yr)==F) {B.Bmsy.sel<-2*quant.P[2,][yr==sel.yr]}
 }
B          <-B.Bmsy*Bmsy;lcl.B<-lcl.B.Bmsy*Bmsy;ucl.B<-ucl.B.Bmsy*Bmsy
B.last     <-B[nyr];lcl.B.last<-lcl.B[nyr];ucl.B.last<-ucl.B[nyr]
B.Bmsy.last<-B.Bmsy[nyr];lcl.B.Bmsy.last<-lcl.B.Bmsy[nyr];ucl.B.Bmsy.last<-ucl.B.Bmsy[nyr]
```

```
Fm          <- ct.raw/B;lcl.F<-ct.raw/ucl.B;ucl.F<-ct.raw/lcl.B
Fmsy.vec     <- ifelse(B.Bmsy>0.5,Fmsy,Fmsy*2*B.Bmsy)
lcl.Fmsy.vec <- ifelse(B.Bmsy>0.5,lcl.Fmsy,lcl.Fmsy*2*B.Bmsy)
ucl.Fmsy.vec <- ifelse(B.Bmsy>0.5,ucl.Fmsy,ucl.Fmsy*2*B.Bmsy)
F.Fmsy       <- Fm/Fmsy.vec; lcl.F.Fmsy<-lcl.F/Fmsy.vec; ucl.F.Fmsy<-ucl.F/Fmsy.vec

F.last     <-Fm[nyr];lcl.F.last<-lcl.F[nyr];ucl.F.last<-ucl.F[nyr]
Fmsy.last  <-Fmsy.vec[nyr];lcl.Fmsy.last<-lcl.Fmsy.vec[nyr];ucl.Fmsy.last<-ucl.Fmsy.vec[nyr]
F.Fmsy.last<-F.Fmsy[nyr];lcl.F.Fmsy.last<-lcl.F.Fmsy[nyr];ucl.F.Fmsy.last<-ucl.F.Fmsy[nyr]

if(is.na(sel.yr)==F){
  B.sel<-B.Bmsy.sel*Bmsy
  F.sel<-ct.raw[yr==sel.yr]/B.sel
  F.Fmsy.sel<-F.sel/Fmsy.vec[yr==sel.yr]
}

# --------------------------------------------
# print input and results to screen
#---------------------------------------------
cat("--------------------------------------\n")
cat("Species:", cinfo$ScientificName[cinfo$Stock==stock], ", stock:",stock,"\n")
cat(cinfo$Name[cinfo$Stock==stock], "\n")
cat("Region:",cinfo$Region[cinfo$Stock==stock],",",cinfo$Subregion[cinfo$Stock==stock],"\n")
cat("Catch data used from years", min(yr),"-", max(yr),", abundance =", btype, "\n")
cat("Prior initial relative biomass =", startbio[1], "-",
startbio[2],ifelse(is.na(stb.low)==T,"default","expert"), "\n")
cat("Prior intermediate rel. biomass=", intbio[1], "-", intbio[2], "in year",
int.yr,ifelse(is.na(intb.low)==T,"default","expert"), "\n")
cat("Prior final relative biomass   =", endbio[1], "-",
endbio[2],ifelse(is.na(endb.low)==T,"default","expert"), "\n")
cat("Prior range for r =", format(start.r[1],digits=2), "-",
format(start.r[2],digits=2),ifelse(is.na(r.low)==T,"default","expert,"),
    ", prior range for k =", start.k[1], "-", start.k[2],"\n")
# if Schaefer and CPUE, print prior range of q
if(FullSchaefer==T & btype=="CPUE") {
  cat("Prior range of q =",q.prior[1],"-",q.prior[2],"\n")
}
# results of CMSY analysis
cat("\nResults of CMSY analysis \n")
cat("------------------------\n")
cat("Altogether", n.viable.b, "viable trajectories for", n.viable.pt," r-k pairs were found \n")
cat("r   =", r.est,", 95% CL =", lcl.r.est, "-", ucl.r.est,", k =", k.est,", 95% CL =", lcl.k.est, "-",
ucl.k.est,"\n")
cat("MSY =", MSY.est,", 95% CL =", lcl.MSY.est, "-", ucl.MSY.est,"\n")
cat("Relative biomass in last year =", median.btv.lastyr, "k, 2.5th perc =", lcl.median.btv.lastyr,
    ", 97.5th perc =", ucl.median.btv.lastyr,"\n")
```

```
cat("Exploitation F/(r/2) in last year =", (F.CMSY/Fmsy.CMSY)[nyr],"\n\n")

# print results from full Schaefer if available
if(FullSchaefer==T) {
  cat("Results from Bayesian Schaefer model (BSM) using catch &",btype,"\n")
  cat("---------------------------------------------------------------\n")
  if(btype == "CPUE") cat("q   =", mean.q,", lcl =", lcl.q, ", ucl =", ucl.q,"\n")
  cat("r   =", r.jags,", 95% CL =", lcl.r.jags, "-", ucl.r.jags,", k =", k.jags,", 95% CL =", lcl.k.jags,
"-", ucl.k.jags,"\n")
  cat("MSY =", MSY.jags,", 95% CL =", lcl.MSY.jags, "-", ucl.MSY.jags,"\n")
  cat("Relative biomass in last year =", quant.P[2,][nyr], "k, 2.5th perc =",quant.P[1,][nyr],
      ", 97.5th perc =", quant.P[3,][nyr],"\n")
  cat("Exploitation F/(r/2) in last year =", (ct.raw[nyr]/(quant.P[2,][nyr]*k.jags))/(r.jags/2) ,"\n\n")
}

# print results to be used in management
cat("Results for Management (based on",ifelse(FullSchaefer==F |
force.cmsy==T,"CMSY","BSM"),"analysis) \n")
cat("--------------------------------------------------------------\n")
if(force.cmsy==T) cat("Mangement results based on CMSY because abundance data seem
unrealistic\n")
cat("Fmsy =",Fmsy,", 95% CL =",lcl.Fmsy,"-",ucl.Fmsy,"(if B > 1/2 Bmsy then Fmsy = 0.5 r)\n")
cat("Fmsy =",Fmsy.last,", 95% CL =",lcl.Fmsy.last,"-",ucl.Fmsy.last,"(r and Fmsy are linearly
reduced if B < 1/2 Bmsy)\n")
cat("MSY  =",MSY,", 95% CL =",lcl.MSY,"-",ucl.MSY,"\n")
cat("Bmsy =",Bmsy,", 95% CL =",lcl.Bmsy,"-",ucl.Bmsy,"\n")
cat("Biomass in last year =",B.last,", 2.5th perc =", lcl.B.last, ", 97.5 perc =",ucl.B.last,"\n")
cat("B/Bmsy in last year  =",B.Bmsy.last,", 2.5th perc =", lcl.B.Bmsy.last, ", 97.5 perc
=",ucl.B.Bmsy.last,"\n")
cat("Fishing mortality in last year =",F.last,", 2.5th perc =", lcl.F.last, ", 97.5 perc
=",ucl.F.last,"\n")
cat("Exploitation F/Fmsy  =",F.Fmsy.last,", 2.5th perc =", lcl.F.Fmsy.last, ", 97.5 perc
=",ucl.F.Fmsy.last,"\n")

# show stock status and exploitation for optional selected year
if(is.na(sel.yr)==F) {
  cat("\nStock status and exploitation in",sel.yr,"\n")
  cat("Biomass =",B.sel, ", B/Bmsy =",B.Bmsy.sel,", F =",F.sel,", F/Fmsy =",F.Fmsy.sel,"\n") }

# indicate if less than 5 years of biomass or CPUE are available
if(btype !="None" & length(bt[is.na(bt)==F])<nab) {
  cat("Less than",nab,"years with abundance data available, shown on second axis\n")
}
cat("Comment:", comment,"\n")
cat("------------------------------------------------------------\n")
```

```
# ----------------------------------------
# Plot results
# ----------------------------------------
# Analysis of viable r-k plot
# ---------------------------
max.y    <- max(c(ifelse(FullSchaefer==T,ucl.k.jags,NA), max(kv.all)),
              ifelse(substr(id_file,1,3)=="Sim",1.2*true.k,max(kv.all)),
              na.rm=T)
min.y    <- min(c(ifelse(FullSchaefer==T,lcl.k.jags,NA), 0.9*min(kv.all)),
              ifelse(substr(id_file,1,3)=="Sim",0.8*true.k,0.9*min(kv.all)),
              na.rm=T)

plot(x=rv.all, y=kv.all, xlim=start.r,
     ylim=c(min.y,max.y),
     pch=16, col="gray",log="xy", bty="l",
     xlab="r", ylab="k", main="C: Analysis of viable r-k")

# plot r-k pairs from MCMC
if(FullSchaefer==T) {points(x=r_out, y=k_out, pch=16,cex=0.5)}

# plot best r-k from full Schaefer analysis
if(FullSchaefer==T) {
  points(x=r.jags, y=k.jags, pch=19, col="red")
  lines(x=c(lcl.r.jags, ucl.r.jags),y=c(k.jags,k.jags), col="red")
  lines(x=c(r.jags,r.jags),y=c(lcl.k.jags, ucl.k.jags), col="red")
}

# plot blue dot for CMSY r-k, with 95% CL lines
points(x=r.est, y=k.est, pch=19, col="blue")
lines(x=c(lcl.r.est, ucl.r.est),y=c(k.est,k.est), col="blue")
lines(x=c(r.est,r.est),y=c(lcl.k.est, ucl.k.est), col="blue")


# Pred. biomass plot
#-------------------
# determine k to use for red line in b/k plot
if(FullSchaefer==T)  {k2use <- k.jags} else {k2use <- k.est}
# determine hight of y-axis in plot
max.y  <- max(c(ifelse(btype=="biomass",max(bt/k2use,na.rm=T),NA),
              ifelse(btype=="CPUE",max(bt/(mean.q*k2use),na.rm=T),NA),
              max(ucl.btv),0.6,startbio[2], endbio[2]),
            ifelse(FullSchaefer==T &
btype=="biomass",max(bt[is.na(bt)==F]/lcl.k.jags,na.rm=T),NA),
            ifelse(FullSchaefer==T &
btype=="CPUE",1.1*max(bt/(mean.q*lcl.k.jags),na.rm=T),NA), na.rm=T)
```

```
# Main plot of relative CMSY biomass
plot(x=yr,y=median.btv[1:nyr], lwd=1.5, xlab="Year", ylab="Relative biomass B/k", type="l",
     ylim=c(0,max.y), bty="l", main="D: Biomass",col="blue")
lines(x=yr, y=lcl.btv[1:nyr],type="l",lty="dotted",col="blue")
lines(x=yr, y=ucl.btv[1:nyr],type="l",lty="dotted",col="blue")
# plot lines for 0.5 and 0.25 biomass
abline(h=0.5, lty="dashed")
abline(h=0.25, lty="dotted")
# plot biomass windows
lines(x=c(yr[1],yr[1]), y=startbio, col="blue")
lines(x=c(int.yr,int.yr), y=intbio, col="blue")
lines(x=c(max(yr),max(yr)), y=endbio, col="blue")

# if observed biomass is available, plot red biomass line (use non-smoothed bt)
if(btype=="biomass" & FullSchaefer==T) {
  lines(x=yr, y=bt/k.jags,type="l", col="red", lwd=1)
  lines(x=yr, y=bt/ucl.k.jags,type="l",col="red",lty="dotted")
  lines(x=yr, y=bt/lcl.k.jags,type="l",col="red",lty="dotted")
}

# if observed CPUE is available, plot red biomass line
if(btype=="CPUE" & FullSchaefer==T) {
  lines(x=yr, y=bt/(mean.q*k.jags),type="l", col="red", lwd=1)
  lines(x=yr, y=bt/(mean.q*ucl.k.jags),type="l",col="red",lty="dotted")
  lines(x=yr, y=bt/(mean.q*lcl.k.jags),type="l",col="red",lty="dotted")
}

# if biomass or CPUE data are available but fewer than 5 years, plot on second axis
if(btype != "None" & FullSchaefer==F) {
  par(new=T) # prepares for new plot on top of previous
  plot(x=yr, y=bt, type="l", col="red", lwd=1,
       ann=F,axes=F,ylim=c(0,1.2*max(bt, na.rm=T))) # forces this plot on top of previous one
  axis(4, col="red", col.axis="red")
}

# Exploitation rate plot
# -------------------------

# if CPUE data are available but fewer than nab years, plot on second axis
if(btype == "CPUE") {
  q=1/(max(median.btv[1:nyr][is.na(bt)==F],na.rm=T)*k.est/max(bt,na.rm=T))
  u.cpue      <- q*ct/bt
}

# determine upper bound of Y-axis
```

```
max.y <- max(c(1.5, 1.2*F.CMSY/Fmsy.CMSY,max(F.CMSY/Fmsy.CMSY),
            ifelse(btype=="biomass" & FullSchaefer==T,max(F.bt[is.na(F.bt)==F]/Fmsy.bt),0),
            ifelse(FullSchaefer==T & btype=="CPUE",max(F.bt.cpue/Fmsy.cpue,na.rm=T),0),
            na.rm=T))

# plot F from CMSY
plot(x=yr,y=F.CMSY/Fmsy.CMSY, type="l", bty="l", lwd=1.5, ylim=c(0,max.y), xlab="Year",
    ylab="F / (r/2)", main="E: Exploitation rate", col="blue")
abline(h=1, lty="dashed")

# plot F from observed biomass
if(btype == "biomass" & FullSchaefer==T) lines(x=yr, y=F.bt/Fmsy.bt, col="red")

# plot F from observed CPUE
if(FullSchaefer==T & btype == "CPUE") lines(x=yr, y=F.bt.cpue/Fmsy.cpue, col="red")

# plot F from CPUE on second axis if less than 5 years
if(FullSchaefer==F & btype == "CPUE") {
  par(new=T) # prepares for new plot on top of previous
  plot(x=yr, y=F.bt.cpue, type="l", col="red", ylim=c(0,
1.2*max(F.bt.cpue,na.rm=T)),ann=F,axes=F)
  axis(4, col="red", col.axis="red")
}

# Parabola plot
#-------------------------
max.y <- max(c(max(ct/MSY.est),ifelse(btype=="biomass",max(ct/MSY.jags),NA),1.2),na.rm=T)
# plot parabola
x=seq(from=0,to=2,by=0.001)
y.c  <- ifelse(x>0.25,1,ifelse(x>0.125,4*x,exp(-10*(0.125-x))*4*x)) # correction for low
recruitment below half and below quarter of Bmsy
y=(4*x-(2*x)^2)*y.c
plot(x=x, y=y, xlim=c(1,0), ylim=c(0,max.y), type="l", bty="l",xlab="Relative biomass B/k",
    ylab="Catch / MSY", main="F: Equilibrium curve")

# plot catch against CMSY estimates of relative biomass
points(x=median.btv[1:nyr], y=ct/MSY.est, pch=16, col="blue")

# plot catch scaled by BSM MSY against observed biomass scaled by BSM k
if(btype == "biomass") {
  points(x=bt/k.jags, y=ct/MSY.jags, pch=16, cex=0.5, col="red")
}

# for CPUE, plot catch scaled by BSM MSY against observed biomass derived as q * CPUE
scaled by BSM k
if(FullSchaefer==T & btype=="CPUE") {
```

```
  points(x=bt/(mean.q*k.jags), y=ct/MSY.jags, pch=16, cex=0.5, col="red")
}

#save analytic chart to JPEG file
if (save.plots==TRUE)
{
  jpgfile<-paste(stock,"_AN.jpeg",sep="")
  dev.copy(jpeg,jpgfile,
           width = 1024,
           height = 768,
           units = "px",
           pointsize = 18,
           quality = 95,
           res=80,
           antialias="cleartype")
  dev.off()
}

#--------------------------------------------
# Plot Management-Graphs if desired
#--------------------------------------------
if(mgraphs==T) {
  # open window for plot of four panels
  if(grepl("win",tolower(Sys.info()['sysname']))) {windows(14,12)}
  par(mfrow=c(2,2))
  # make margins narrower
  par(mar=c(3.1,4.1,2.1,2.1))

  #---------------------
  # plot catch with MSY
  #---------------------
  max.y <- max(c(1.1*max(ct.raw),ucl.MSY),na.rm=T)
  plot(x=yr,rep(0,nyr),type="n",ylim=c(0,max.y), bty="l", main=paste("Catch",stock),
       ylab="Catch in 1000 t")
  rect(yr[1],lcl.MSY,yr[nyr],ucl.MSY,col="lightgray", border=NA)
  lines(x=c(yr[1],yr[nyr]),y=c(MSY,MSY),lty="dashed", col="black", lwd=1.5)
  lines(x=yr, y=ct.raw, lwd=2)
  text("MSY",x=end.yr-1.5, y=MSY+MSY*0.1)

  #----------------------------------------
  # plot estimated biomass relative to Bmsy
  #----------------------------------------
  # plot empty frame
  plot(yr, rep(0,nyr),type="n", ylim=c(0,max(c(2, max(ucl.B.Bmsy)))), ylab="B /
Bmsy",xlab="Year", main="Biomass", bty="l")
  # plot gray area of uncertainty in predicted biomass
```

```
  polygon(c(yr,rev(yr)), c(lcl.B.Bmsy,rev(ucl.B.Bmsy)),col="lightgray", border=NA)
  # plot median biomass
  lines(yr,B.Bmsy,lwd=2)
  # plot lines for Bmsy and 0.5 Bmsy
  lines(x=c(yr[1],yr[nyr]),y=c(1,1), lty="dashed", lwd=1.5)
  lines(x=c(yr[1],yr[nyr]),y=c(0.5,0.5), lty="dotted", lwd=1.5)

  # plot exploitation rate
  # -------------------------
  # plot empty frame
  plot(yr, rep(0,nyr),type="n", ylim=c(0,max(c(2,
ifelse(max(ucl.F.Fmsy)<5,max(ucl.F.Fmsy),5)))),
      ylab="F / Fmsy",xlab="Year", main="Exploitation", bty="l")
  # plot gray area of uncertainty in predicted exploitation
  polygon(c(yr,rev(yr)), c(lcl.F.Fmsy,rev(ucl.F.Fmsy)),col="lightgray", border=NA)
  # plot median exploitation rate
  lines(x=yr,y=F.Fmsy,lwd=2)
  # plot line for u.msy
  lines(x=c(yr[1],yr[nyr]),y=c(1,1), lty="dashed", lwd=1.5)

  #><><><><><><><><><><><><><><><><><><><><><><><><><><>
  # plot stock-status graph
  #---------------------------
  if(FullSchaefer==T & force.cmsy==F) {x.F_Fmsy = all.F_Fmsy[,nyr]
  y.b_bmsy = all.b_bmsy[,nyr]} else {
    log.sd.B.Bmsy = (log(ucl.B.Bmsy.last+0.0011)-log(lcl.B.Bmsy.last+0.001))/(2*1.96)
    log.sd.F.Fmsy = (log(ucl.F.Fmsy.last+0.005)-log(lcl.F.Fmsy.last+0.001))/(2*1.96)
    x.F_Fmsy= rlnorm(20000,log(F.Fmsy.last+0.001),log.sd.F.Fmsy)
    y.b_bmsy =rlnorm(20000,log(B.Bmsy.last+0.001),log.sd.B.Bmsy)
  }
  kernelF <-
ci2d(x.F_Fmsy,y.b_bmsy,nbins=201,factor=2.2,ci.levels=c(0.50,0.80,0.75,0.90,0.95),show="non
e")
  c1 <- c(-1,100)
  c2 <- c(1,1)

  max.x1   <- max(c(2, max(kernelF$contours$"0.95"$x,ucl.F.Fmsy.last),na.rm =T))
  max.x    <- ifelse(max.x1 > 5,min(max(5,F.Fmsy*2),8),max.x1)
  max.y    <- max(max(2,quantile(y.b_bmsy,0.96)))

  #Create plot
  plot(1000,1000,type="b", xlim=c(0,max.x), ylim=c(0,max.y),lty=3,xlab="",ylab="", bty="l")
  mtext("F / Fmsy",side=1, line=2)
  mtext("B / Bmsy",side=2, line=2)

  # extract interval information from ci2d object
```

```
  # and fill areas using the polygon function
  polygon(kernelF$contours$"0.95",lty=2,border=NA,col="cornsilk4")
  polygon(kernelF$contours$"0.8",border=NA,lty=2,col="grey")
  polygon(kernelF$contours$"0.5",border=NA,lty=2,col="cornsilk2")

  ## Add points and trajectory lines
  lines(c1,c2,lty=3,lwd=0.7)
  lines(c2,c1,lty=3,lwd=0.7)
  lines(F.Fmsy,B.Bmsy, lty=1,lwd=1.)

  points(F.Fmsy,B.Bmsy,cex=0.8,pch=4)
  points(F.Fmsy[1],B.Bmsy[1],col=1,pch=22,bg="white",cex=1.9)

points(F.Fmsy[which(yr==int.yr)],B.Bmsy[which(yr==int.yr)],col=1,pch=21,bg="white",cex=1.9
)
  points(F.Fmsy[nyr],B.Bmsy[nyr],col=1,pch=24,bg="white",cex=1.9)

  ## Add legend
  legend('topright', c(paste(start.yr),paste(int.yr),paste(end.yr),"50% C.I.","80% C.I.","95% C.I."),
        lty=c(1,1,1,-1,-1,-
1),pch=c(22,21,24,22,22,22),pt.bg=c(rep("white",3),"cornsilk2","grey","cornsilk4"),
        col=1,lwd=1.1,cex=0.9,pt.cex=c(rep(1.3,3),1.7,1.7,1.7),bty="n",y.intersp = 0.9)
  #><> End of Biplot

} # end of management graphs

# save management chart to JPEG file
if (save.plots==TRUE & mgraphs==TRUE)
{
  jpgfile<-paste(stock,"_MAN.jpeg",sep="")
  dev.copy(jpeg,jpgfile,
          width = 1024,
          height = 768,
          units = "px",
          pointsize = 18,
          quality = 95,
          res=80,
          antialias="cleartype")
  dev.off()
}

# -------------------------------------
## Write some results into csv outfile
# -------------------------------------
if(write.output == TRUE) {
```

```
  # write data into csv file
  output = data.frame(as.character(cinfo$Group[cinfo$Stock==stock]),
                      as.character(cinfo$Region[cinfo$Stock==stock]),
                      as.character(cinfo$Subregion[cinfo$Stock==stock]),
                      as.character(cinfo$Name[cinfo$Stock==stock]),
                      cinfo$ScientificName[cinfo$Stock==stock],
                      stock, start.yr, end.yr, btype,
                      max(ct.raw),ct.raw[nyr],
                      ifelse(FullSchaefer==T,MSY.jags,NA), # full Schaefer
                      ifelse(FullSchaefer==T,lcl.MSY.jags,NA),
                      ifelse(FullSchaefer==T,ucl.MSY.jags,NA),
                      ifelse(FullSchaefer==T,r.jags,NA),
                      ifelse(FullSchaefer==T,lcl.r.jags,NA),
                      ifelse(FullSchaefer==T,ucl.r.jags,NA),
                      ifelse(FullSchaefer==T,k.jags,NA),
                      ifelse(FullSchaefer==T,lcl.k.jags,NA),
                      ifelse(FullSchaefer==T,ucl.k.jags,NA),
                      ifelse(FullSchaefer==T & btype=="CPUE",mean.q,NA),
                      ifelse(FullSchaefer==T & btype=="CPUE",lcl.q,NA),
                      ifelse(FullSchaefer==T & btype=="CPUE",ucl.q,NA),
                      ifelse(FullSchaefer==T,quant.P[2,][nyr],NA), # last B/k JAGS
                      ifelse(FullSchaefer==T,quant.P[1,][nyr],NA),
                      ifelse(FullSchaefer==T,quant.P[3,][nyr],NA),
                      ifelse(FullSchaefer==T,(ct.raw[nyr]/(quant.P[2,][nyr]*k.jags))/(r.jags/2),NA), # last
F/Fmsy JAGS
                      r.est, lcl.r.est, ucl.r.est, # CMSY r
                      k.est, lcl.k.est, ucl.k.est, # CMSY k
                      MSY.est, lcl.MSY.est, ucl.MSY.est, # CMSY MSY
                      median.btv.lastyr, lcl.median.btv.lastyr,ucl.median.btv.lastyr, # CMSY B/k in last
year with catch data
                      (F.CMSY/Fmsy.CMSY)[nyr],
                      Fmsy,lcl.Fmsy,ucl.Fmsy,Fmsy.last,lcl.Fmsy.last,ucl.Fmsy.last,
                      MSY,lcl.MSY,ucl.MSY,Bmsy,lcl.Bmsy,ucl.Bmsy,
                      B.last, lcl.B.last, ucl.B.last, B.Bmsy.last, lcl.B.Bmsy.last, ucl.B.Bmsy.last,
                      F.last, lcl.F.last, ucl.F.last, F.Fmsy.last, lcl.F.Fmsy.last, ucl.F.Fmsy.last,
                      ifelse(is.na(sel.yr)==F,B.sel,NA),
                      ifelse(is.na(sel.yr)==F,B.Bmsy.sel,NA),
                      ifelse(is.na(sel.yr)==F,F.sel,NA),
                      ifelse(is.na(sel.yr)==F,F.Fmsy.sel,NA),

ifelse(yr[1]>2000,NA,ct.raw[yr==2000]),ifelse(yr[1]>2001,NA,ct.raw[yr==2001]),ifelse(yr[1]>2
002,NA,ct.raw[yr==2002]), ifelse(yr[1]>2003,NA,ct.raw[yr==2003]),# allow missing 2000-2002

ct.raw[yr==2004],ct.raw[yr==2005],ct.raw[yr==2006],ct.raw[yr==2007],ct.raw[yr==2008],ct.ra
w[yr==2009],ct.raw[yr==2010],
```

```
ifelse(yr[nyr]<2011,NA,ct.raw[yr==2011]),ifelse(yr[nyr]<2012,NA,ct.raw[yr==2012]),ifelse(yr[n
yr]<2013,NA,ct.raw[yr==2013]),ifelse(yr[nyr]<2014,NA,ct.raw[yr==2014]),ifelse(yr[nyr]<2015,
NA,ct.raw[yr==2015]), # allow missing 2011-2015

ifelse(yr[1]>2000,NA,F.Fmsy[yr==2000]),ifelse(yr[1]>2001,NA,F.Fmsy[yr==2001]),ifelse(yr[1]
>2002,NA,F.Fmsy[yr==2002]),ifelse(yr[1]>2003,NA,F.Fmsy[yr==2003]), # allow missing 2000-
2002

F.Fmsy[yr==2004],F.Fmsy[yr==2005],F.Fmsy[yr==2006],F.Fmsy[yr==2007],F.Fmsy[yr==2008],
F.Fmsy[yr==2009],F.Fmsy[yr==2010],

ifelse(yr[nyr]<2011,NA,F.Fmsy[yr==2011]),ifelse(yr[nyr]<2012,NA,F.Fmsy[yr==2012]),ifelse(y
r[nyr]<2013,NA,F.Fmsy[yr==2013]),ifelse(yr[nyr]<2014,NA,F.Fmsy[yr==2014]),ifelse(yr[nyr]<
2015,NA,F.Fmsy[yr==2015]),# allow missing 2011-2015

ifelse(yr[1]>2000,NA,B[yr==2000]),ifelse(yr[1]>2001,NA,B[yr==2001]),ifelse(yr[1]>2002,NA,
B[yr==2002]),ifelse(yr[1]>2003,NA,B[yr==2003]), # allow missing 2000-2002

B[yr==2004],B[yr==2005],B[yr==2006],B[yr==2007],B[yr==2008],B[yr==2009],B[yr==2010],

ifelse(yr[nyr]<2011,NA,B[yr==2011]),ifelse(yr[nyr]<2012,NA,B[yr==2012]),ifelse(yr[nyr]<201
3,NA,B[yr==2013]),ifelse(yr[nyr]<2014,NA,B[yr==2014]),ifelse(yr[nyr]<2015,NA,B[yr==2015]
)) # allow missing 2011-2015

  write.table(output, file=outfile, append = T, sep = ",",
            dec = ".", row.names = FALSE, col.names = FALSE)

  output2 <-data.frame(mdat.all) #juliana

  write.table(output2, file="output2.csv",  sep = ";", dec=".",
            row.names=T, col.names=T)#juliana


  # write screen text into text outfile.txt

  cat("Species:", cinfo$ScientificName[cinfo$Stock==stock], ", stock:",stock,"\n",
      cinfo$Name[cinfo$Stock==stock], "\n",
      "Source:",cinfo$Source[cinfo$Stock==stock],"\n",
      "Region:",cinfo$Region[cinfo$Stock==stock],",",cinfo$Subregion[cinfo$Stock==stock],"\n",
      "Catch data used from years", min(yr),"-", max(yr),", abundance =", btype, "\n",
      "Prior initial relative biomass =", startbio[1], "-",
startbio[2],ifelse(is.na(stb.low)==T,"default","expert"), "\n",
      "Prior intermediate rel. biomass=", intbio[1], "-", intbio[2], "in year",
int.yr,ifelse(is.na(intb.low)==T,"default","expert"), "\n",
      "Prior final relative biomass   =", endbio[1], "-", endbio[2],ifelse(is.na(endb.low)==T,",
default","expert"), "\n",
```

```
      "Prior range for r =", format(start.r[1],digits=2), "-",
format(start.r[2],digits=2),ifelse(is.na(r.low)==T,"default","expert,"),
      ", prior range for k  =", start.k[1], "-", start.k[2],
      file=outfile.txt,append=T)

  if(FullSchaefer==T & btype=="CPUE") {
    cat("\n Prior range of q =",q.prior[1],"-",q.prior[2],file=outfile.txt,append=T)
  }
  cat("\n\n Results of CMSY analysis with altogether",n.viable.b, "viable trajectories for",
n.viable.pt,"r-k pairs \n",
      "r =", r.est,", 95% CL =", lcl.r.est, "-", ucl.r.est,
      ", k =", k.est,", 95% CL =", lcl.k.est, "-", ucl.k.est,"\n",
      "MSY =", MSY.est,", 95% CL =", lcl.MSY.est, "-", ucl.MSY.est,"\n",
      "Relative biomass last year =", median.btv.lastyr, "k, 2.5th =", lcl.median.btv.lastyr,
      ", 97.5th =", ucl.median.btv.lastyr,"\n",
      "Exploitation F/(r/2) in last year =", (F.CMSY/Fmsy.CMSY)[length(median.btv)-1],"\n",
      file=outfile.txt,append=T)

    if(FullSchaefer==T) {
    cat("\n Results from Bayesian Schaefer model using catch &",btype,"\n",
        "r =", r.jags,", 95% CL =", lcl.r.jags, "-", ucl.r.jags,
        ", k =", k.jags,", 95% CL =", lcl.k.jags, "-", ucl.k.jags,"\n",
        "MSY =", MSY.jags,", 95% CL =", lcl.MSY.jags, "-", ucl.MSY.jags,"\n",
        "Relative biomass in last year =", quant.P[2,][nyr], "k, 2.5th perc =",quant.P[1,][nyr],
            ", 97.5th perc =", quant.P[3,][nyr],"\n",
        "Exploitation F/(r/2) in last year =", (ct.raw[nyr]/(quant.P[2,][nyr]*k.jags))/(r.jags/2) ,
        file=outfile.txt,append=T)
     if(btype == "CPUE") {cat("\n q =", mean.q,", lcl =", lcl.q, ", ucl =", ucl.q,
        file=outfile.txt,append=T)}
  }

  cat("\n\n Results for Management (based on",ifelse(FullSchaefer==F |
force.cmsy==T,"CMSY","BSM"),"analysis) \n",
      "Fmsy =",Fmsy,", 95% CL =",lcl.Fmsy,"-",ucl.Fmsy,"(if B > 1/2 Bmsy then Fmsy = 0.5 r)\n",
      "Fmsy =",Fmsy.last,", 95% CL =",lcl.Fmsy.last,"-",ucl.Fmsy.last,"(r and Fmsy are linearly
reduced if B < 1/2 Bmsy)\n",
      "MSY  =",MSY,",  95% CL =",lcl.MSY,"-",ucl.MSY,"\n",
      "Bmsy =",Bmsy,",  95% CL =",lcl.Bmsy,"-",ucl.Bmsy,"\n",
      "Biomass in last year  =",B.last,", 2.5th perc =", lcl.B.last, ", 97.5 perc =",ucl.B.last,"\n",
      "B/Bmsy in last year   =",B.Bmsy.last,", 2.5th perc =", lcl.B.Bmsy.last, ", 97.5 perc
=",ucl.B.Bmsy.last,"\n",
      "Fishing mortality in last year =",F.last,", 2.5th perc =", lcl.F.last, ", 97.5 perc
=",ucl.F.last,"\n",
      "F/Fmsy  =",F.Fmsy.last,", 2.5th perc =", lcl.F.Fmsy.last, ", 97.5 perc =",ucl.F.Fmsy.last,"\n",
      file=outfile.txt,append=T)
  # show stock status and exploitation for optional selected year
```

```
  if(is.na(sel.yr)==F) {
    cat("\n Stock status and exploitation in",sel.yr,"\n",
    "Biomass =",B.sel, ", B/Bmsy =",B.Bmsy.sel,", fishing mortality F =",F.sel,", F/Fmsy
=",F.Fmsy.sel,"\n",
    file=outfile.txt,append=T) }

  if(btype !="None" & length(bt[is.na(bt)==F])<nab) {
    cat(" Less than",nab,"years with abundance data available, shown on second
axis\n",file=outfile.txt,append=T) }

  cat(" Comment:", comment,"\n","---------------------------------------------------------\n\n",
      file=outfile.txt,append=T)
 }# end of loop to write text to file

 if(close.plots==T) graphics.off() # close on-screen graphics windows after files are saved

} # end of stocks loop

#stop parallel processing clusters
stopCluster(cl)
stopImplicitCluster()

#to get unique r-k pairs:
write.table(unique.rk, file="unique.rk.pairs-jau.csv", dec=".", sep=";")
```

Código do método COM-SIR (retirado de Rosenberg *et al.*, 2014):

```
#################COM SIR ###########################################
#  Catch only model implemented by C.V.Minte-Vera
#  Version June 10, 2013                                  <><   <><
#  Vasconcellos and Cochrane 2005                 <><                              <><
#  Biomass dynamic (Schaefer) and harvest dynamic model (logistic)
#  assumed the initial harvest rate equals Catch first year / Biomass first year
#  Biomass first year = carrying capacity                              <><
#  lognormal likehood for catch data w/ observation error CV =0.4
#  Estimation using Bayesian Sampling Importance Resampling         <><
#  Joint prior is the important function, i.e. resampling proportional to the likelihood
#################   <><   <><   <><   ####################################

#  <>< #  COUNTER,  counter for stock = i
i <- 1

# <>< # Directories
# for Procedure
ProcDir="C:\\Users\\Juliana\\OneDrive\\doutorado\\Data-poor methods\\COM-SIR method\\"
```

```
# for Results
ResDir="C:\\Users\\Juliana\\OneDrive\\doutorado\\Data-poor methods\\COM-SIR method\\"
# for Data
MyDir="C:\\Users\\Juliana\\OneDrive\\doutorado\\Data-poor methods\\COM-SIR method\\"

#file with inputs data, the R object is called "input",it is a list
filename="jau.csv" #ju
input=read.csv(filename, header=T, dec=".") #já lê no formato list
is.list(input)

# <>< # SIR Controls
My.N.Sim= 5000000 # numbers of samples from the importance function
My.N.Post= 5000 # number of samples from the posterior (ressampling part)
My.seed= ceiling(runif(1,0,1e6))# random seed same procedure as ThorII
My.CV = 0.4 ## CV for observations - i.e. for Catch data


# <>< # PROCEDURE section
#load the functions needed for COM SIR
source("FunctionsCOM.R")
###


# <>< # DATA section
# stocks
#"input" is the name of the list with the input data
stocks_id=names(input) #stock names
StockName=stocks_id[i]
ct <- input$ct #ju
yr <- input$yr #ju
n <- length(yr)
MyData <- data.frame(catch=ct,year=yr) #ju
MyData
# <>< # PRIORs section
# Prior for K is ln(K) ~ U( ln(min.K), ln(max.K))
# bound follows Martell and Froese 2012
min.K=max(ct)
max.K=100*min.K

# Prior on r based on "resilience" following Froese 2012 Table 1
res <- "Very low"
res <- "Low"
res <- "Medium"
res <- "High"
#Resilience according to FishBase:
start_r <- c(0.015, 0.1) #start_r for res == "Very low"
```

```
start_r  <- c(0.05,0.5) #res == "Low"
start_r <-  c(0.2,1) #res = Medium
start_r  <- c(0.6,1.5) #res == "High"
# <>< # RESULTS section
## Unquote if there is a need to create a directory for results
#ResultDir<- paste(ResDir,stock_id[i],"\\",sep="")
#dir.create(ResultDir,showWarnings = FALSE)
#setwd(ResultDir)

###My.Par is used when plots of the model are done, need it here because is passed as argument
#these values are used to compute the relative values from prior and posteriors
#plotted to see the gain in information from the inclusion of the data
My.Par<-c(800,800,0.6,1.0,0.8,0.5,0)
My.Par<-t(My.Par)
My.Par<-as.data.frame(My.Par)
names(My.Par)<-c( "N1",   "K",    "r",    "z",    "a",    "x",    "h")
Time=system.time(suppressWarnings(
  COM<-
DoProject(MyFile="teste",Myseed=My.seed,TruePar=My.Par,MyData=MyData,EstLogisticM=T,

LogisticModel=T,MyCV=My.CV,NormalL=F,Nsim=My.N.Sim,Npost=My.N.Post,logK=T,Norm
K=F,Normr=F,
                start.r=start_r,minK=min.K, maxK=max.K,MyYLim=c(-2,8),Obs=F)
))
Results= suppressWarnings(data.frame('stock_id'=
StockName,'b_bmsy'=apply(COM$BoverBmsy,MARGIN=1,FUN=median),
                                  'b_bmsyUpper'
=apply(COM$BoverBmsy,MARGIN=1,FUN=quantile,prob=0.925),
                                  'b_bmsyLower'=
apply(COM$BoverBmsy,MARGIN=1,FUN=quantile,prob=0.075),

'b_bmsy_iq25'=apply(COM$BoverBmsy,MARGIN=1,FUN=quantile,prob=0.25) ,

'b_bmsy_iq75'=apply(COM$BoverBmsy,MARGIN=1,FUN=quantile,prob=0.75),
                                  'E'=apply(COM$E,MARGIN=1,FUN=median),
                                  'E_Upper'=apply(COM$E,MARGIN=1,FUN=quantile,prob=0.925),
                                  'E_Lower'=apply(COM$E,MARGIN=1,FUN=quantile,prob=0.075),
                                  'E_iq25'=apply(COM$E,MARGIN=1,FUN=quantile,prob=0.25),
                                  'E_iq75'=apply(COM$E,MARGIN=1,FUN=quantile,prob=0.75),
                                  'year'=MyData[,2],

'seed'=My.seed,'convergence'=ifelse(COM$Diagno['ESS']>200,"Strong",ifelse(COM$Diagno['ES
S']>30,"Weak","Not")),'n_iterations'=My.N.Post,
'effective_sample_size'=COM$Diagno['ESS'],'run_time'=Time['elapsed'],'method_id'="COM.SIR
"))
```

3 AVALIAÇÃO DOS ESTOQUES PESQUEIROS DO RESERVATÓRIO DE ITAIPU: MODELO BASEADO EM CAPTURAS E INDICADORES BASEADOS NO TAMANHO

Resumo

A pesca profissional no reservatório de Itaipu é desenvolvida logo após a formação do reservatório e abriga cerca de 700 pescadores, sendo uma atividade muito importante para a geração de renda e como fonte de proteína. A sustentabilidade dos recursos pesqueiros depende de diversos fatores, entre eles o conhecimento dos níveis atuais de biomassa, captura e mortalidade por pesca. Os principais estoques pesqueiros do reservatório de Itaipu foram avaliados por meio de um modelo baseado em dados de captura e indicadores baseados no tamanho. Os dados de captura para algumas espécies continham muita informação, enquanto que para outras, os resultados foram sensíveis às distribuições a priori assumidas. A mortalidade por pesca estimada foi alta para todas as espécies analisadas, pelo menos em algum momento da série temporal. Ainda assim, os níveis de biomassa estimados estão acima do recomendando para algumas delas. A análise da composição de tamanhos identificou que a proporção de indivíduos capturados, maiores que o comprimento de primeira maturação, esteve acima de 0.5 somente para duas espécies. Já a proporção de indivíduos capturados com tamanho ótimo foi abaixo de 0.5. Sugere-se que seja revisado o tamanho mínimo de captura para duas espécies (*Hypophthalmus edentatus* e *Plagioscion squamosissimus*).

Palavras-chave modelo de Schaefer, pesca de água doce, pesca de pequena escala, rendimento máximo sustentável.

3.1 INTRODUÇÃO

A captura mundial total proveniente da pesca em águas continentais vem aumentando nos últimos anos, e apesar do Brasil ocupar a 11ª posição entre os países com maior produção, a captura diminuiu nos anos de 2013 e 2014 (FAO 2016). A produção pesqueira continental no Brasil é afetada negativamente pela falta de gestão adequada, e, entre outros fatores, pelos impactos causados pela construção de barragens. No Brasil, usinas hidroelétricas são a principal fonte energética para o país, porém afetam negativamente a diversidade dos ecossistemas aquáticos brasileiros, como também a produção pesqueira (Agostinho *et al*. 2005, Winemiller *et al*. 2016).

A construção de barragens obstrui a rota migratória de espécies com alto valor comercial, controla pulsos de inundação, afetando negativamente o recrutamento das espécies que têm seu ciclo reprodutivo associado a planícies de inundação, e muda a composição do pescado para espécies com menor valor econômico (Hoeinghaus *et al*. 2009, Oliveira *et al*. 2015, Agostinho *et al*. 2016).

Por sua vez, a gestão pesqueira no Brasil muitas vezes não é eficiente para proteger os recursos naturais. A abordagem adotada atualmente ainda é um sistema *top-down*, e as principais medidas de ordenamento estão voltadas ao controle do esforço de pesca, e proteção da época reprodutiva das espécies. Os recursos humanos são escassos para a fiscalização, e na maioria das pescarias não existem programas de monitoramento contínuos e eficazes, como também avaliações da situação dos estoques pesqueiros, principalmente para pescarias continentais. Portanto, as decisões são baseadas em pouca ou nenhuma informação científica (Castello 2007, Viana 2013).

A importância em avaliar a situação dos estoques pesqueiros, não se justifica somente pela conservação dos recursos naturais. A pesca de pequena escala (PPE), comercial ou de subsistência, desenvolve um papel relevante para a segurança alimentar, principalmente em países em desenvolvimento, como o Brasil (McIntyre *et al*. 2016). A pesca comercial de pequena escala desenvolvida no reservatório de Itaipu, assim como outras PPE, tem um papel fundamental como fonte de renda e alimento para a população local. Este reservatório encontra-se na bacia do alto rio Paraná, onde a concentração de reservatórios hidroelétricos é alta, e os impactos destes empreendimentos na PPE são acentuados (Agostinho *et al*. 2007, Oliveira *et al*. 2015).

Poucos estoques já foram avaliados no reservatório de Itaipu (Ambrósio *et al*. 2001, Feitosa *et al*. 2004, Santana 2014, Philippsen *et al*. 2016), e considerando que esta PPE explora uma alta diversidade de espécies, a avaliação de uma maior quantidade de estoques permitirá gerar informações úteis para embasar medidas de gestão local. Além disso, métodos que requerem poucos dados (*data-limited methods*), estão atualmente sendo aperfeiçoados e testados (Rosenberg *et al*. 2014, Wetzel & Punt 2015), e são capazes de estimar parâmetros importantes para a gestão. Nesse contexto, o objetivo deste trabalho foi avaliar a situação de alguns dos principais estoques pesqueiros explorados no reservatório de Itaipu, combinando dois métodos limitados em dados. Especificamente, foi adotado o método baseado em capturas (*catch-only models*; Vasconcellos & Cochrane 2005), e indicadores baseados no comprimento (*length-based indicators*; Froese 2004).

3.2 MÉTODOS

3.2.1 ÁREA DE ESTUDO

O reservatório de Itaipu está localizado na bacia do alto rio Paraná, sul do Brasil, na fronteira com o Paraguai (Fig. 1). Este reservatório possui uma área de 1350 Km^2 e é um dos principais em produção de energia elétrica no Brasil (Agostinho *et al*. 2007). A pesca comercial no reservatório de Itaipu começou oficialmente em 1985, três anos após o término da construção da barragem, em 1982 (Okada *et al*. 2005, Okada *et al*. 2012). A pesca desenvolvida no reservatório de Itaipu é de pequena escala, tem várias espécies-alvo, e adota principalmente redes de malha e espinhel (Okada *et al*. 2012). Ao longo dos anos, houve uma mudança expressiva na composição das capturas, que inicialmente era composta por espécies migradoras de longa distância, e de alto valor comercial. Atualmente, a captura é composta, principalmente, por espécies sedentárias com baixo valor comercial (Hoeinghaus *et al*. 2009).

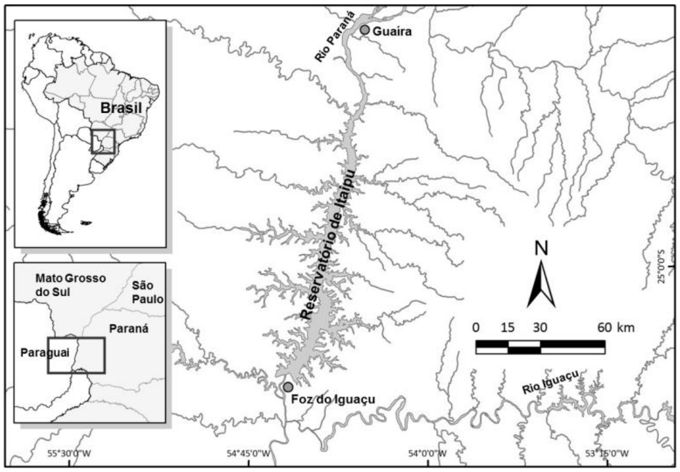


Figura 1. Reservatório de Itaipu, localizado na fronteira entre Brasil e Paraguai.

3.2.2 Origem dos dados

Os dados de captura analisados são provenientes de um programa de monitoramento desenvolvido em parceira entre a Itaipu Binacional e o Núcleo de Pesquisas em Limnologia, Ictiologia e Aquacultura (Nupélia), da Universidade Estadual de Maringá. A série temporal de capturas abrange dados entre 1987 e 2011, enquanto que os dados de comprimento compreendem os anos de 1988 até 2010 (Okada *et al*. 2005, Okada *et al*. 2012). Os estoques analisados foram *Pterodoras granulosus*, *Prochilodus lineatus*, *Hypophthalmus edentatus*, *Pinirampus pirinampu*, *Plagioscion squamosissimus*, que foram as espécies mais capturas em 2010 (Okada *et al*. 2012), e *Salminus brasiliensis*, *Pseudoplatystoma corruscans* e *Zungaro jahu*, que são espécies de alto valor econômico, porém suas capturas mostraram expressiva redução após a construção do reservatório.

3.2.3 Análise dos dados

Os dados de captura foram analisados com um modelo baseado em capturas (de aqui em diante referido como método COM-SIR), proposto por Vasconcellos & Cochrane (2005), e implementado por Minte-Vera (Rosenberg *et al*. 2014). O método COM-SIR estima a captura ao longo do tempo, com um sistema acoplado de equações sobre o esforço e a dinâmica de biomassa, e permite a obtenção de estimativas dos parâmetros: taxa intrínseca de crescimento da população (*r*), e capacidade de suporte (*K*). Estes parâmetros são úteis para obter indicadores sobre o estado de explotação dos recursos pesqueiros, como por exemplo, o rendimento máximo sustentável (MSY), e a biomassa que produz o rendimento máximo sustentável (B_{MSY}) (Vasconcellos & Cochrane 2005, Rosenberg *et al*. 2014).

O modelo de dinâmica de biomassa de Schaefer (equação 1) e um modelo da taxa de captura (equação 2) são combinados para predizer a captura ao longo do tempo (equação 3), permitindo inferir sobre o *status* do estoque, a produção e a taxa de explotação (Vasconcellos & Cochrane 2005). O modelo de Schaefer de dinâmica de biomassa é dado por:

$$B_{t+1} = B_t + rB_t\left(1 - \frac{B_t}{K}\right) - C_t \qquad (1)$$

onde B_{t+1} é a biomassa no ano seguinte $t+1$, B_t é a biomassa atual, e C_t é a captura no ano t.

A taxa de captura evolui ao longo do tempo, de acordo com um modelo logístico (Minte-

Vera dados não publicados, Vasconcellos & Cochrane 2005):

$$P_{t+1} = P_t \left[1 + x \left(\frac{B_t}{aK} - 1 \right) \right] \qquad (2)$$

onde P_t é a proporção da biomassa capturada no tempo *t*, *a* (0 < *a* < 1) é o equilíbrio bioeconômico como proporção de *K*, assumindo que não há subsídios ou que os subsídios são constantes, e *x* é a taxa de mudança do esforço. A taxa de captura inicial é dada por $P_0 = {C_0}/{B_0}$. Assume-se que a captura inicial, C_0, é igual à primeira captura observada da série temporal, e que a biomassa inicial é igual à capacidade de suporte ($B_0 = K$).

As capturas são preditas pela seguinte equação:

$$\hat{C}_{t+1} = P_{t+1} \left[B_t + rB_t \left(1 - \frac{B_t}{K} \right) - \hat{C}_t \right] \qquad (3)$$

onde $\hat{C}_{t+1}$ é a captura predita no ano $t+1$, P_{t+1} é a taxa de captura ou proporção da biomassa capturada no ano $t+1$, *K* é a capacidade de suporte ou a biomassa da população quando o crescimento populacional é nulo, e *r* é a taxa intrínseca de crescimento da população. Os parâmetros que foram estimados são *r*, *K*, *x*, e *a*.

Para estimar tais parâmetros foi adotada uma abordagem Bayesiana usando o algoritmo de re-amostragem por importância (*sampling importance resampling algorithm*, SIR; McAllister *et al*. 1994, Gelman *et al*. 2004), implementado no software R (R Development Core Team 2013).

Foi assumido que a captura observada segue uma função de verossimilhança lognormal (Casella & Berger 2002), sendo os valores esperados iguais à captura predita pelo modelo baseado em capturas:

$$L(\phi|w) = \prod_{t=1}^{n} \frac{1}{\sigma C_t \sqrt{2\pi}} \exp\left[-\frac{1}{2\sigma^2} \left(\ln C_t - \mu \right)^2 \right]$$

onde $\mu = \ln E(C_t) - \frac{\sigma^2}{2}$, *n* é o tamanho da amostra, C_t é a captura observada no ano *t*, $E(C_t)$ é a captura esperada para o ano *t* dada a equação 3, e σ^2 é o parâmetro de variabilidade que assumido ser conhecido e igual a 0.4 (Vasconcellos & Cochrane 2005).

As distribuições a priori para os parâmetros a e x foram assumidas como $a \sim Uniform(0,1)$ e $x \sim Uniform(0.000001,1)$. Para *K* foi assumido uma distribuição uniforme no espaço logarítmico, onde os limites inferior e superior foram delimitados pela captura máxima observada e 100 vezes esta captura máxima, respectivamente: $Ln(K) \sim Uniforme\left(ln(captura\ máxima), ln(100 captura\ máxima)\right)$. Para a distribuição a priori de *r*, foi assumida uma distribuição uniforme, com os limites inferior e superior definidos pela resiliência da espécie. A resiliência de cada espécie foi determinada de acordo com as categorias apresentadas no FishBase (Froese & Pauly 2016; Tabela 1).

Tabela 1. Intervalos inferior e superior para a distribuição a priori de *r*, conforme a resiliência da espécie (resiliência obtida no FishBase; intervalos para cada categoria da resiliência foram retirados de Froese *et al*. 2016).

Resiliência	**Intervalos superior e inferior**
Muito baixa (*Z. jahu*)	$0.015, 0.1$
Baixa (*P. pirinampu* e *P. corruscans*)	$0.05, 0.5$
Média (*P. lineatus*, *P. granulosus*, *P. squamosissimus*, *H. edentatus*, *S. brasiliensis*)	$0.2, 1$

A função de importância foi definida como sendo igual à função priori conjunta, e assim, a razão de importância foi igual à verossimilhança. Foi considerado um total de 500.000 vetores amostrados randomicamente da distribuição a priori conjunta, e deles, 5.000 amostras foram retiradas com reposição e probabilidade proporcional a razão de importância. Para verificar se a amostra de parâmetros foi obtida de uma função de importância similar à distribuição posterior, foram consideradas as seguintes medidas: (i) a densidade máxima (*maximum single density*, MSD) foi menor que 1%, o que significa que a re-amostragem foi realizada até que nenhum vetor fosse designado mais que 1% da distribuição de probabilidade a posterior (Punt & Hilborn 1997); e (ii) a entropia relativa à uniformidade (ERU), que descreve o grau de proximidade entre a função de importância e a distribuição a posterior; quanto mais próximo de 1 o valor de ERU for, mais próximas elas estão (Kinas 1996). O código para rodar o modelo foi escrito por Minte-Vera (Rosenberg *et al*. 2014), e está disponível em Rosenberg *et al*. (2014). Para avaliar o ajuste do modelo, foi realizada uma "*posterior predictive check*". Para tanto, dados de captura foram simulados a partir de uma distribuição lognormal, com esperança igual à captura estimada, e desvio padrão igual ao assumido no modelo, de 0.4. Os dados simulados foram comparados com a captura observada, e se o intervalo de credibilidade de 95% continha os dados observados, o ajuste foi considerado adequado. Para investigar a sensibilidade dos resultados em relação às distribuições a priori assumidas para r e K, foram analisadas diferentes combinações de distribuições a priori para estes parâmetros: distribuição normal para r e uniforme no espaço logarítmico para K (DP1; o valor médio entre os valores da resiliência foi assumido como média e desvio padrão considerando o coeficiente de variação assumido no modelo: 0.4); distribuição normal para r e uniforme para K (DP2); distribuição uniforme para r e para K (DP3). A distribuição a priori *default* é distribuição uniforme para r e uniforme no espaço logarítmico para K. Somente diferentes distribuições de probabilidade foram testadas, os valores dos parâmetros destas distribuições foram os mesmos, conforme a tabela 1. Os resultados para r, K e MSY obtidos com as diferentes distribuições a priori foram apresentados em relação aos valores obtidos com a distribuição priori default (distribuição uniforme para r e distribuição uniforme no espaço logarítmico para K).

Foram aplicados indicadores baseados no comprimento, formulados por Froese (2004), para avaliar a estrutura das populações exploradas na pesca de Itaipu. O indicador Pmat mede a proporção de indivíduos maduros no desembarque, ou seja, a fração da captura que é maior que o tamanho de primeira maturação (Lm). O objetivo é permitir que todos os indivíduos se reproduzam antes de serem capturados pela pesca. O indicador Popt mede a proporção de indivíduos capturados que possuam comprimento entre $0.9Lopt$ e $1.1Lopt$, onde $Lopt$ é o comprimento ótimo, sendo obtido com a seguinte equação proposta por Beverton (1992):

$$Lopt = \frac{3L_{\infty}}{3 + (M/k)}$$

onde L_{∞} é o comprimento assintótico, e k é a taxa de crescimento, ambos obtidos com a curva de crescimento de von Bertallanfy; M é a mortalidade natural obtida com a equação proposta por Then *et al*. (2015):

$$M = 4.118(k^{0.73})(L_{\infty}^{-0.333})$$

O indicador Pmega mede a proporção de indivíduos maiores e mais velhos nas capturas, ou seja, os indivíduos maiores que $1.1Lopt$. Os anos com amostras menores que 10 não foram analisados. Os parâmetros de história de vida das espécies analisadas foram retirados da bibliografia, e quando não havia informação disponível, as equações de Froese e Binohlan (2002) foram utilizadas (Tabela 2).

Tabela 2. Parâmetros de história de vida das espécies analisadas. TM: tamanho mínimo de captura (em centímetros), de acordo com a IN n^{o} 26/2009 Ibama. *registro de normativa apenas para o gênero *Hypophthalmus* para as bacias do rio Araguaia e Tocantins (Dias Neto & Dias 2015). k e $\boldsymbol{L_{\infty}}$ correspondem a taxa de crescimento e ao comprimento assintótico, ambos provenientes do modelo de von Bertalanffy. Lm é o tamanho de primeira maturação.

Espécie	**TM**	$\boldsymbol{k}$	$\boldsymbol{L_{\infty}}$	**Lm**	**Fonte**
P. lineatus	38	0.23	63.95	23	A
P. granulosus	40	0.135	56.8	31.4	B
P. squamosissimus	25	0.17	78.75	26	C
H. edentatus	29*	0.2	61.15	26	D
S. brasiliensis	60	0.27	80.42	42.9	E
P. pirinampu	50	0.22	72.9	40	F
P. corruscans	90	0.17	164.3	81.5	G
Z. jahu	90	0.29	149.3	74.8	H

A k, $\boldsymbol{L_{\infty}}$, $\boldsymbol{L_m}$: Santana (2014); **B** k e $\boldsymbol{L_{\infty}}$: Feitoza *et al.* (2008); $\boldsymbol{L_m}$: Okada *et al.* 2012; **C** k e $\boldsymbol{L_{\infty}}$: Castro (1998); $\boldsymbol{L_m}$: Okada *et al.* (2012); **D** k e $\boldsymbol{L_{\infty}}$: Ambrósio *et al.* (2003); $\boldsymbol{L_m}$: Okada *et al.* 2012; **E** k e $\boldsymbol{L_{\infty}}$: Feitosa *et al.* 2004; $\boldsymbol{L_m}$: Froese e Binohlan (2002); **F** k: Angelini e Agostinho (2005); $\boldsymbol{L_{\infty}}$: Froese e Binohlan (2002); $\boldsymbol{L_m}$: Okada *et al.* (2012); **G** k: Angelini e Agostinho (2005); $\boldsymbol{L_{\infty}}$ e $\boldsymbol{L_m}$: Froese e Binohlan (2002); **H** k: Angelini e Agostinho (2005); $\boldsymbol{L_{\infty}}$ e $\boldsymbol{L_m}$: Froese e Binohlan (2002).

A mortalidade total (Z) foi estimada com a equação de Beverton-Holt (Quinn & Deriso 1999), implementada na função bheq, do pacote fishmethods (Nelson 2016), no software R (R Core Team 2016):

$$Z = \frac{k(L_{\infty} - \bar{L})}{(\bar{L} - L_c)}$$

Os parâmetros da equação são comprimento assintótico (L_{∞}) e o coeficiente de crescimento (k), ambos provenientes do modelo de crescimento de von Bertalanffy, e o comprimento de primeira captura (L_c), e o comprimento médio dos dados de captura ($\bar{L}$). O comprimento de primeira captura foi obtido como a moda dos valores de comprimento. A mortalidade por pesca (F) pode ser estimada subtraindo-se a mortalidade natural da mortalidade total. Considera-se que um estoque esteja experimentando sobrepesca, quando F é maior que M (Babcock *et al*. 2013).

3.3 RESULTADOS

O diagnóstico de convergência da distribuição posterior evidenciou convergência das distribuições, com valores de MSD menores do que um, e pesos próximos a um (Tabela 3). O modelo estimou valores de captura próximos dos valores observados para a maioria das espécies (Figura 2 e Figura S1 no material suplementar).

Tabela 3. Diagnóstico de convergência usado no método COM-SIR.

Espécie	**MSD**	**ERU**
Prochilodus lineatus	0.32	0.92
Pterodoras granulosus	0.18	0.94
Plagioscion squamosissimus	0.42	0.96
Hypophthalmus edentatus	0.54	0.96
Salminus brasiliensis	0.22	0.96
Pinirampus pirinampu	0.08	0.95
Pseudoplatystoma corruscans	0.37	0.95
Zungaro jahu	0.20	0.96

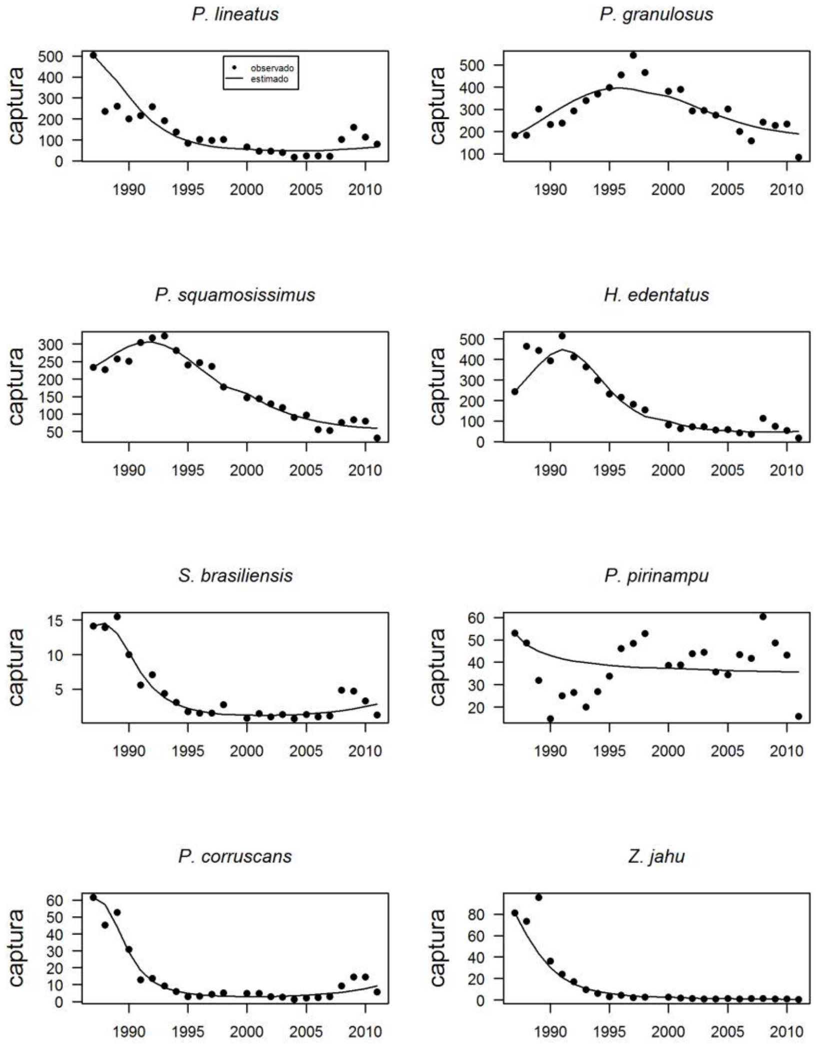


Figura 2. Captura observada (pontos) e estimada (linha sólida) pelo método COM-SIR.

A análise de sensibilidade evidenciou que as estimativas dos parâmetros para *P. granulosus* e *P. squamosissimus*, foram os mais sensíveis à escolha da distribuição a priori utilizada (Figura 3). Os modelos com distribuições a priori diferentes da distribuição a priori *default* não convergiram para *P. lineatus*, enquanto que para *H. edentatus* somente a distribuição a priori DP1 convergiu (ver tabela S1 no material suplementar). As razões entre os parâmetros estimados entre as distribuições a priori default e DP1 para *H. edentatus* foram 0.80, 1.14, e 0.92 para *r*, *K* e MSY, respectivamente.

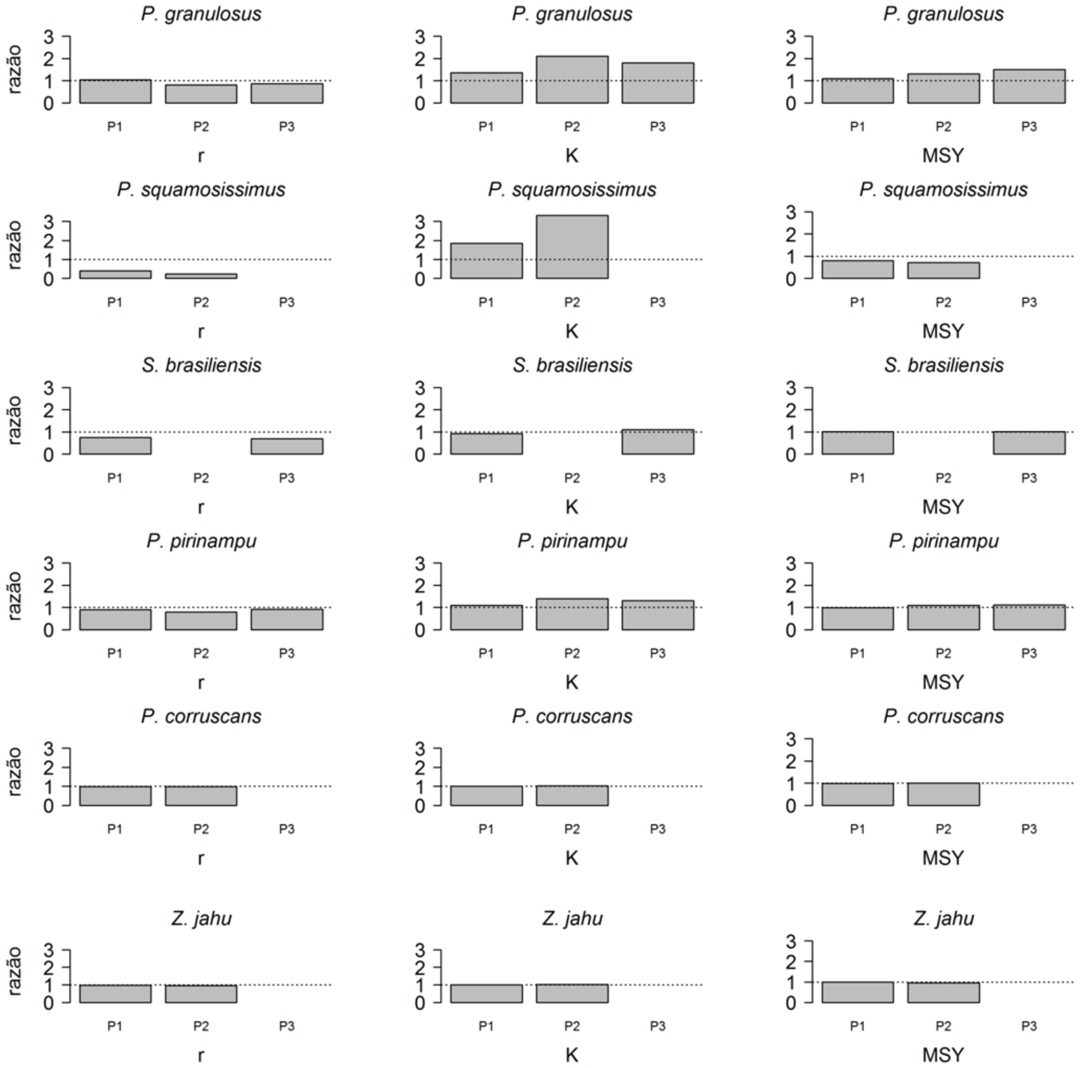


Figura 3. Razão entre as estimativas obtidas utilizando diferentes distribuições a priori. As barras ausentes são para modelos que não convergiram. Razão entre os valores obtidos com as distribuições a priori *default* e as combinações de distribuições a priori DP1 (razão P1), DP2 (razão P2), e DP3 (razão P3). Priori *default*: distribuição uniforme para *r* e uniforme no espaço logarítmico para *K*; DP1: distribuição normal para *r* e uniforme no espaço logarítmico para *K*; DP2: distribuição normal para *r* e uniforme para *K*; DP3: distribuição uniforme para *r* e para *K*.

A captura esteve acima de MSY nos primeiros anos da série temporal, para a maioria das espécies (Fig. 4, Tabela 4). Somente para *P. pirinampu* a captura esteve acima de MSY, durante alguns poucos anos.

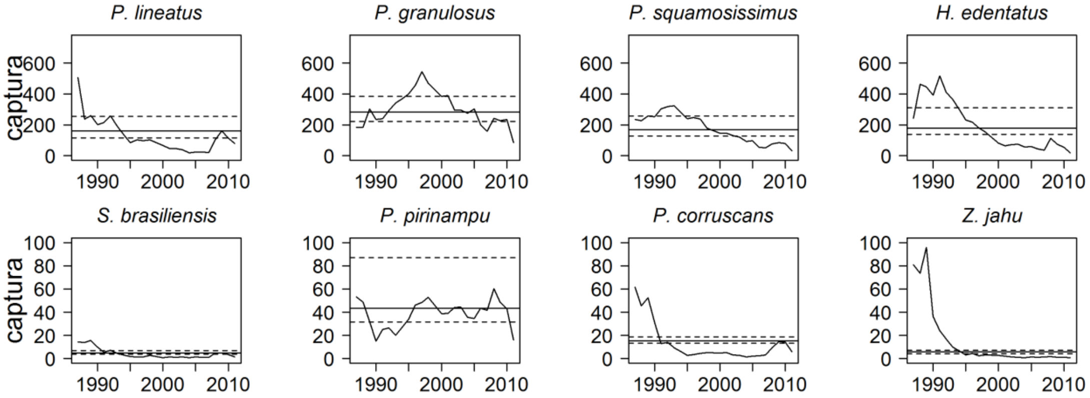


Figura 4. Captura (em toneladas) e MSY estimado pelo COM-SIR para os estoques pesqueiros do reservatório de Itaipu. As linhas contínua e tracejada representam a mediana e o intervalo de credibilidade de 95%, respectivamente.

A biomassa estimada pelo método COM-SIR apresentou amplos intervalos de credibilidade, principalmente para as estimativas nos anos finais da série temporal (Fig. 5, Tabela 4). Considerando o último ano de dados disponíveis (2011), os estoques de *P. granulosus*, *P. squamosissimus*, *H. edentatus* e *Z. jahu* estão com biomassa abaixo do limite (*overfished*; $B_{2011}/B_{MSY} < 0.5$).

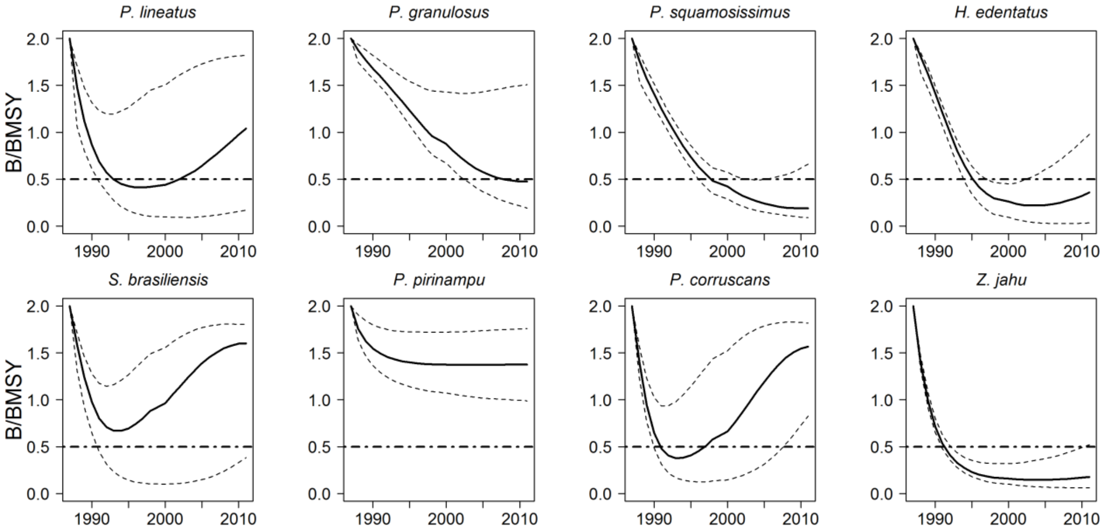


Figura 5. Biomassa em relação à B_{MSY} estimadas pelo método COM-SIR para os estoques pesqueiros do reservatório de Itaipu. As linhas contínua e tracejada representam a mediana e o intervalo de credibilidade de 95%, respectivamente. A linha ponto-tracejada representa o ponto de referência limite para o estoque estar sobrepescado ($B_t/B_{MSY} < 0.5$: *overfished*).

As espécies explotadas no reservatório de Itaipu mostraram diferentes tendências de mortalidade por pesca em relação à F_{MSY} (Fig. 6, Tabela 4). Para os estoques de *P. lineatus*, *S.brasiliensis*, *P. corruscans* e *Z. jahu* houve mortalidade por pesca maior que F_{MSY} (*overfishing was occuring*) nos primeiros anos da série temporal, com uma redução ao longo dos anos. Em contrapartida, o padrão inverso foi observado para *P. granulosus*, *P. squamosissimus* e *H. edentatus*. *Pinirampus pirinampu* foi a única que não experimentou *overfishing* durante 1987 e 2011.

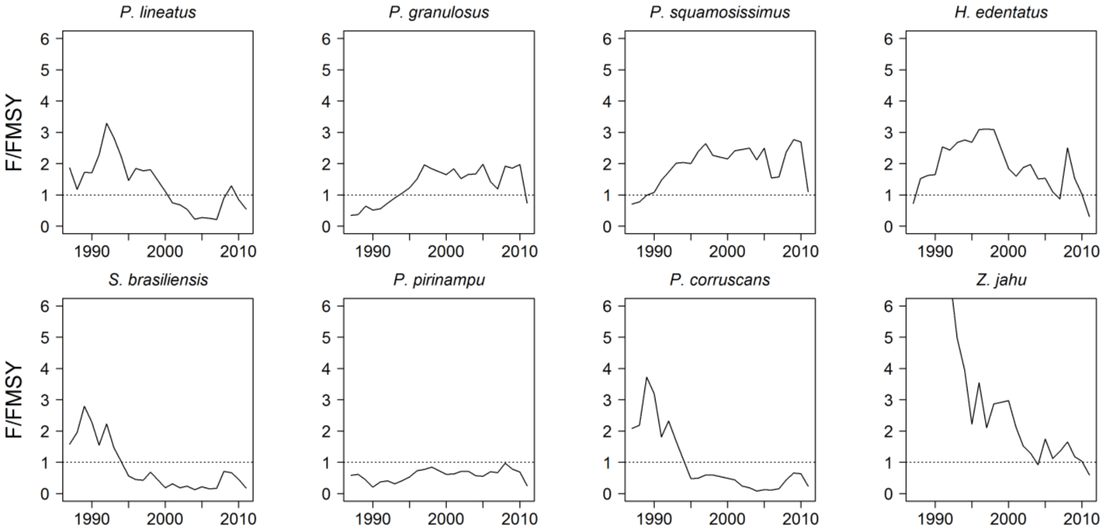


Figura 6. Mortalidade por pesca relativa à F_{MSY}, estimadas método COM-SIR para os estoques pesqueiros do reservatório de Itaipu.

Tabela 4. Estimativas dos parâmetros e dos pontos de referência para os estoques pesqueiros do reservatório de Itaipu.

Espécie/Parâmetro	***r***	***K***	**MSY**	**B_{MSY}**	**F_{MSY}**
P. lineatus	0.279 (0.21-0.86)	1936 (1072-3396)	161 (114-255)	968 (536-1698)	0.139 (0.106-0.432)
P. granulosus	0.369 (0.208-0.898)	2904 (1441-5972)	283 (221-383)	1452 (720-2986)	0.184 (0.102-0.449)
P. squamosissimus	0.341 (0.207-0.933)	1955 (1021-2803)	168 (128-256)	978 (510-1402)	0.170 (0.103-0.467)
H. edentatus	0.262 (0.204-0.916)	2570 (1356-3351)	179 (137-311)	1285 (678-1676)	0.131 (0.102-0.458)
S. brasiliensis	0.262 (0.220-0.691)	68.5 (41-98)	4.76 (3.82-6.68)	34 (20.5-48.8)	0.131 (0.110-0.346)
P. pirinampu	0.412 (0.209-0.493)	436 (292-1133)	43.3 (31.5-87.2)	218 (146-567)	0.206 (0.104-0.246)
P. corruscans	0.290 (0.25-0.385)	205 (164-269)	15 (13-19)	102 (82-135)	0.145 (0.125-0.192)
Z. jahu	0.088 (0.057-0.099)	271 (243-311)	5.8 (4-7.2)	135 (121-155)	0.044 (0.028-0.049)

A análise conjunta do nível de biomassa e da mortalidade por pesca, para o ano de 2011, revelou que as espécies com maior probabilidade de estarem com biomassa abaixo de B_{MSY} e mortalidade acima de F_{MSY} são *P. squamosissimus*, *P. lineatus* e *Z. jahu* (Fig. 7). Em contrapartida, os estoques de *S. brasiliensis*, *P. pirinampu* e *P. corruscans* apresentaram alta probabilidade de estarem em boas condições.

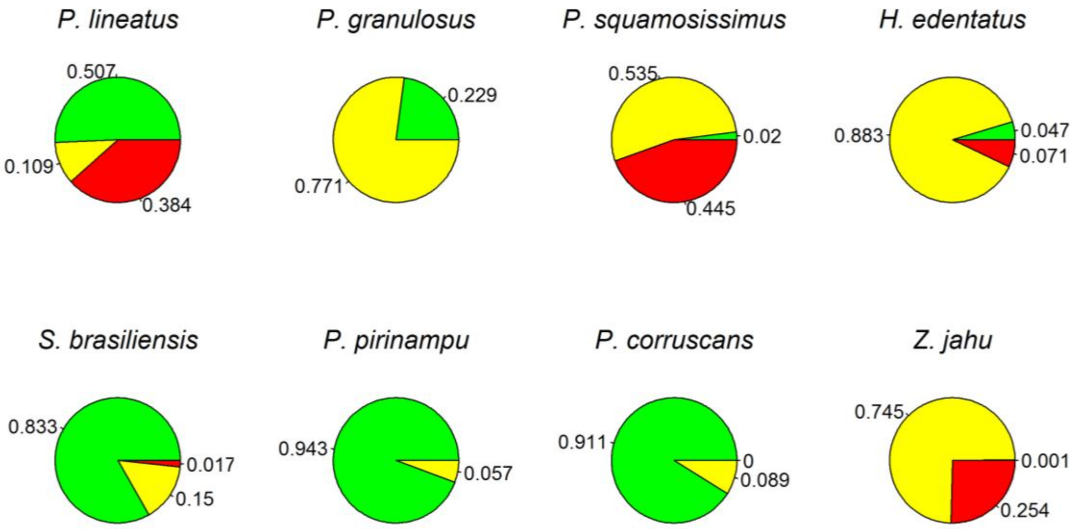


Figura 7. *Status* atual (2011) dos estoques pesqueiros do reservatório de Itaipu, com as respectivas probabilidades: $P((B_{2011}/B_{MSY} > 1)$ & $(F_{2011}/F_{MSY} < 1))$ = verde; $P((B_{2011}/B_{MSY} > 1)$ & $(F_{2011}/F_{MSY} > 1))$ = laranja; $P((B_{2011}/B_{MSY} < 1)$ & $(F_{2011}/F_{MSY} < 1))$ = amarelo; $P((B_{2011}/B_{MSY} < 1)$ & $(F_{2011}/F_{MSY} > 1))$ = vermelho. $B_{2011}/B_{MSY} > 1$= não está sobrepescado (*not overfished*), e $F_{2011}/F_{MSY} < 1$= sobrepresca não está acontecendo (*overfishing is not occuring*).

Os indicadores baseados no tamanho indicaram que a pesca no reservatório de Itaipu é responsável por capturar, predominantemente, indivíduos que não atingiram o comprimento de primeira maturação e abaixo do comprimento ótimo de cada espécie (Fig. 8). A única espécie que apresentou maior proporção de indivíduos maiores e mais velhos (Pmega) no desembarque, durante a maioria da série temporal analisada foi *P. lineatus* (Fig. 8). Somente a pesca de *H. edentatus* e *P. lineatus* apresentou proporção de indivíduos maduros (Pmat) próxima de um nos desembarques. Foi observado um aumento na proporção de indivíduos capturados com comprimento ótimo a partir de 2001 para *H. edentatus*, enquanto que para *P. lineatus* houve diminuição. Os estoques de *S. brasiliensis*, *P. pirinampu*, *P. corruscans*, e *Z. jahu* foram capturados abaixo do tamanho de primeira maturação (Fig. 9).

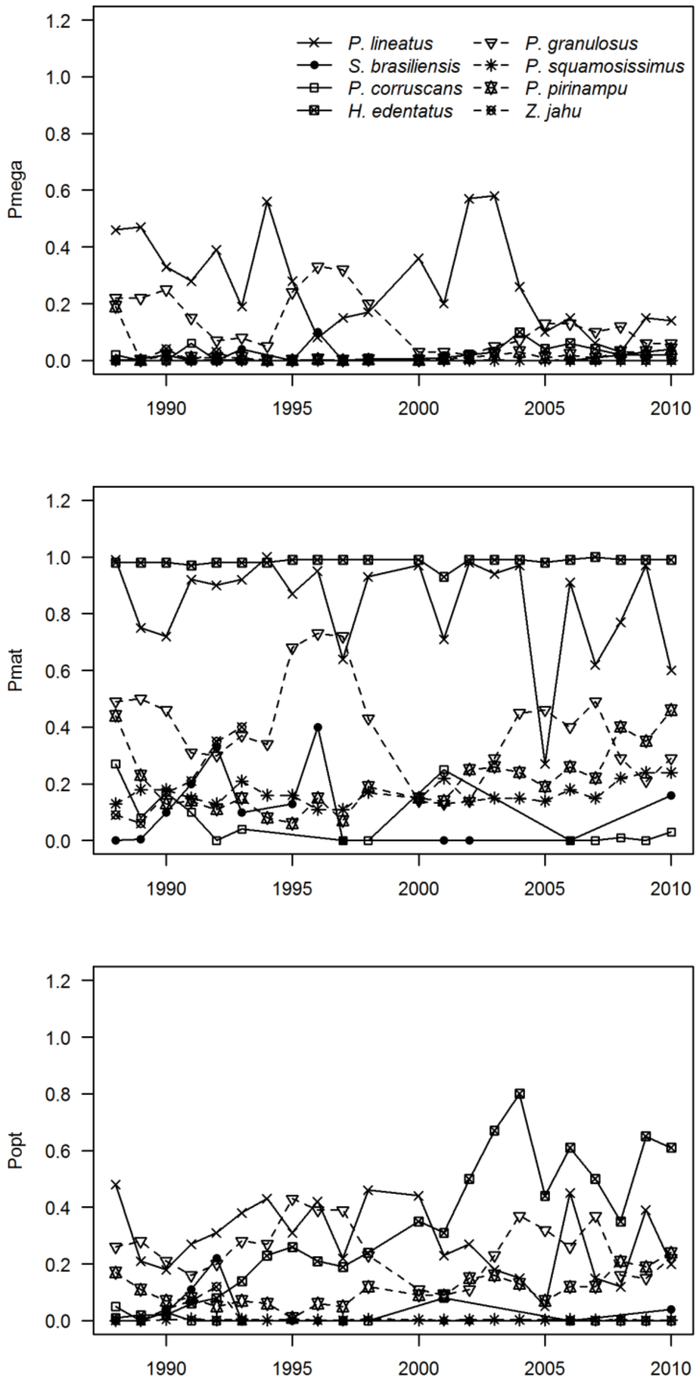


Figura 8. Indicadores baseados no tamanho (Froese 2004) para as espécies analisadas do reservatório de Itaipu. Pmega: proporção de indivíduos capturados maiores que 1.1Lopt; Pmat: proporção de indivíduos capturados maiores que o tamanho de primeira maturação; Popt: proporção de indivíduos capturados com tamanho entre 0.9 de Lopt e 1.1 de Lopt.

As estimativas de mortalidade obtidas usando os dados de comprimento evidenciaram que a mortalidade por pesca excede a mortalidade natural, para todas as espécies analisadas, exceto para *P. granulosus* (Tabela 5).

Tabela 5. Estimativas de tamanho ótimo ($Lopt$, em centímetros), mortalidade natural (M) e total (Z), e razão entre mortalidade por pesca e mortalidade natural (F/M).

Espécie/Parâmetro	$Lopt$	**M**	**Z**	**F/M**
P. lineatus	42.32	0.35	0.85	1.41
P. granulosus	35.19	0.25	0.41	0.65
P. squamosissimus	52	0.26	1.31	4.03
H. edentatus	39.74	0.32	1.45	3.49
S. brasiliensis	55.33	0.37	1.65	3.49
P. pirinampu	48.75	0.33	0.78	1.39
P. corruscans	116.93	0.21	1.10	4.32
Z. jahu	109.62	0.31	0.86	1.73

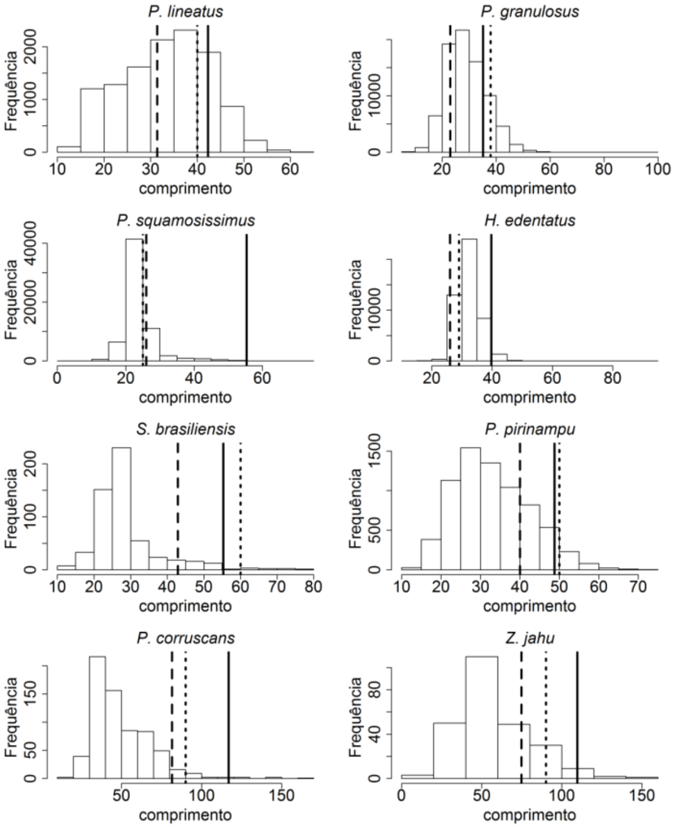


Figura 9. Histograma dos dados de comprimento (centímetros) das espécies analisadas. As linhas verticais sólida, pontilhada e tracejada representam o comprimento ótimo ($Lopt$), o tamanho mínimo de captura (TM), e o tamanho de primeira maturação (Lm), respectivamente, para as espécies do reservatório de Itaipu.

3.4 DISCUSSÃO

Embasar medidas de gestão com conhecimento científico, em pescarias que não possuem programas de monitoramento, e ausência de informações biológicas sobre as espécies exploradas é um dos desafios atuais na ciência pesqueira. Diferentes métodos e estratégias têm sido discutidos e investigados, e neste trabalho foram adotados dois métodos que usam tipos diferentes de dados, permitindo uma avaliação complementar da situação dos estoques pesqueiros explorados no reservatório de Itaipu.

Considerando o método COM-SIR, a análise de sensibilidade evidenciou que os dados de captura das espécies *S. brasiliensis*, *P. pirinampu*, *P. corruscans*, e *Z. jahu*, foram informativos, uma vez que os valores estimados para os parâmetros de interesse não variaram muito, com as diferentes distribuições a priori assumidas (McAllister & Kirkwood 1998). Já as estimativas de *P. granulosus* e *P. squamosissimus* variaram em maior grau, dependendo da distribuição a priori assumida. Além disso, modelos com diferentes distribuições a priori não convergiram para *P. lineatus* e *H. edentatus*. O uso da abordagem Bayesiana têm auxiliado nos casos conhecidos como limitados em dados. Esta abordagem permite a inclusão de conhecimento a priori, sendo possível avaliar a plausibilidade dos dados e a influência da informação a priori nas estimativas dos parâmetros de interesse (Punt & Hilborn 1997; McAllister & Kirkwood 1998). Para as espécies que tiveram as estimativas dos parâmetros influenciadas fortemente pela distribuição a priori assumida, é preciso mais cautela ao adotar estes valores para embasar as medidas de gestão.

Os indicadores baseados no comprimento mostraram que a explotação dos estoques analisados não atende as sugestões de sustentabilidade propostas por Froese (2004). Já as estimativas obtidas com o método COM-SIR evidenciaram que os estoques que não sofreram mortalidade por pesca maior que F_{MSY} nos últimos anos, apresentaram biomassa acima dos níveis sugeridos (*P. lineatus*, *S. brasiliensis*, *P. pirinampu*, e *P. corruscans*).

Embora os dados de captura (método COM-SIR) tenham indicado que estes estoques estejam em boas condições, os indicadores de comprimento mostraram que a maior parte da captura foi composta por indivíduos com comprimento abaixo do tamanho de primeira maturação (Lm), para *S. brasiliensis*, *P. pirinampu*, e *P. corruscans*, o que pode causar sobrepesca de recrutamento. Considerando a discrepância nos resultados, e a alta incerteza nas estimativas de biomassa (amplos intervalos de credibilidade), o aumento de esforço de pesca deve ser cauteloso para estes estoques, enquanto que a diminuição da captura de jovens deve ser uma medida urgente.

Não é fácil distinguir os efeitos ambientais dos efeitos da pesca sobre as populações de peixes. Embora as populações de grandes migradores tenham sofrido consideráveis impactos negativos devido à construção da usina hidrelétrica de Itaipu (Agostinho *et al*. 2008, Hoeinghaus *et al*. 2009), os resultados obtidos com os dois métodos evidenciaram que a pressão pesqueira também foi acentuada sobre elas. As estimativas de mortalidade por pesca, obtidas com dados de comprimento (razão F/M), estiveram de acordo com as mortalidades por pesca estimadas com o método COM-SIR. Foi possível observar diferentes tendências temporais de mortalidade por pesca estimada entre as espécies explotadas. Os estoques de grandes migradores sofreram altos níveis de mortalidade por pesca nos primeiros anos de exploração, enquanto que a mortalidade por pesca sobre os estoques de *P. granulosus*, *P. squamosissimus* e *H. edentatus* aumentou a partir de 1990. Este padrão é mais uma evidência da mudança que ocorreu nas espécies alvo da pesca após a formação do reservatório de Itaipu, relatada por pescadores e constatada por alguns trabalhos científicos (Hoeinghaus *et al*. 2009, Philippsen *et al*. 2016).

Os estoques que apresentaram os piores *status* foram *P. squamosissimus* e *Z. jahu*. Para ambos a mortalidade por pesca estimada esteve acima de F_{MSY}, ao longo de toda a série temporal, como também níveis de biomassa abaixo do recomendado ($Bt/B_{MSY} < 0.5$). Além disso, a proporção de indivíduos capturados abaixo do tamanho de primeira maturação foi muito alta. Medidas de gestão devem priorizar ações para proteger estes estoques urgentemente.

O princípio de proteger indivíduos jovens de serem capturados é antigo, e tem como objetivo prevenir o sobrepesca de recrutamento (Vasilakopoulos *et al*. 2011). Ainda, populações com elevada abundância de indivíduos maiores e mais velhos, são mais estáveis e menos suscetíveis ao excesso de explotação (Hixon *et al*. 2014). Nesse sentido, a adoção de medidas que limitem o tamanho mínimo e o tamanho máximo de captura (*harvest slots*), pode aumentar a probabilidade de conservar as populações (Gwinn *et al*. 2015).

A adoção de análises que são alimentadas com diferentes tipos de dados, como as adotadas neste estudo, por exemplo, permitiu concluir que a mortalidade por pesca é alta para a maioria dos estoques no reservatório de Itaipu. Estes resultados são corroborados por outra abordagem, a percepção dos pescadores, que também revelou diminuição da captura das espécies exploradas pela pesca (Philippsen *et al*. 2016). Além disso, os pescadores entrevistados citaram que entre as causas para a diminuição dos estoques estão a ausência de fiscalização e o uso de malhas que capturam juvenis.

Simulações com os indicadores de Froese (2004) sugerem que se somente indivíduos maduros são capturados, mas não no comprimento ótimo (indicador Popt), a melhor estratégia seria capturar indivíduos próximos de Lopt (Cope & Punt 2009). Este cenário parece ser o caso da pesca de *H. edentatus*, que captura praticamente 100% de indivíduos maiores que Lm, mas muito abaixo de Lopt. Ainda, o modelo baseado em capturas mostrou que a biomassa deste estoque está abaixo do recomendado. Portanto, concentrar as capturas em Lopt pode ser uma estratégia para aumentar a biomassa do estoque. Uma outra alternativa para tentar reestabelecer níveis sustentáveis de biomassa para esta espécie, seria reduzir o esforço de pesca.

Dados de comprimento são relativamente fáceis de serem obtidos, portanto, métodos baseados neste tipo de dados podem ser mais adequados para avaliar pescarias limitadas em dados (Prince *et al*. 2015). Os indicadores de Froese fornecem somente uma avaliação superficial da composição de tamanhos vulnerável a pesca, porém não seja possível acessar o estado de um estoque em relação a pontos de referência (Cope & Punt 2009). Recentemente, foi desenvolvido um método para inferir a razão F/M e o potencial desovante (*spawning potential ratio*) de determinado estoque, utilizando dados de comprimento e parâmetros de história de vida (Hordyk *et al*. 2015). Este método parece ser uma boa opção para avaliar futuramente os estoques pesqueiros do reservatório de Itaipu, que possuem dados disponíveis para tal avaliação. Com estes resultados, será possível avaliar se os dados de captura e comprimento estão “contando a mesma história” sobre os estados destes estoques.

Os dois métodos empregados neste estudo possuem pressupostos que nem sempre são atendidos e podem enviesar as estimativas obtidas (Cope & Punt 2009, Rosenberg *et al*. 2014). Ainda que resultados discrepantes tenham sido obtidos em relação à sustentabilidade dos estoques, dependendo do método utilizado, a abordagem adotada neste estudo permitiu avaliar a situação dos estoques pesqueiros sob diferentes aspectos. As principais sugestões de medidas de gestão baseadas nos resultados encontrados neste estudo são: (i) implementar um tamanho máximo de captura para proteger os indivíduos maiores e mais velhos; (ii) estabelecer um tamanho mínimo de captura para *H. edentatus* (35 cm); (iii) aumentar o tamanho mínimo de captura de *P. squamosissimus* (35 cm); (iv) aumentar a fiscalização para impedir a captura de indivíduos abaixo do tamanho permitido; (v) investigar o uso de buffers para contabilizar as incertezas envolvidas com as estimativas obtidas com métodos limitados em dados, como é feito por exemplo, na pesca do Pacífico nos Estados Unidos (Wetzel & Punt 2015).

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Jr., M., Zarfl, C., Mulligan, M., Sullivan, J. P., Arantes, C. C.; Sousa, L. M., Koning, A. A., Hoeinghaus, D. J., Sabaj, M., Lundberg, J. G.; Armbruster, J.; Thieme, M. L.; Petry, P., Zuanon, J., Torrente Vilara, G., Snoeks, J., Ou, C., Rainboth, W., Pavanelli, C. S., Akama, A., van Soesbergen, A., Sáenz, L. 2016. Balancing hydropower and biodiversity in the Amazon, Congo, and Mekong. **Science**, 351: 128-129.

APÊNDICE B – Avaliação dos estoques pesqueiros do reservatório de Itaipu: modelo baseado em capturas e indicadores baseados no tamanho

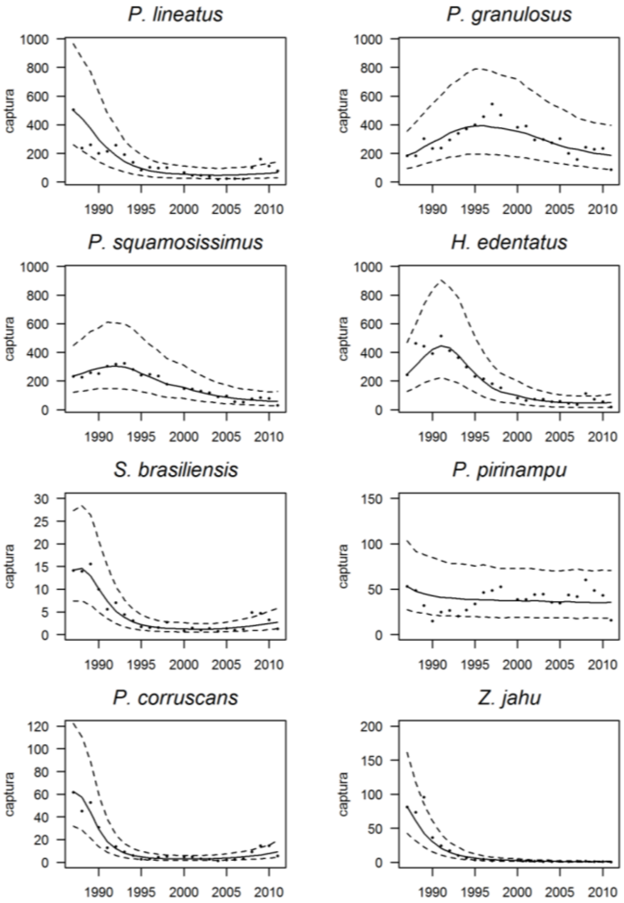
P. lineatus
P. granulosus
P. squamosissimus
H. edentatus
S. brasiliensis
P. pirinampu
P. corruscans
Z. jahu

Figura S1. *Posterior predictive checking* para os dados de captura obtidos com o método COM-SIR. As linhas sólida e pontilhada representam a mediana e o intervalo de credibilidade de 95%. Os pontos representam a captura observada. Note que os intervalos do eixo vertical são diferentes.

Tabela S1. Diagnóstico de convergência para as diferentes distribuições a priori assumidas. Priori *default*: distribuição uniforme para *r* e uniforme no espaço logarítmico para *K*; DP1: distribuição normal para *r* e uniforme no espaço logarítmico para *K*; DP2: distribuição normal para *r* e uniforme para *K*; DP3: distribuição uniforme para *r* e para *K*.

	DP1		**DP2**		**DP3**	
	MSD	**Entropia**	**MSD**	**Entropia**	**MSD**	**Entropia**
P. lineatus	1.600	0.884	2.660	0.906	3.560	0.867
P. granulosus	0.060	0.954	0.080	0.962	0.080	0.962
P. squamosissimus	0.280	0.966	0.360	0.962	1.260	0.960
H. edentatus	0.460	0.961	1.820	0.960	1.860	0.962
S. brasiliensis	0.380	0.960	1.300	0.960	0.860	0.962
P. pirinampu	0.100	0.947	0.100	0.926	0.120	0.930
P. corruscans	0.220	0.951	0.920	0.947	1.220	0.952
Z. jahu	0.320	0.933	1.280	0.948	1.160	0.952

ANEXO B – Código do método COM-SIR (retirado de Rosenberg *et al.*, 2014)

```
################COM SIR ###########################################
#  Catch only model implemented by C.V.Minte-Vera
#  Version June 10, 2013                                   <><   <><
#  Vasconcellos and Cochrane 2005                 <><                         <><
#  Biomass dynamic (Schaefer) and harvest dynamic model (logistic)
#  assumed the initial harvest rate equals Catch first year / Biomass first year
#  Biomass first year = carrying capacity                                <><
#  lognormal likehood for catch data w/ observation error CV =0.4
#  Estimation using Bayesian Sampling Importance Resampling          <><
#  Joint prior is the important function, i.e. resampling proportional to the likelihood
#################   <><   <><   <><   ####################################

#  <>< #  COUNTER,  counter for stock = i
i <- 1

# <>< # Directories
# for Procedure
ProcDir="C:\\Users\\Juliana\\OneDrive\\doutorado\\Data-poor methods\\COM-SIR method\\"
# for Results
ResDir="C:\\Users\\Juliana\\OneDrive\\doutorado\\Data-poor methods\\COM-SIR method\\"
# for Data
MyDir="C:\\Users\\Juliana\\OneDrive\\doutorado\\Data-poor methods\\COM-SIR method\\"

#file with inputs data, the R object is called "input",it is a list
filename="jau.csv" #ju
input=read.csv(filename, header=T, dec=".") #já lê no formato list
is.list(input)

# <><  # SIR Controls
My.N.Sim= 5000000  # numbers of samples from the importance function
My.N.Post= 5000 # number of samples from the posterior (ressampling part)
My.seed= ceiling(runif(1,0,1e6))# random seed same procedure as ThorII
My.CV = 0.4 ## CV for observations - i.e. for Catch data

#  <>< #  PROCEDURE section
#load the functions needed for COM SIR
source("FunctionsCOM.R")
###
#  <>< #  DATA section
# stocks
#"input" is the name of the list with the input data
stocks_id=names(input) #stock names
StockName=stocks_id[i]
```

```
ct <- input$ct #ju
yr <- input$yr #ju
n <- length(yr)
MyData <- data.frame(catch=ct,year=yr) #ju
MyData
#  <>< # PRIORs section
# Prior for K  is ln(K) ~ U( ln(min.K), ln(max.K))
# bound follows Martell and Froese 2012
min.K=max(ct)
max.K=100*min.K

# Prior on r based on "resilience" following Froese 2012 Table 1
res <- "Very low"
res <- "Low"
res <- "Medium"
res <- "High"
#Resilience according to FishBase:
start_r  <- c(0.015, 0.1) #start_r for res == "Very low"
start_r  <- c(0.05,0.5) #res == "Low"
start_r <-  c(0.2,1) #res = Medium
start_r  <- c(0.6,1.5) #res == "High"

# <>< # RESULTS section
## Unquote if there is a need to create a directory for results
#ResultDir<- paste(ResDir,stock_id[i],"\\",sep="")
#dir.create(ResultDir,showWarnings = FALSE)
#setwd(ResultDir)

###My.Par is used when plots of the model are done, need it here because is passed as argument
#these values are used to compute the relative values from prior and posteriors
#plotted to see the gain in information from the inclusion of the data
My.Par<-c(800,800,0.6,1.0,0.8,0.5,0)
My.Par<-t(My.Par)
My.Par<-as.data.frame(My.Par)
names(My.Par)<-c( "N1",   "K",    "r",    "z",    "a",    "x",    "h")
Time=system.time(suppressWarnings(
  COM<-
DoProject(MyFile="teste",Myseed=My.seed,TruePar=My.Par,MyData=MyData,EstLogisticM=T,

LogisticModel=T,MyCV=My.CV,NormalL=F,Nsim=My.N.Sim,Npost=My.N.Post,logK=T,Norm
K=F,Normr=F,
              start.r=start_r,minK=min.K, maxK=max.K,MyYLim=c(-2,8),Obs=F)
))

Results= suppressWarnings(data.frame('stock_id'=
StockName,'b_bmsy'=apply(COM$BoverBmsy,MARGIN=1,FUN=median),
```

```
                              'b_bmsyUpper'
=apply(COM$BoverBmsy,MARGIN=1,FUN=quantile,prob=0.925),
                              'b_bmsyLower'=
apply(COM$BoverBmsy,MARGIN=1,FUN=quantile,prob=0.075),

'b_bmsy_iq25'=apply(COM$BoverBmsy,MARGIN=1,FUN=quantile,prob=0.25) ,

'b_bmsy_iq75'=apply(COM$BoverBmsy,MARGIN=1,FUN=quantile,prob=0.75),
                              'E'=apply(COM$E,MARGIN=1,FUN=median),
                              'E_Upper'=apply(COM$E,MARGIN=1,FUN=quantile,prob=0.925),
                              'E_Lower'=apply(COM$E,MARGIN=1,FUN=quantile,prob=0.075),
                              'E_iq25'=apply(COM$E,MARGIN=1,FUN=quantile,prob=0.25),
                              'E_iq75'=apply(COM$E,MARGIN=1,FUN=quantile,prob=0.75),
                              'year'=MyData[,2],

'seed'=My.seed,'convergence'=ifelse(COM$Diagno['ESS']>200,"Strong",ifelse(COM$Diagno['ES
S']>30,"Weak","Not")),'n_iterations'=My.N.Post,

'effective_sample_size'=COM$Diagno['ESS'],'run_time'=Time['elapsed'],'method_id'="COM.SIR
"))
```

4 FOOD-WEB MODELING APPROACH TO ASSESS THE STOCK STATUS OF A RESERVOIR FISHERY

Abstract

Ecological models are increasingly being adopted to evaluate alternative fisheries management scenarios. This study adopted an ecosystem modeling approach to address the possible impacts of fishing on the structure and functioning of a tropical reservoir (Itaipu reservoir). We found that fishing effects, along with predator-prey relationships, were the main factors that contributed to explain catch trends in Itaipu fishery. Catches and diversity declined significantly between 1988 and 2011, even though the rates of change were small. In contrast, the mean Trophic Level of Catch and the L index did not show any significant change along the same period, indicating that Itaipu fishery has been sustainable in terms of ecosystem effects. Simulations revealed that ecosystem and species are not greatly affected by increased fishing effort, although, simulations with fishing at F_{MSY}, resulted in biomass decline for species that are important for the fishery, and some of them have a key role in ecosystem structure, such as *Z. jahu*. In terms of management advice, our results indicated that fishing effort should not increase upon *P. lineatus*, *P. corruscans* and *Z. jahu*. The enforcement of the law to protect mainly *Z. jahu* is very advisable, because it was identified as a keystone species in Itaipu reservoir. The severe decline of this species will result not just in loss to fishery yields but also can impact the structure and functioning of the ecosystem. The same is true for *S. brasiliensis*, but this species seems to afford more fishing effort than is currently applied.

Keywords: ecological modeling, ecosystem-based management, inland fisheries, L index, maximum sustainable yield.

4.1 INTRODUCTION

Inland capture fisheries commonly are small-scale, spatially spread, involve a large number of artisanal or subsistence fishers, and their products are usually marketed and consumed locally (Welcomme 2011). Most tropical freshwater fisheries exploit many species of fishes, often with the same fishing gear (Smith *et al*. 2005). The global total capture fishery production from freshwater in 2014 was 11.9 million tonnes, representing about 13% of total catch (FAO 2016).

Although the small production and the reduced overall economic value compared to marine fisheries, inland capture fisheries play a vital social role, because they are the main source of income and protein for hundreds of rural households in remote areas (Smith *et al.* 2005; Bartley *et al*. 2015). The majority of the catch from inland capture fisheries comes from developing countries, where fishing is key to achieve food security and poverty alleviation (Cooke *et al*. 2016).

Fishing may harmfully impact not only the fish population being exploited, but also the ecosystem structure and function (Coll *et al*. 2016). Apart from fishing, freshwater systems are subject to several other impacts, such as invasion by non-native species, climate change and habitat alteration (Agostinho *et al*. 2016; Walsh *et al*. 2016). Fishing, in turn, may also be negatively impacted by habitat alteration and climate change. For example, dam construction is known to negatively affect the relative species composition and yield of inland fisheries. Furthermore, reservoirs impact in particular migratory species, which frequently are those with highest commercial value. Migratory species are affected in many ways by reservoirs, first because the dam is a physical barrier to migration, then because the reservoir decreases the suitable habitat for spawning, finally the natural mortality of larvae migrating downstream is increased: in the calmer water of the reservoir even the small minnow can predate larvae (Agostinho *et al*. 2008; Hoeinghaus *et al*. 2009).

Despite the sizable contribution inland fisheries make to society, the sector is often neglected in national and international agendas, and stock status of the majority of the inland fisheries is unknown (De Graaf *et al*. 2015; FAO 2016). Besides, when dealing with fisheries in reservoirs, water demands as hydropower production, usually take precedence over biodiversity conservation and fishery activities in policy priorities, especially in developing countries (Winemiller *et al*. 2016).

When it takes place, fishery management in reservoirs is usually done by the traditional way through either input or output controls (Arlinghaus *et al*. 2016; Agostinho *et al*. 2016). The main input regulations can be restrictions on fishing gears, access control and fishing seasons. The output controls may be limits on minimum size of fish and on catch per fisher. These controls may be insufficient to ensure population sizes that can sustain sizable production over time, for the majority of the target species. Fish species in reservoirs, usually need at least some degree of habitat connection with upstream rivers to complete reproduction. Large migratory species usually disappear or sharply decrease in abundance after a river impoundment, because the new habitat does not have the adequate lotic characteristics that they require to complete their life cycle (Agostinho *et al*. 2008). Some sedentary fish species spawn in the littoral zone, which may have wide and frequent water level fluctuations caused by the hydropower generation (Nagrodski *et al*. 2012). In this context, it is clear that fisheries management in reservoirs should be done along with habitat management (through dam operation), and should take into account the negative impact that water level oscillation has on recruitment of fish species (Arlinghaus *et al*. 2016; Oliveira *et al*. 2015).

Inland capture fisheries can be viewed as a coupled social-ecological system with dynamics that depend upon human behavior, societal norms and environmental quality (Beard *et al*. 2011). The ecosystem approach to fisheries (EAF) may be a way to implement sustainable development and management of inland fisheries, by addressing both human and ecological aspects (FAO 2003; Suuronen and Bartley 2014). The ecological dimension aims to conserve the ecosystem structure, diversity and functioning, meanwhile the societal and human objectives focus on attain food and livelihood. In this way, management actions under EAF try to balance these dimensions (Pikitch *et al*. 2004).

In regard to the ecological dimension, food web modeling can be adopted as a tool to understand ecological processes, and to investigate the fishing impacts on ecosystems (Angelini *et al*. 2013; Coll *et al*. 2016). The knowledge produced under this approach can inform and promote sound management and policy decisions, in regard of ecological aspects. Besides, ecosystem modeling can contextualize and be integrated to single-species management, by considering impacts on non-target species and on structural elements of the ecosystem, as well as the trophic interactions among species (Hilborn 2011; Collie *et al*. 2016; Gascuel *et al*. 2016).

This study adopted an ecosystem modeling approach to address the possible impacts of fishing on the structure and functioning of Itaipu Reservoir (Brazil). This commercial small-scale fishery has a fundamental role for providing livelihood and protein source for almost 700 fishers, with the majority of catch concentrated mainly in 10 species (Okada *et al*. 2012). Changes in catch composition, as well as catch decline after the construction of Itaipu reservoir, have affected negatively the income of these local fishers (Hoeinghaus *et al*. 2009). Moreover, low water level in the reservoir due to high demand of energy production, during the reproductive season of some target species, has been claimed by fishers to make the situation worse. Local fishery management have been done solely based on traditional strategies (input and output controls), and a more holistic approach such as EAF, may provide a comprehensive understanding of the effects of fishing on the ecosystem, providing knowledge to support future management decisions. In this way, we aimed to: (i) develop a new Ecopath model to Itaipu reservoir based on a previous model (Angelini *et al*. 2006), but now calibrating the model using a time series of landings and fishing effort; (ii) to assess the role of fishing on ecosystem structure, using ecological indicators, (iii) to perform simulations changing fishing effort and to estimate maximum sustainable yield (MSY), in an ecosystem context; and (iv) discuss ecosystem management for fishing activities in Itaipu reservoir.

4.2 METHODS

4.2.1 Study area and local fishery

The Itaipu reservoir was filled in 1982 and it is located on the Brazil-Paraguay border (Fig. 1), in the Upper Paraná River, a region that has a high concentration of hydroelectric dams (Agostinho *et al*. 2007). Itaipu Reservoir has a surface area of 1350 km^2, mean depth of 22 m and an average hydraulic retention time of approximately 40 days. The fishery composition had changed markedly after the impoundment: from large migratory species with high commercial value, to sedentary ones with lower values (Hoeinghaus *et al*. 2009). The main fishing gears used in Itaipu fisheries are gillnets and longlines (Okada *et al*. 2012). Itaipu Reservoir is connected upstream to an extensive floodplain, which is essential to maintain the abundance of reservoir fish populations, especially the migratory ones (Oliveira *et al*. 2015).

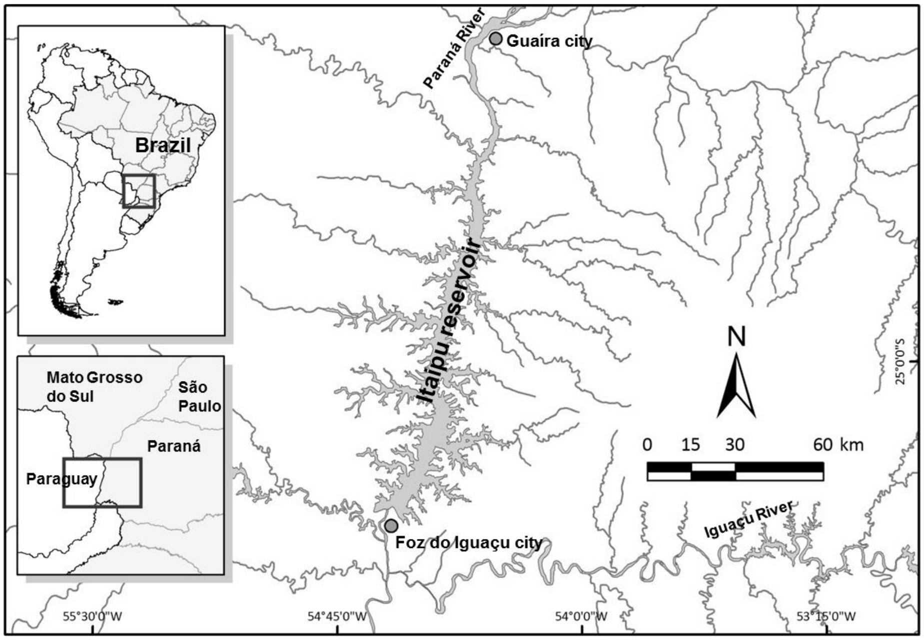

Fig. 1. Itaipu reservoir in the Brazil- Paraguay border.

4.2.2 Modeling approach and Itaipu reservoir food web model

The Ecopath model represents a static portray of an ecosystem, quantifying the energy flows among the functional groups included in the model. The Ecopath parameterization is based on the assumption of energy balance, in a given time period, being implemented by two main equations (Christensen and Walters 2004). The first equation describes the production of a functional group:

$$B_i \cdot \left(\frac{P}{B}\right)_i = \sum_j B_j \cdot \left(\frac{Q}{B}\right)_j \cdot DC_{ji} + \left(\frac{P}{B}\right)_i \cdot B_i \cdot (1 - EE_i) + Y_i + E_i + BA_i \quad \text{(Eq. 1)}$$

where $\left(\frac{P}{B}\right)_i$ is the production/biomass ratio of group (i), and B_i is its biomass, B_j is the biomass of predator (j), $\left(\frac{Q}{B}\right)_j$ is the consumption/biomass ratio of predator (j), and DC_{ji} is the fraction of prey (i) in the diet of predator (j); Y_i is the catch of functional group (i), E_i is the migration rate (emigration – immigration), BA_i is the biomass accumulation rate for group (i). Other types of mortality, or mortality that is not explained by the model, is represented by $(1 - EE_i)_i$, where EE_i is the ecotrophic efficiency of group (i), that means, is the proportion of annual productivity $\left(\frac{P}{B}\right)_i$ that is consumed in the ecosystem by predators and/or exported from the ecosystem by fishing. Under these mass balance conditions, it is assumed that the annual production/biomass ratio $\left(\frac{P}{B}\right)_i$ is equivalent to the total mortality (Z) (Allen 1971; Christensen *et al*. 2008).

The second equation describes the energy balance of each functional group(i), where its consumption $\left(\frac{Q}{B}\right)_i$, equals the production rate $\left(\frac{P}{B}\right)_i$, the non-assimilated food (UN_i) and respiration (R_i):

$$\left(\frac{Q}{B}\right)_i \cdot B_i = \left(\frac{P}{B}\right)_i \cdot B_i + R_i + UN_i \quad \text{(Eq. 2)}$$

The algorithm implemented in EwE solves a system of linear equations for each of the following parameters: B_i, $\left(\frac{P}{B}\right)_i$, $\left(\frac{Q}{B}\right)_i$ and EE_i. Usually the ecotrophic efficiency parameter is estimated by the EwE software, because it is very difficult to measure it in the nature (Christensen *et al*. 2008;

Heymans *et al*. 2016).

The food web model of Itaipu reservoir developed here is an updated version of the model constructed by Angelini *et al*. (2006), using the same software. The major modifications made were: (i) alteration of fish functional groups, to represent especially the main species in the landings; (ii) better Biomass (B) input estimates than available in Angelini *et al*. (2006; see below); (iii) P/B parameters estimates calculated from Beverton-Holt equilibrium estimator of instantaneous total mortality (Z) (Quinn and Deriso 1999), for fish functional groups that had length data available (since P/B corresponds to Z, according to Allen (1971) and Christensen *et al*. (2008)); (iv) revision of the diet matrix used in Angelini *et al*. (2006); (v) use of different gear types (see below); and, finally (vi) a calibration of the model in the Ecosim module using an annual time series of catches and fishing effort (from 1988 to 2011).

The Ecopath model of Itaipu reservoir represents the 1988 year and contains 31 functional groups, being 24 fish functional groups (18 are fishing target species), one group representing detritus and three primary producers: phytoplankton, periphyton and macrophytes (Table 1).

The biomass estimates for fish functional groups which had catch data available, were obtained from a catch-only model (COM-SIR), which uses the Schaefer biomass dynamic model (Vasconcellos and Cochrane 2005; Rosenberg *et al*. 2014). The input data necessary for the COM-SIR model is a times series of catch and, information about the resilience of the species, which was obtained for each species from FishBase (Froese and Pauly 2016). The biomass estimate for *A. lacustris* was taken from Angelini *et al*. (2006). The biomasses of fish species that are not predators, and did not have catch data available, were estimated by Ecopath model.

Production/Biomass ratio (P/B) for the fish functional groups that had length data available, were estimated as total mortality (Z), using the Beverton-Holt equilibrium estimator of instantaneous total mortality (Quinn and Deriso 1999) with bias-correction, as suggested by Ehrhardt and Ault (1992). This equation is implemented in the function bheq, from fishmethods package (Nelson 2016), in R software (R Core Team 2016). The parameters for this function are the asymptotic length, and the growth coefficient (both from the von Bertalanffy growth model), the length at first capture, and the largest length at the sample (to include a maximum size of capture). The majority of these parameters were obtained from literature (see Section 4 in Supplementary Material) and from empirical equations (Froese and Binohlan 2000). P/B ratio for the fish functional groups that did not have length data available were obtained from the literature (Angelini and Agostinho 2005; Gubiani *et al*. 2012): *Astyanax altiparanae*, *Roeboides descalvadensis*, *Moenkhausia intermedia*, *Steindachneria* spp., *Hoplosternum littorale*, *Gymnotus* spp.

The fishing fleets were considered by gear type: handline (to catch *Salminus brasiliensis*, *Zungaro jahu* and *Pseudoplatystoma corruscans*), longline and longline2, used to capture *Pterodoras granulosus* and *Pinirampus pirinampu*, respectively (with different baits), and gillnet to capture other species (Okada *et al*. 2012). Time series of catch (1988-2011) and length data (1988-2010) were obtained from the landing monitoring program performed by the Nucleus of Research in Limnology, Ichthyology and Aquaculture (Nupélia), from the Universidade Estadual de Maringá (Nupélia/UEM).

The consumption/biomass ratio (Q/B) for fish functional groups were obtained with the equation proposed by Palomares and Pauly (1998). Biomass, P/B, and Q/B ratios for primary producers, and benthos were obtained from Angelini *et al*. (2006). Insects and zooplankton biomasses were estimated by Ecopath.

The diet matrix was obtained from the published literature, mainly from the local study area (the initial diet matrix is in Section 1 in Supp. Material, and for the references used see Table S5/Section 4 in Supp. Material). As migratory species did not spend all the time in the Itaipu reservoir area, a proportion of their diet compositions were considered as import, to take this characteristic into account (Christensen *et al*. 2008; Corrales *et al*. 2015).

The Itaipu reservoir model was balanced when Ecotrophic Efficiency (EE) values were lower than 1 (Christensen *et al*. 2008). The steps necessary to balance the model were described in the Supplementary Material (section 1). The Pre-Balance tool was used to evaluate the input parameters, biomass and vital rates, according to Link (2010) (Section 2 in the Supp. Material).

The ecosystem structure and functioning of the Itaipu reservoir model (static version) were analyzed by attributes, which are related to Odum's theory about the ecosystem development (Odum 1969): (a) the ratio of Total Primary Production/Total Respiration: index of relative maturity of the system, if ratio is greater than one, ecosystem is considered in succession, ratio approaching one, mature; (b) Finn's cycling index: is the fraction of total flows that is recycled; (c) Total System Throughput (TST) is the sum of all flows in the system, an indirect indicator of the size of the ecosystem; (d) Mean Length of Pathways is the average number of groups that inflow or outflow passes through, and as diversity of flows and recycling is expected to increase with maturity; (e) Ascendency and Overhead are related with the average mutual information in a system, scaled by the TST; (f) Flow from Detritus to Trophic Level II/ Flow from Primary Producers to TL II rate, because mature ecosystem are detritus-based, while in the initial stages of development, the grazing food chains are predominant (Odum 1969; Christensen 1995; Christensen *et al*. 2008). We compare these attributes values to outputs from Angelini *et al*. (2006).

In the static version analysis we also considered three attributes for each functional groups: (i) Omnivory Index (OI) which indicates trophic specialization with zero for restrict specialist, and higher values for consumers that feeds on many trophic levels; (ii) Net efficiency which is the net food conversion efficiency, calculated as the production divided by the assimilated part of the food; (iii) Flow to detritus which consists of amount material egested (the non-assimilated food) and those elements of the component, which die of old age or diseases (Christensen *et al.* 2008). We also analyzed the following rates: F/Z: Fishing Mortality/Total Mortality and R/B: Respiration/Biomass (/year).

4.2.3 Ecosim: fitting time series in the Itaipu reservoir model

The Ecosim interface provides a dynamic simulation capability at the ecosystem level, with key initial parameters inherited from the base Ecopath model. A system of differential equations that express rates of biomass flows among functional groups, as a function of time varying biomass and harvest rates, is implemented (Walters *et al*. 1997; Christensen and Walters 2005; Christensen *et al*. 2008). The equation is derived of the equation 1 from Ecopath, and takes the form:

$$\frac{dB_i}{dt} = g_i \sum_j Q_{ji} - \sum_j Q_{ij} + I_i - (MO_i + F_i + e_i) \cdot B_i \qquad \text{(Eq.3)}$$

where ${dB_i}/{dt}$ is the change in the biomass of functional group *i* (B_i) over time *t*, g_i is the net growth efficiency (production/consumption ratio), Q_{ji} is the consumption of group *j* by group *i*, Q_{ij} is the consumption of group *i* by group *j*, I_i is the extent of immigration of functional group *i*, MO_i, F_i and e_i are, respectively, the non-predation rate of natural mortality, the fishing mortality and emigration of functional group *i*. The consumption rates, Q_{ij}, are calculated based on the foraging arena concept, where the biomasses are divided into vulnerable and invulnerable states. The transfer rate, v_{ij}, between these two states determines the predator-prey interactions (top-down, bottom-up or mixed) (Christensen *et al*. 2008; Ahrens *et al*. 2012):

$$Q_{ij} = \frac{a_{ij} \cdot v_{ij} \cdot B_i \cdot P_j}{2v_{ij} + a_{ij} \cdot P_j} \qquad \text{(Eq. 4)}$$

where a_{ij} is the effective search rate of predator *j* feeding on prey *i*, B_i is the biomass of the prey, P_j is the biomass of predator, and v_{ij} is the vulnerability of prey *i* to predator *j*. The values that the vulnerabilities assume indicate the type of flow control, with $v_{ij} = 2$, $v_{ij} = 1$ and, $v_{ij} > 2$ representing a mixed flow control, a bottom-up, and a top-down control, respectively (Walters and Martell 2004; Christensen and Pauly 2004; Ahrens *et al*. 2012).

In the time series fitting procedure we used fishing effort data as driving factor, to fit the catch data from 1988 to 2011. Fishing effort was given in number of days fishing (sum of fishing days of all fishers per year). The absolute observed catch data were compared to predicted catch to assess the fit of the model. Ecosim interface uses the sum of squared deviations of log catches from log predicted catches (Christensen *et al*. 2008). The fitting procedure was done using an integrated plug-in, the Stepwise Fitting Procedure (Scott *et al*. 2016). This tool automates the search for the best fitting of the model to observed data, testing a set of hypotheses, to assess the impact of fishing (through fishing mortality/effort times series), changes in the predator-prey dynamics (vulnerability settings), and changes in primary production (PP anomaly function). Each hypothesis testing represents a combination of these three variables (following Mackinson *et al*. 2009a). The best-fit model is found and determined by the minimum difference between model predictions to time series observations using a weighted sum of squared differences (SS), and the Akaike Information Criterion (AIC), which penalizes for fitting too many parameters based on the number of time series available for estimating the SS (Scott *et al*. 2016). The Itaipu model was calibrated using 12 time series of catches, allowing the estimation of 11 parameters during the fitting procedure. From the 12 species, only the five main species caught at Itaipu fishery were analyzed (*Prochilodus lineatus*, *Hypophthalmus edentatus, Pterodoras granulosus*, *Plagioscion squamosissimus*, and *Pinirampus pirinampu*). Besides those species, *S. brasiliensis*, *Z. jahu*, and *P. corruscans* were analyzed due to their economic importance, although their landings dropped since the construction of Itaipu dam.

After the calibration of the ecosystem model with time series of catch, the fishing mortality that produces the maximum sustainable yield (F_{MSY}), and the maximum sustainable yield (MSY), were estimated for the main target species (listed above). The Ecosim equilibrium analysis estimates F_{MSY} and MSY under two approaches, stationary and full compensation. Under the stationary approach, an estimate of MSY and F_{MSY} for each harvested group was obtained running the Ecosim model to equilibrium, for a range of fishing mortality values while holding biomasses of all other groups constant (this means that food availability and predation impacts are constant; the fishing mortality of all other groups are hold constant at the Ecopath base values). The full compensation approach allows the biomasses of all groups to vary, but only in response to fishing-driven changes in the biomass of the harvested group. Estimates of F_{MSY} and MSY were obtained by running a simulation with 1000 years, in which the fishing mortality value of the species analyzed was incremented and decremented (Christensen *et al*. 2008; Mackinson *et al*. 2009b).

Using the F_{MSY} estimates obtained from the Ecosim equilibrium analysis, we analyzed if the main stocks of Itaipu fisheries would be subject to overfishing. To do so, we considered that overfishing was occurring for the stocks that showed fishing mortality above the reference levels F_{MSY} (stationary and full compensation) ($F > F_{MSY}$). To classify the stocks regarding their biomass levels, we follow the procedure of Forrest *et al*. (2015) to defining reference points for biomass limit (30%) and target (50%) of the biomass in the first year of the model ($0.3B_{1988}$ and $0.5B_{1988}$). Forrest *et al*. (2015) had considered lowest percentages of biomass to the first year (20 and 40%) and we increased these values in order to have a more severe overfishing threshold, since it is known that there was already fishing in Itaipu reservoir, even before its construction (Agostinho *et al*. 1999), and as a way to account for uncertainties, since biomass was estimated from the model. Stocks with biomass below $0.3B_{1988}$ were considered as overfished.

4.2.4 Ecological indicators

After the model with the lowest AIC was identified, ecological indicators were analyzed to investigate possible impacts of fishing on the ecosystem. The indicators were selected based on literature (Coll *et al*. 2008; Corrales *et al*. 2015).

The mixed trophic impact (MTI) analysis is based on Leontief method (1951), to assess the effect that changes in the biomass of a group will have on the biomass of other groups in a system. It is implemented on EwE software based on the approach developed by Ulanowicz and Puccia (1990). The MTI is calculated by constructing a *n* x *m* matrix, where the *i*, *jth* elements represent the interaction between the impacting group *i* and the impacted group *j*:

$$MTI_{i,j} = DC_{i,j} - FC_{j,i} \qquad \text{(Eq. 5)}$$

where $DC_{i,j}$ is the diet composition term expressing how much *j* contributes to the diet of *i*, and $FC_{j,i}$ is a term giving the proportion of the predation on *j* that is due to *i* as a predator. The fishing fleets are included as "predators" (Christensen *et al*. 2008).

The keystoneness index (KS_i) identifies keystone species in the food web model by balancing the effects of (i) the direct and indirect trophic impacts that each impacting group *i* has on any impacted group *j* of the food web (obtained through the MTI matrix), and (ii) the biomass of the impacting group. We analyzed the KS index implemented in the last version of EwE software, developed by Valls *et al*. (2015). This KS index was proposed with the aim to give a more balanced contribution between the trophic impact and biomass components in the estimation of species keystoneness, without over representing abundant or rare species (Valls *et al*. 2015):

$$KS = \log(IC_L x BC_0) \qquad \text{(Eq. 6)}$$

where $IC_L = \varepsilon_i$, and ε_i is the measure of the overall effect of each group as $\varepsilon_i = \sqrt{\sum_{j \neq i}^{n} m_{ij}^2}$ (from the mixed trophic impact matrix). BC_0 is the descending order rank of the biomass of the functional groups.

4.2.5 Fishing effects

The primary production required to sustain the fishery (PPR), is obtained as the sum from the primary production and the detritus back calculated for all the pathways from the caught species:

$$PPR = \frac{1}{9} \cdot \sum_i \left[Y_i \cdot \left(\frac{1}{TE} \right)^{TL_i - 1} \right] \quad \text{(Eq. 7)}$$

where Y_i is the catch of the functional group *i*, TE is the mean transfer efficiency, TL_i is the trophic level of the functional group *i*, and 1/9 is the average conversion coefficient from wet weight to gC (Pauly and Christensen 1995).

The mean trophic level of catches (TLc) reflects the strategy of the fishery, taking into account trophic levels of the species in the catches. It is obtained as a weighted average of TL of the species in the catches:

$$TLc = \frac{\sum_{i=1}^{m} Y_{ik} \cdot TL_i}{\sum_{i=1}^{m} Y_{ik}} \quad \text{(Eq. 8)}$$

where Y_{ik} is the catches of functional group *i* in year *k*, and TL_i is the trophic level of the functional group *i*.

The Kempton index (Q) is a measure of biomass diversity that describes the slope of a cumulative group abundance curve (Christensen *et al*. 2008). The Q index is developed to measure the effects of mortality from fishing or climate on species diversity in ecosystem simulation models, considering only species with trophic level higher than 3 (Ainsworth and Pitcher 2006; Christensen *et al*. 2008).

The theoretical quantification of the loss in the secondary production due to exploitation is given by the L index (Libralato *et al*. 2008). This index takes into account both ecosystem properties (primary production and transfer efficiency), and features of the fishing activities (trophic level of catches and primary production required) to quantify the loss in secondary production as a proxy for quantifying effects of fishing. It is calculated by:

$$L = -\frac{1}{P_1 \cdot \ln TE} \cdot \sum_{i}^{m} \left(PPR_i \cdot TE^{TL_i - 1} \right) \qquad \text{(Eq. 9)}$$

where P_1 indicates the autotrophic and detritus production ($P_1 = PP + FD$, PP is the calculated net primary production and FD is flows to detritus), TE is average transfer efficiency between the trophic levels, PPR_i and TL_i are the Primary Production Required Trophic Level for functional group *i*, respectively (Libralato *et al*. 2008).

To test if the temporal trends of indicators were significant, we performed an ordinary least squared (OLS) regression, following the procedure in Coll *et al*. (2008, 2016). To test for autocorrelation in residuals of the OLS regression, we performed a Durbin-Watson test, implemented on package car (Fox and Weisberg 2011). If the residuals were auto correlated we proceeded to a generalized least squares regression, which allows the errors to be correlated and/or have unequal variance (Venables and Ripley 2002). These analyses were performed in R (R Core Team 2016), with lm and gls functions from packages MASS (Venables and Ripley 2002) and nlme (Pinheiro *et al*. 2016), respectively.

4.2.6 Simulation of fishing effort scenarios

We performed a series of fishing simulations on Itaipu Reservoir model to assess any possible change in ecosystem characteristics due to increasing or decreasing fishing effort, using the dynamic module Ecosim (Christensen *et al*. 2008). We used the Ecosim model that was previous fitted to a time series of catch data from 1988 to 2011 (section 2.3), to develop different scenarios modifying the fishing effort of gillnet, longline, longline2 and handline gears. For these different gears we increased the baseline (2011) fishing effort (FE) in 25% (scenario 1), 50% (scenario 2), 75% (scenario 3), and 100% (scenario 4), as well as we reduced FE in 10% (scenario 5) and 20% (scenario 6). The simulations were performed from 2011, with duration of 30 years.

The comparative results of the simulated scenarios were shown for catch, biomass, diversity (Kempton index), TLc, and L index. Temporal trends of indicators were tested with ordinary least squares or generalized least squares, as explained in section 2.5, considering the times series between 2011 and 2041.

We also made two simulations with the F_{MSY} estimates obtained from the Ecosim equilibrium analysis: one was applying the estimated F_{MSY} full compensation (scenario 7), and the second one applying the estimated F_{MSY} stationary (scenario 8). To investigate the impacts of these scenarios on the main targeted species, we analyzed the trends of their estimated biomass and estimated catches. There is a schematic diagram showing the modeling approach adopted in this study (see Fig. S2 in Supp. Material).

4.3 RESULTS

4.3.1 Overall outputs of Ecopath

The functional groups that showed highest Ecotrophic Efficiency (EE) values were species exploited by fisheries as well as species important as prey (Table 1). The highest trophic level was 4.37 for *S. brasiliensis* (Fig. 2), while the species *Acestrorhyncus lacustris* and *Serrasalmus* spp. showed the lowest values for the Omnivory Index (OI) (Table 1), suggesting a specialized diet. Detritus and Phytoplankton are the main sources of energy (Fig. 2).

The pre-balance analysis showed the biomass decomposition through upper trophic levels, as well as for P/B and R/B. Q/B did not show a clear pattern across trophic levels (Supp. Material). To balance the model we first modified the diet matrix, especially the diet composition for piscivores species: *Plagioscion squamosissimus*, *Zungaro jahu*, and *Hoplias* spp., in an attempt to reduce the predation mortality caused by these species on other functional groups (final diet matrix is shown in Table S2 in Supp. Material; see Table S1 in Supp. Material for input diet matrix). Modifications were made on biomass for *Serrasalmus* spp., and on P/B and Q/B values for other functional groups (see Section 1 in Supp. Material for more detailed information).

Table 1. Basic output estimates of Itaipu model. FG #: Functional group number; TL: Trophic Level; B: Biomass (t/km²); P/B: Production/Biomass (/year); Q/B: Cosumption/Biomass (/year); EE: Ecotrophic Efficiency; FD: Flow to Detritus (t/km²/year); NE: Net Efficiency; OI: Omnivory Index; F: Fishing Mortality rate (/year); F/Z: Fishing Mortality/Total Mortality rate; R/B: Respiration/Biomass (/year). Values in bold were estimated by Ecopath.

FG #	Functional Group	TL	B	P/B	Q/B	EE	FD	NE	OI	F	F/Z	R/B
1	Phytoplankton	1	0.36	250	0	**0.47**	47.37	-	0	0	0	-
2	Macrophytes	1	100	30	0	**0.06**	2822.55	-	0	0	0	-
3	Periphyton	1	14.8	40	0	**0.16**	496	-	0	0	0	-
4	Zooplankton	2	**0.11**	54	250	0.7	6.97	0.27	0	0	0	146
5	Benthos	2	4.8	10.4	40	**0.27**	75.04	0.33	0	0	0	21.6
6	Insects	2	**3.34**	25	250	0.7	192.01	0.13	0	0	0	175
7	*Prochilodus lineatus*	2.18	1.14	0.82	13.36	**0.99**	3.05	0.08	0.15	0.15	0.19	9.87
8	*Leporinus elongatus*	2.6	0.6	1.25	6.44	**0.45**	1.18	0.24	0.24	0	0	3.9
9	*Schizodon borelli*	2.1	0.26	1.41	30.54	**0.55**	1.75	0.06	0.09	0.04	0.03	23.02
10	*Roeboides descalvadensis*	2.7	**1.96**	1.99	19.99	0.7	9.02	0.12	0.21	0	0	14
11	*Hoplias* spp.	3.77	0.34	1.6	5.98	**0.98**	0.42	0.33	0.31	0.04	0.03	3.18
12	*Pseudoplatystoma corruscans*	3.72	0.11	0.51	3.52	**0.53**	0.1	0.18	0.54	0.27	0.53	2.31
13	*Zungaro jahu*	3.35	0.14	1.13	3.89	**0.34**	0.21	0.36	0.16	0.39	0.34	1.98
14	*Salminus brasiliensis*	4.37	0.04	0.4	4.4	**0.63**	0.04	0.11	0.3	0.25	0.63	3.12
15	*Hypopthalmus edentatus*	2.7	1.66	1.5	7.14	**0.99**	2.38	0.26	0.21	0.21	0.14	4.21
16	*Pinirampus pirinampu*	3.2	0.37	1.01	5.87	**0.1**	0.77	0.22	0.35	0.1	0.1	3.69
17	*Moenkhausia intermedia*	2.2	**2.46**	1.3	13.2	0.7	7.44	0.12	0.16	0	0	9.26
18	*Plagioscion squamosissimus*	3.48	1.29	1.4	5.51	**0.15**	2.96	0.32	0.08	0.13	0.09	3.01
19	*Leporinus fridericci*	2.39	0.26	1.3	7.55	**0.97**	0.4	0.22	0.29	0.04	0.03	4.74
20	*Hypostomus* spp.	2.2	0.78	2.7	15.92	**0.46**	3.61	0.21	0.16	0.07	0.03	10.04
21	*Pterodoras granulosus*	2.38	1.6	1.02	5.4	**0.22**	3.01	0.24	0.25	0.08	0.08	3.3
22	*Astyanax altiparanae*	2.5	**2.4**	1.6	12.17	0.7	7	0.16	0.25	0	0	8.14
23	*Gymnotus* spp.	2.9	**0.08**	1.25	7	0.7	0.15	0.22	0.09	0	0	4.35
24	*Rhaphiodon vulpinus*	3.56	0.27	1.09	6.53	**0.35**	0.54	0.21	0.32	0.06	0.06	4.13
25	*Acestrorhyncus lacustris*	3.39	0.04	1.05	9.74	**0.48**	0.1	0.13	0.05	0	0	6.74
26	*Serrasalmus* spp.	3.37	0.08	1	10.74	**0.64**	0.2	0.12	0.07	0.2	0.2	7.59
27	*Hemisorubim plathyrhynchos*	3.51	0.01	0.46	6.14	**0.82**	0.01	0.09	0.19	0.2	0.43	4.45
28	*Steindachneria* spp.	2.15	**0.06**	2	23.7	0.7	0.32	0.11	0.13	0	0	16.96
29	*Cichla* spp.	3.18	0.36	1.23	7.97	**0.94**	0.6	0.19	0.12	0	0	5.15
30	*Hoplosternum littorale*	2.8	**0.55**	1.2	9.1	0.7	1.2	0.16	0.16	0	0	6.08
31	Detritus	1	0.04	-	-	**0.23**	0	0	0.1	-	-	-

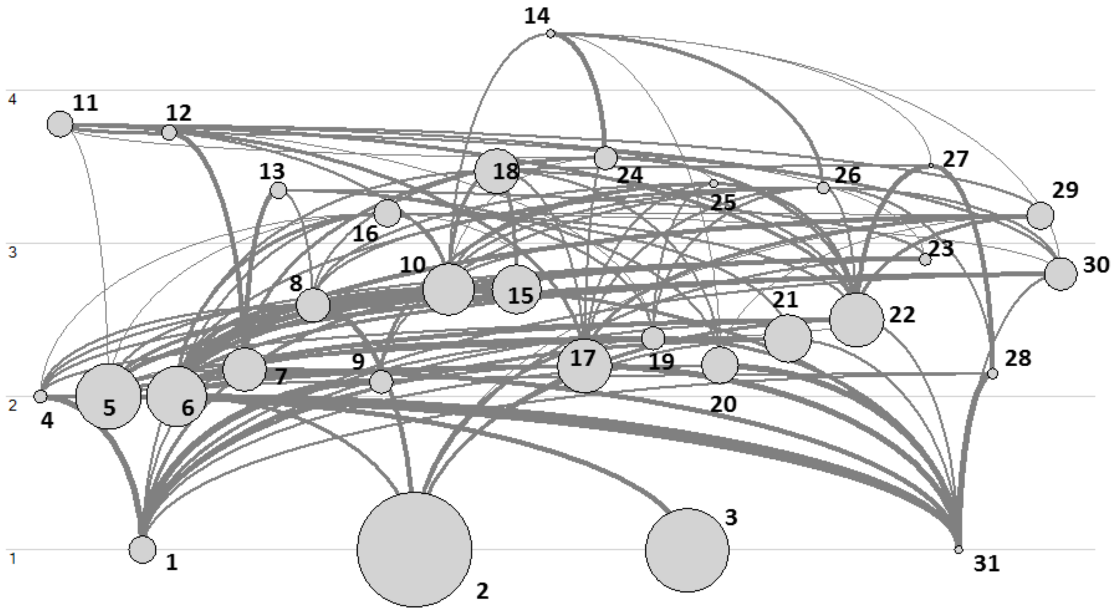

Fig. 2. Food web of Itaipu Reservoir (Ecopath Model). Functional groups numbers are identified in Table 1. The width of the lines represents the magnitude of the flows between functional groups and the size of the circles represents the (log) biomass. Numbers on the left indicate the Trophic Level.

4.3.2 Ecosystem structure

The outputs for the ratio Total Primary Production/Total Respiration was greater than one (Table 3) suggesting that the Itaipu reservoir ecosystem is at a developmental stage, according to Odum's attributes (1969). However, ascendency was high (Table 3), and the flow from detritus is higher than the flow from primary producers, indicating a detritivory dominance, which is a characteristic of mature systems. The majority of ecosystem metrics showed lower values than the model of Itaipu constructed by Angelini *et al*. (2006), Finn's cycling index and total overhead, both higher than the previous model (Table 3). Other attributes values are showed in Table S6/Section 5 in Supplementary Material.

Table 3. Ecosystem attributes of Itaipu Reservoir model (static model) and comparison to Angelini *et al*. (2016) Ecopath models for the same reservoir.

Attributes (unit)	**This study**	**Angelini *et al*. 2006**	
	1988	**1983-1987**	**1988-1992**
Total Primary Production/Total Respiration (TPP/TR)	4.44	6.3	6.8
Finn's cycling index (%)	3.067	1.92	1.78
Total System Throughput ($t/km^2/year$) TST	8614.54	8716.6	8528.9
Mean length of pathways = Total number of arrows / Total number of pathways	4.67	5.01	5.19
Ascendency total (%)	42.74	46	46.8
Connectance Index (dimensionless) CI	0.14	0.16	0.17
System Omnivory Index (dimensionless) SOI	0.15	0.17	0.16
Total number of pathways	530	663	801
(Flow from Detritus / Flow from PP) to TL II	2.62	2.02	1.9
Mean trophic level of the catch (TLc)	2.79	2.91	2.79
TE total (%)	7.36	8.5	9.6

The mixed trophic impact plot shows that a slight positive impact of *S. brasiliensis* upon *Steindachneria* spp., *S. borelli* and *L. elongatus*, probably due to a predation release, since *S. brasiliensis* feed on their predators (*Serrasalmus* spp. and *R. vulpinus*) (Fig. 3). It is also possible to observe high negative impacts from some predators upon their prey.

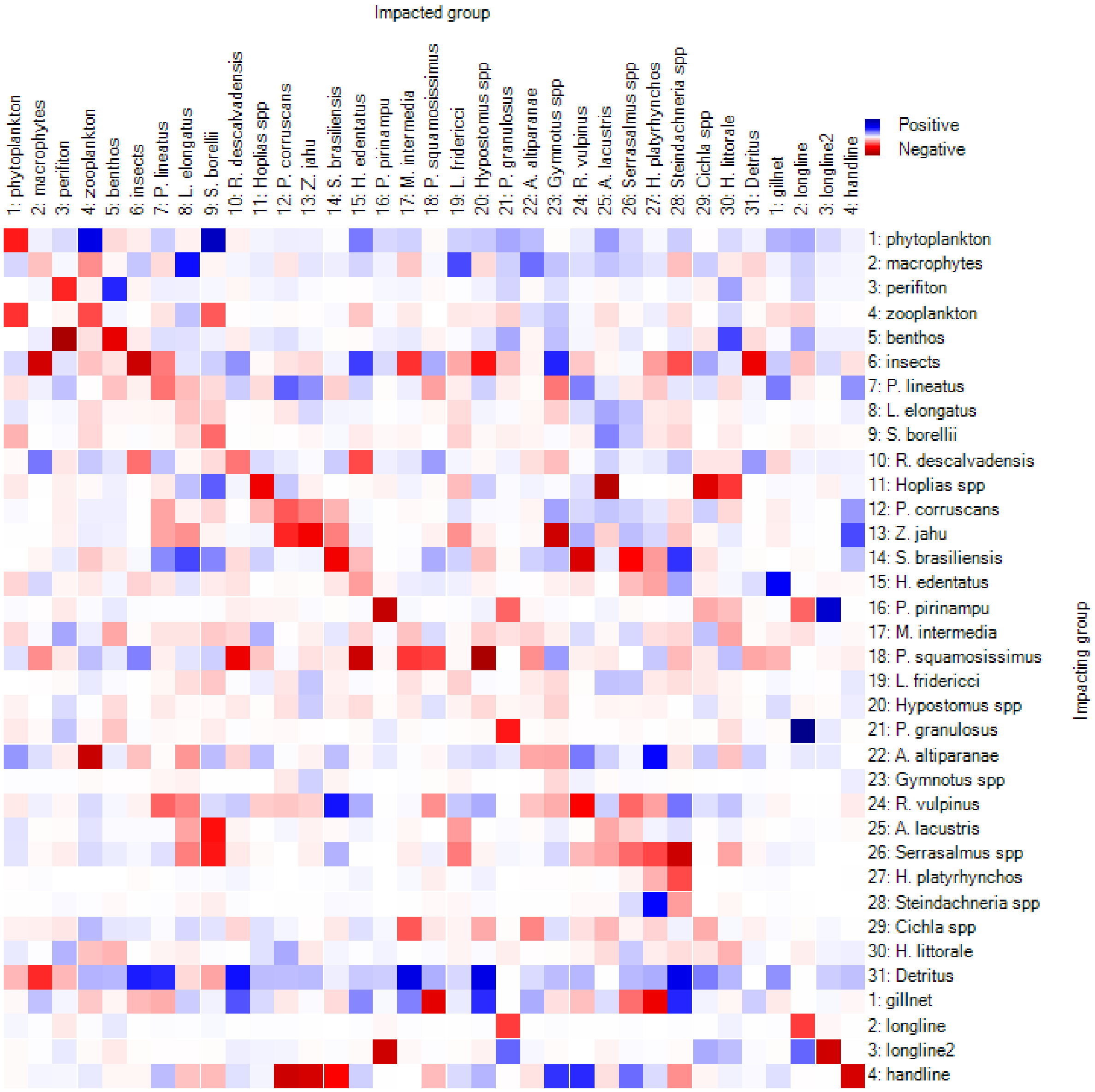

Fig. 3. Mixed trophic impact plot representing the negative (red) and positive (blue) impacts between the functional groups. Impacting groups are in lines and impacted groups are in column.

The KS index identified *S. brasiliensis*, *Serrasalmus* spp., *Z. jahu*, and *Hoplias* spp., as keystone species in Itaipu reservoir ecosystem (Fig. 4).

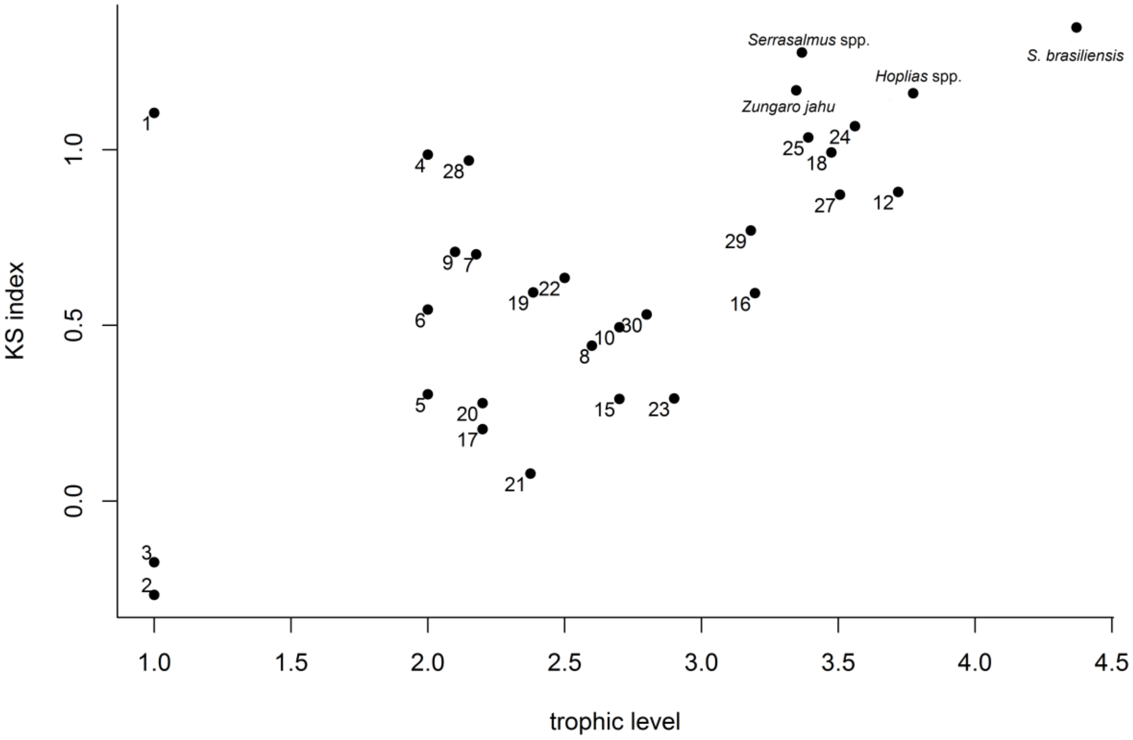

Fig. 4. Keystoneness index for Itaipu reservoir model. For the highest KS values we highlighted the names, to identify the other functional groups see numbers on Table 1.

4.3.3 Fishing effects

Ecopath results for 1988 showed high fishing mortalities rates (F) for *P. corruscans* and *S. brasiliensis* (F/Z > 0.5), moderate F for *Z. jahu* (F/Z=0.34), and a low fishing mortality (F/Z < 0.2) for the other species (*P. lineatus*, *P. pirinampu*, *P. squamosissimus*, *H. edentatus*, *P. granulosus*).

The mixed trophic impact plot shows that gillnet positively impacts *Steindachneria* spp. and *Hypostomus* spp., probably due to a decrease in predation pressure from *H. platyrhynchos* and *P.*

squamosissimus, respectively, which are caught by this fishing gear (Fig. 3). The same effect may occur due to the positive impact of handline on *Gymnotus* spp. and *R. vulpinus*. The mixed trophic impact plot (Fig. 3) shows that gillnet positively impacts on *Steindachneria spp*. and *Hypostomus spp*., probably due to a decrease in predation pressure from *H. platyrhynchos* and *P. squamosissimus*, respectively, which are caught by this fishing gear (Fig. 4). The same effect may occur due to the positive impact of handline on *Gymnotus spp*. and *R. vulpinus*. In this manner, an increase in fishing effort may negatively impact some target species, but at the same time cause a positive impact on other species.

The Primary Production Required (PPR) necessary to sustain the fishery in Itaipu reservoir is practically half of the total primary production (Table 3). The total catch decreased along the time, with some peaks as in 2005 and 2008 (Fig. 5). The mean trophic level of the catch was 2.77 in 1988, ranged between 2.75 and 2.87, showing a small upward trend until 2011 (Fig. 5). Diversity (Kempton index) decreased since 1988, but being a small reduction. L index values were between the references values of $L_{50\%}$ and $L_{75\%}$, indicating a moderate risk of ecosystem overfishing, *sensu* Murawski (2000), in Itaipu reservoir.

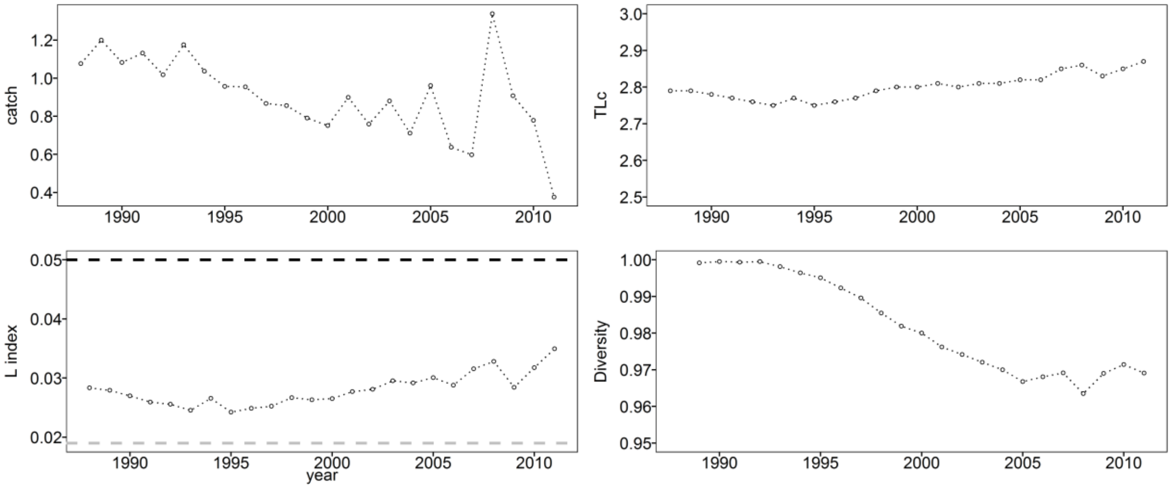

Fig. 5. Time series of total catch (tones/km^2/year), mean trophic level of catch (TLc), L index for Itaipu reservoir model and diversity (Kempton index). In the L index plot the dash lines represent the reference values: $L_{50\%}$ (black) and $L_{75\%}$ (grey).

In Itaipu fishery, total catch and diversity showed a significant decrease between 1988 and 2011, even though they were small changes (catch: slope=-0.018%, p-value = 0.002; diversity: slope=-0.001%, p-value = 0.014). The mean trophic level of catches (TLc), and L index did not showed a significant rate of change across the same period (TLc: slope=0.003%, p-value = 0.267; L index: slope=0.0003, p-value = 0.447).

4.3.4 Ecosim fitting

The model with the lower AICc (6.85) accounted for almost 60% of the variance compared to the baseline model, and included the effects of fishing and trophic interactions (represented by 11 vulnerabilities) (Table 4; see Table S3 in Supp. Material, section 3, for all the combinations tried and their respective SS and AICc values). In this way, the major effects on the trend of time series of catches were fishing and predator-prey interactions.

The functional groups with changed vulnerabilities rates values (v) after the fitting procedure were *P. lineatus*, *Hoplias* spp. and *Cichla* spp. with v=100; *S. brasiliensis*, *H. edentatus*, *P. pirinampu*, *A. altiparanae*, *Gymnotus* spp., *R. vulpinus*, and *Serrasalmus* spp with v=1; *P. corruscans* with v=11.32. The estimated catch of *P. lineatus*, *P. squamosissimus*, *P. pirinampu*, and *S. brasiliensis*, when compared with the observed catch showed a good fitting (Fig. 6, and see Fig. S3 in Supp. material for other species). The model overestimated catches for *P. corruscans* and *Z. jahu*, but with quite similar trend of the observed data, while the fitting for *H. edentatus* and *P. granulosus* were not good.

Table 4. Results from the stepwise fitting procedure for some models tested. Baseline model corresponds to the model without fishing, predator-prey (v) and anomaly primary production (pp) effects. SS: weighted sum of squared differences. AICc: Akaike information criteria corrected for small sample sizes.

Model	**SS**	**AICc**
Baseline	676.71	247.53
Baseline and 11v	676.70	271.35
Baseline and 10pp	571.30	222.30
Fishing	383.60	90.86
Fishing and 11v	259.52	6.84

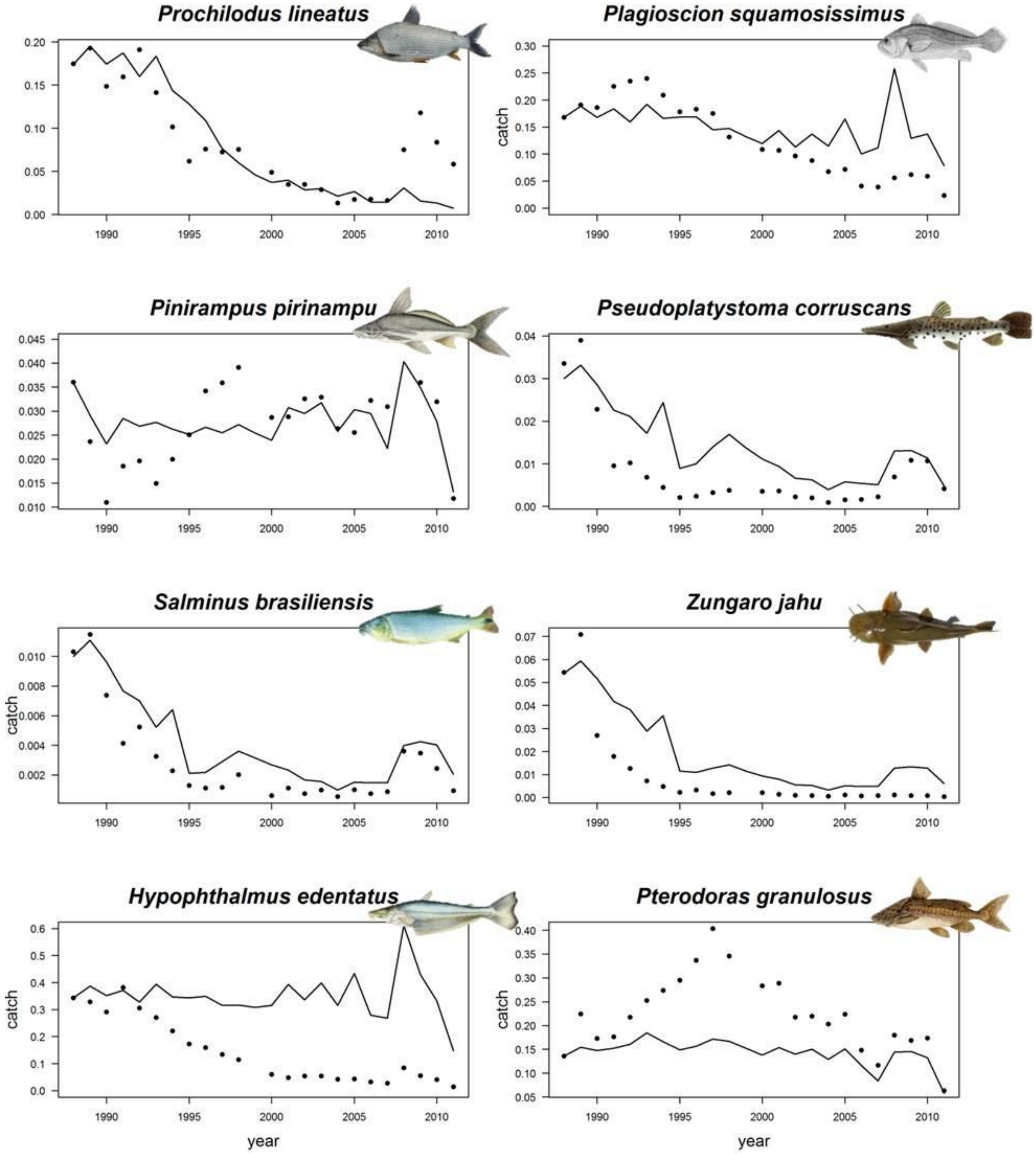

Fig. 6. Catch observed and predicted by EwE model for the main species of Itaipu reservoir fishery (circles: observed catch; line: predicted catch). Catches in tonnes/km^2.

4.3.5 Simulation of fishing scenarios

The simulations performed under scenarios with increased fishing effort (scenarios 1 to 4) resulted in higher catches, as expected (Fig. 7). The mean trophic level of the catch (TLc) was lower in scenarios with increased fishing effort, as well as higher values of L index, indicating that increased fishing effort will have negative effects on the ecosystem of Itaipu reservoir (Fig. 7). Although diversity showed lower values in the scenarios with increased fishing effort, than in the decreased ones (scenarios 5 and 6), diversity increased under all scenarios relative the baseline scenario (same fishing effort from 2011).

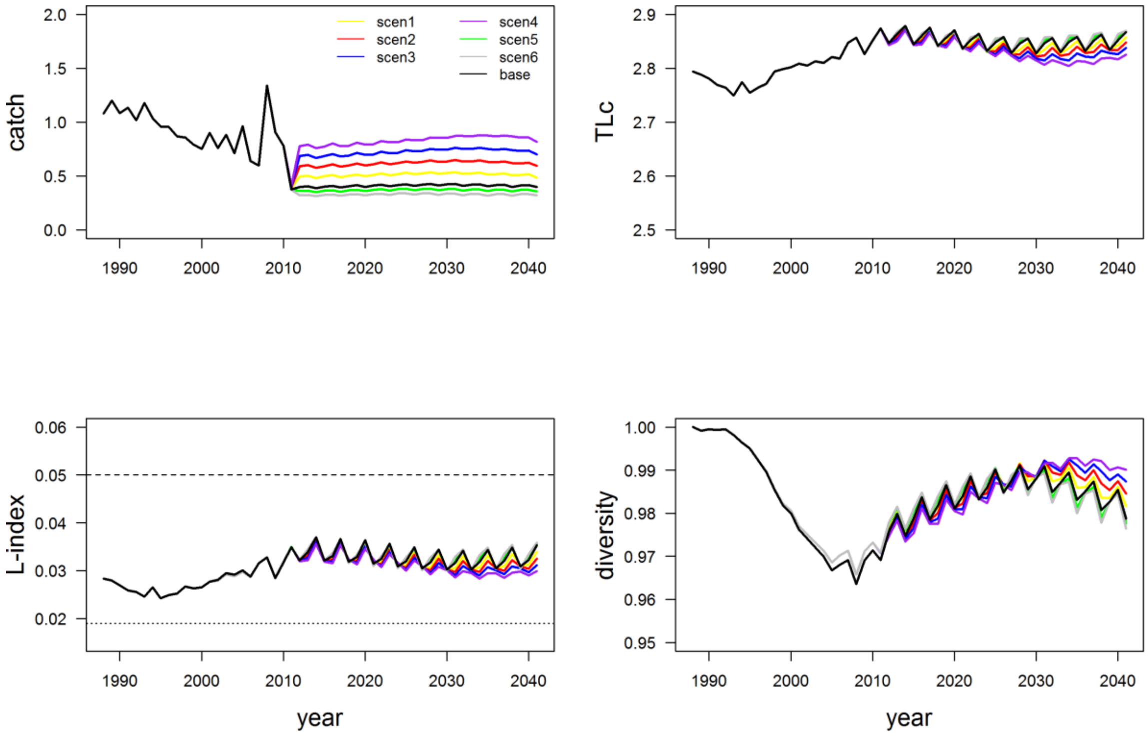

Fig. 7. Indicator trends under different scenarios of fishing effort. Scen1: scenario 1 (+25%), Scen2: scenario 2 (+50%), Scen3: scenario 3 (+75%), Scen4: scenario 4 (+100%), Scen5: scenario 5 (-10%), Scen6: Scenario 6 (-20%), Base: baseline (fishing effort in 2011), Scen7: F_{MSY} full compensation, Scen8: F_{MSY} stationary. Catch is in tonnes/km^2. In the L index plot the dash lines represent the reference values: $L_{50\%}$ (black) and $L_{75\%}$ (grey).

The rate of change in total catch was not significant under all simulated scenarios (see Fig. S4/Section 6 in Supp. material). The TLc indicator decreased with higher fishing effort (scenarios 1, 2, 3 and 4) and increased under lower fishing effort compared to the baseline scenario (Fig. 7). Regarding diversity, the rates of change were positive and significant under scenarios 2, 3, and 4. L index showed no significant rates of change only under scenarios 5 and 6. Again, despite statistically significance in the rates of change of the indicators, it is worth nothing that they were very small changes under all scenarios.

The estimates of maximum sustainable yield (MSY) from the stationary system were lower than the MSY estimated considering the full compensation mode, except for *P. pirinampu* and *S. brasiliensis*, where they were the same (Fig. 8). According to the estimates of MSY for each stock, obtained with the Ecosim equilibrium analysis, catches did not exceed the MSY for any stock, under scenarios of higher fishing effort. On the contrary, when applying the fishing mortality rates that produce the MSY (F_{MSY}), estimated by the equilibrium analysis in Ecosim, catches were above MSY in the last years for *P. lineatus*. Only the stocks of *P. squamosissimus* and *P. pirinampu* produced the yield corresponding to the MSY (Fig. 8). Estimated catches for *P. corruscans* and *S. brasiliensis* did not showed great changes, under the scenario applying F_{MSY}.

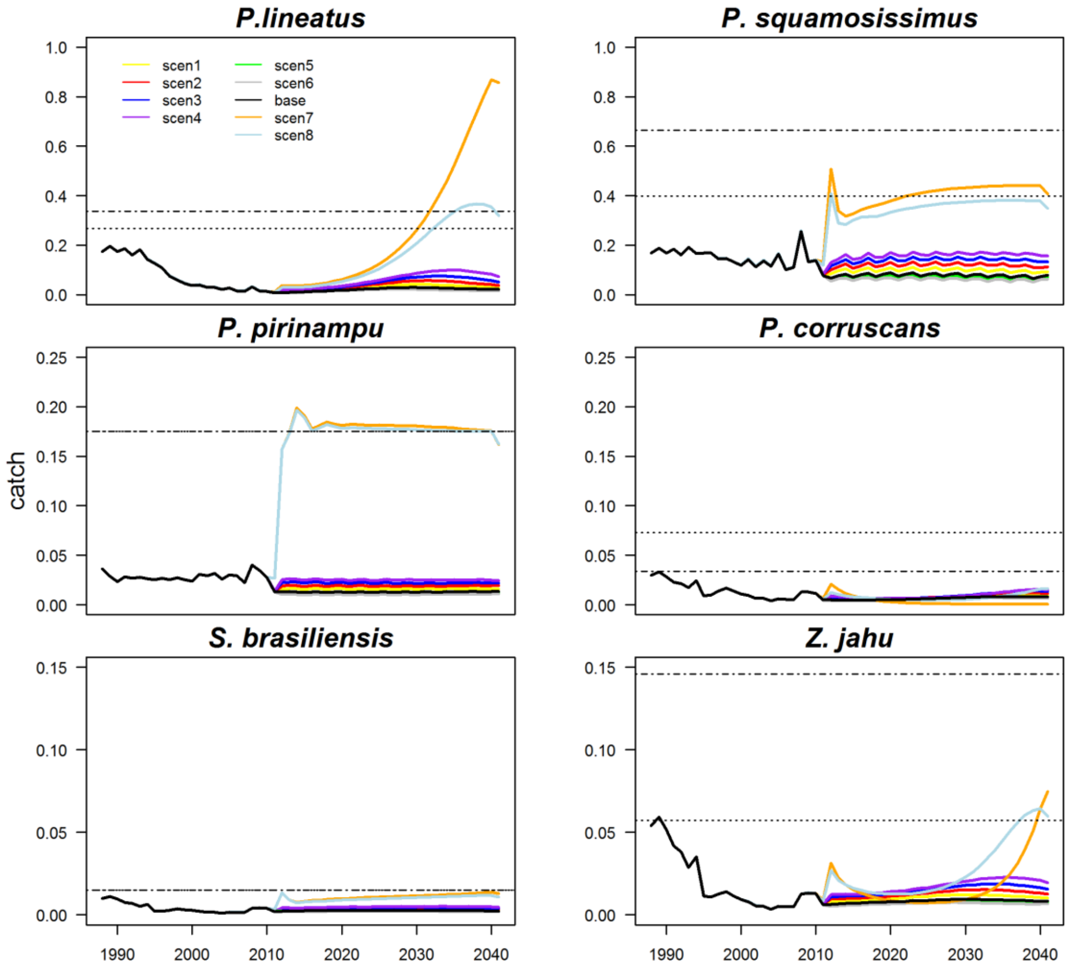

Fig. 8. Estimated catches for the target fishes in Itaipu reservoir under different fishing effort scenarios for the 30 years simulations (2012-2041). Dotted lines and dotdash lines represent MSY from the Ecosim equilibrium analysis, corresponding to the stationary and full compensation mode, respectively. Base: baseline (fishing effort value from 2011), Scen1: scenario 1 (+25%), Scen2: scenario 2 (+50%), Scen3: scenario 3 (+75%), Scen4: scenario 4 (+100%), Scen5: scenario 5 (-10%), Scen6: Scenario 6 (-20%). Catch is in tonnes/km^2.

The simulated biomass, between 2011 and 2041, were higher under increased fishing effort scenarios for *P. lineatus*, *P. squamosissimus* and *Z. jahu* (Fig. 9), while for *P. corruscans and P. pinirampu*, simulated biomasses were higher with lower fishing effort. Biomass along the simulated years, and the different scenarios did not showed great changes. We avoided simulating scenarios for *P. granulosus* and *H. edentatus* since their fitting were not good (Fig. 6). The stocks of *P. squamosissimus*, *P. pirinampu*, and *S. brasiliensis* did not showed estimated biomass below their limit (0.3B_{1988}) and target (0.5B_{1988}), even under scenarios with increased fishing effort (Fig. 9).

The worst stock status was for *P. lineatus*, which since 1999, showed estimated biomass below both the biomass limit and target. After 2020, estimated biomass for this stock went up to the biomass target just with the scenario with highest fishing effort. On the contrary, higher biomass levels were observed under scenarios with decreased fishing effort for *Z. jahu* (until 2030), and *P. corruscans*. This last stock exhibited biomass levels at and below the biomass target for scenarios 3, and 4, respectively (Fig. 9). Regarding, simulations applying F_{MSY} values (scenarios 7 and 8), estimated biomass were below the limit for *P. lineatus*, *P. corruscans*, and *Z. jahu* (Fig. 9). The estimated biomass for *P. squamosissimus* was at and above the biomass target, under F_{MSY} full compensation and stationary, respectively. The stock of *P. pirinampu* was the only one with biomass levels too high above reference points, even with the fishing mortality at F_{MSY} imposed upon it.

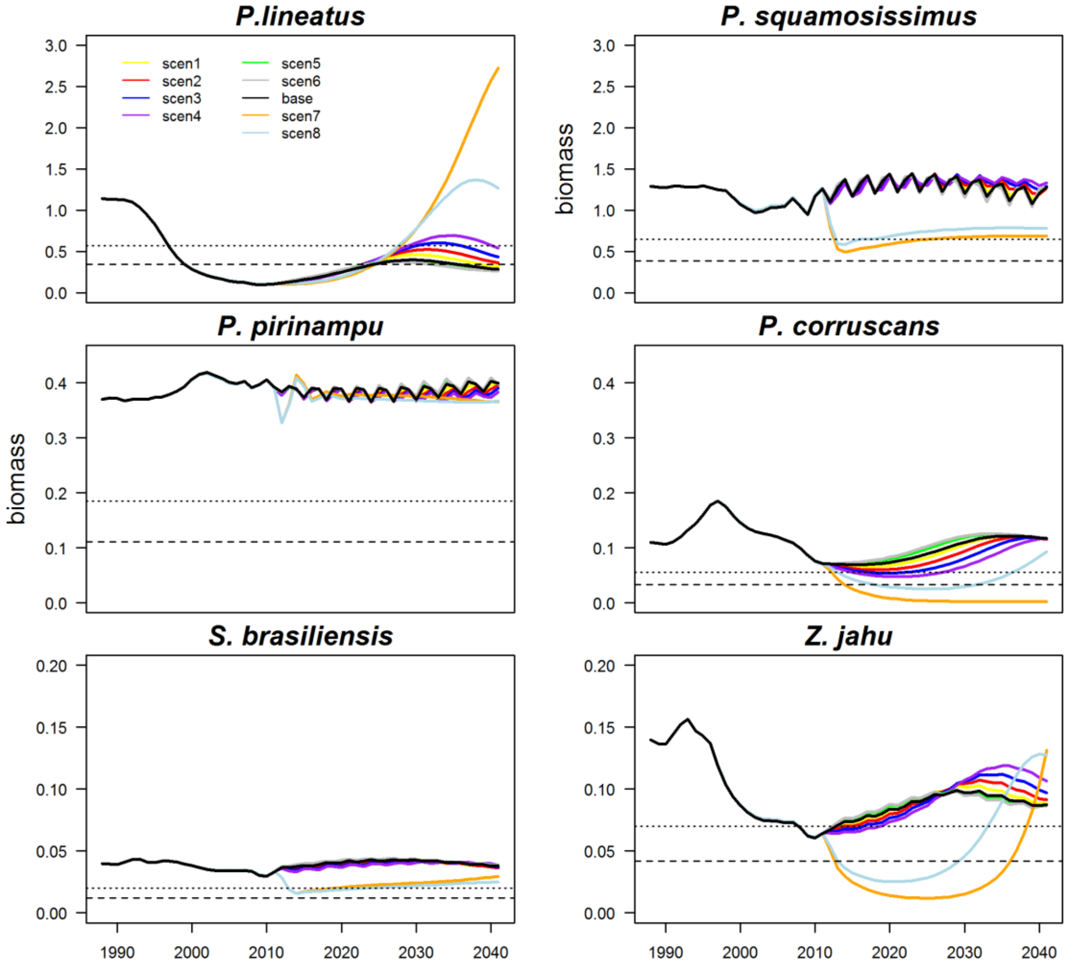

Fig. 9. Biomass estimates from Ecosim simulations for the main target species in Itaipu fisheries. Dashed and dotted lines represent the biomass limit ($0.3B_{1988}$) and the biomass target ($0.5B_{1988}$), respectively.

The fishing mortality rates were higher under scenarios with increased fishing effort for all species analyzed (Fig. 10). The estimates of fishing mortality that produces the maximum sustainable yield (F_{MSY}), as the MSY estimates, were lower for the stationary mode comparing to the full compensation. The only stock with fishing mortality higher than F_{MSY} was *P. corruscans*, in the first years of the time series. Also, under the increased fishing effort scenarios, the fishing mortality for this stock is close to the F_{MSY} reference point. Currently, overfishing is not occurring for any of the target stocks analyzed (Fig. 10).

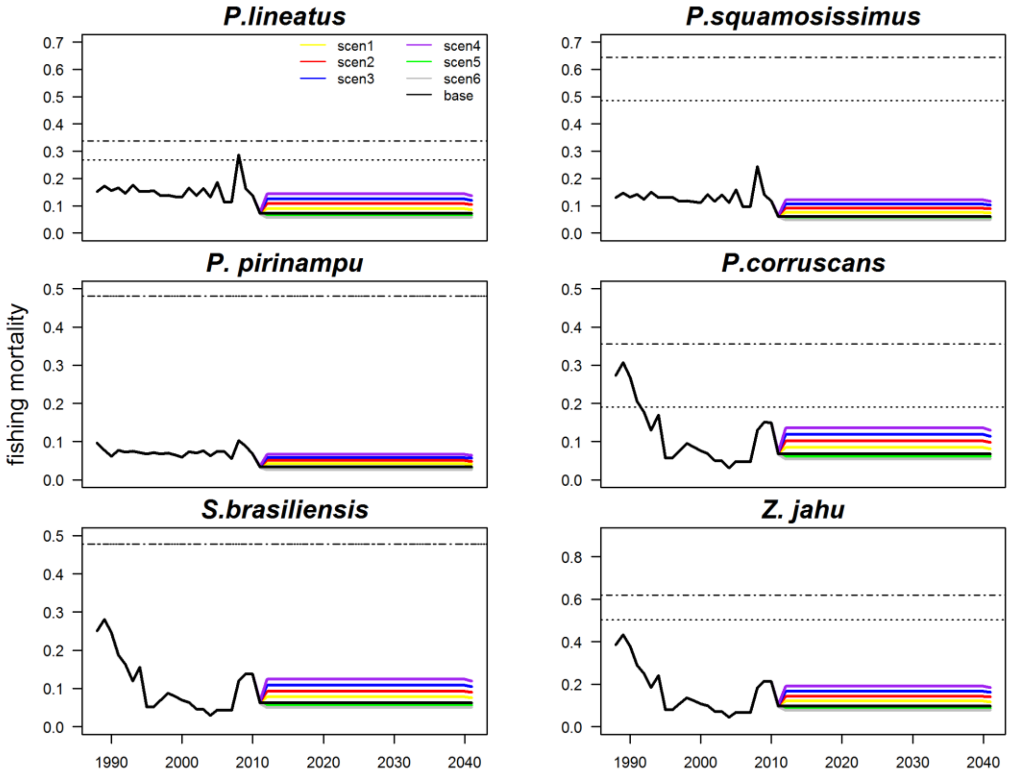

Fig. 10. Fishing mortality (years^{-1}) estimated by the food web model of Itaipu reservoir under different scenarios of fishing effort for the 30 years simulations (2012-2041). Dotted lines and dotdashed lines represent F_{MSY} from the Ecosim equilibrium analysis, corresponding to the stationary and full compensation mode, respectively.

4.4 DISCUSSION

Fishing effects, along with predator-prey relationships, were the main factors that contributed to explain catch trends in Itaipu fishery. Catches and diversity declined significantly between 1988 and 2011, even though the rates of change were small. In contrast, the mean Trophic Level of Catch (TLc) and the L index did not showed any significant change along the same period, indicating that Itaipu fishery has been sustainable in terms of ecosystem effects. Simulations revealed that ecosystem and species are not greatly affected by increased fishing effort, although, simulations with fishing at F_{MSY}, resulted in biomass decline for species that are important for the fishery, and some of them have a key role in ecosystem structure, such as *Z. jahu*.

4.4.1 Overall outputs of Ecopath and Ecosystem structure

Itaipu food web is supported mostly by a detritus-based chain, with a high recycling index, compared to other reservoirs (Gubiani *et al*. 2011). This could indicate a fast development *sensu* Odum's theory (1969), however reservoirs are systems that are constantly under disturbances, due to dam operations, which affect water level (Agostinho *et al*. 2007), so they can take more time to reach maturity, or even can be at an intermediate point between initial stage and maturity (Gubiani *et al*. 2011).

Top-down process were evident in Itaipu reservoir, where *S. brasiliensis* could be defined as an apex predator (Wallach *et al*. 2015), and exhibited a positive effect on species with lower trophic levels (*Leporinus elongatus*, *Schizodon borellii*), probably due the predation on those species' predators (*Rhaphiodon vulpinus*, *Serrasalmus* spp.). Among the other species identified as keystone species, *Hoplias* spp. was already identified to affect the structure of fish assemblage in floodplain lakes (Petry *et al*. 2010). In this way, the keystoneness results highlighted the importance of these species not just for the fishery, but also for the maintenance of the food web structure, despite their low biomass.

4.4.2 Fishing effects

After impoundment it is expected a shift in fish assemblages from migratory and large-bodied species, to sedentary, medium-sized species (Agostinho *et al*. 2016). So, it would be expected that the mean trophic level of catches in Itaipu reservoirs also showed a decrease in this indicator, but a constant trend for TLc was observed between 1988 and 2011. Even with the absence of large migratory piscivores (*S. brasiliensis* and *P. corruscans*), among the most caught species in the beginning of the time series (Philippsen *et al*. 2016), there was other three species with high trophic level (*P. squamosissimus*, *P. pinirampu* and *Hoplias* spp.) among the most caught species in landings. Considering that from 1988, there was no expressive change, in terms of composition of the main species caught in Itaipu reservoir (*P. granulosus*, *P. lineatus*, *H. edentatus*, *P. squamosissimus*, *P. pinirampu* and *Hoplias* spp.; Okada *et al*. 2012), this could be the explanation for why the TLc did not change. Also, according to Essington *et al*. (2006), only declines in TLc higher than 0.15 are indicative of ecologically significant fishing down the food web process, which did not happen in Itaipu fishery.

4.4.3 Ecosim fitting

The fitted model of Itaipu reservoir with lowest AICc, exhibited in a general way a mixed flow control (v=2), with some bottom-up (7 groups with v=1), and top-down flow controls (4 groups with v > 2). The lack of model fit for *H. edentatus* and *P. granulosus* could be an evidence that fishing is not the main driver for their population dynamics. Itaipu reservoir had an expressively decrease in primary productivity and consequently zooplankton (Abujanra and Agostinho 2002) which could negatively influence the abundance of *H. edentatus* (a planktivorous species). The predation by *P. squamosissimus* on *H. edentatus* was suggested as another factor influencing its abundance (Ambrósio *et al*. 2001), but our model estimated the vulnerability of *H. edentatus* as 1 (low influence of predation on it), going against the hypothesis of predation effects. It is interesting to notice that between 1988 and 1993, the model fit was good in our study, and in this same period, results from a single-species model showed that catches were higher than the maximum sustainable yield (Ambrósio *et al*. 2001). In this way, it is likely that population dynamics of *H. edentatus* was first driven by fishing and, after 1993 other factors than fishery had a main role.

For *P. granulosus*, the lack of fitting suggests that fishing could not explain its temporal dynamics, despite the importance of this species to total catch in Itaipu fishery. This population experienced a great increase in catches between 1988 and 1997, followed by a decrease. In this same period, an invader mollusk (*Corbicula fluminae*) had its abundance increased, associated with water levels dynamics in Itaipu reservoir, and contributed markedly for the diet of *P. granulosus* (90%). In 1996, abundance of *C. fluminae* decreased in Itaipu reservoir, and accounted only for 1% in the diet of *P. granulosus* (Gaspar da Luz *et al*. 2002). Bottom-up effects seems to have important roles in shaping the population dynamics of *H. edentatus* and *P. granulous*, and our model could not be able to represent these effects, resulting in lack of model fit.

4.4.4 Simulation of fishing scenarios

The majority of stocks in Itaipu fishery were not overfished and overfishing was not occurring under all scenarios, during the simulation phase of this study. Exceptions were *P. lineatus* which was overfished until 2030, *P. corruscans* was overfished only when F_{MSY} full compensation was applied (scenario 7), and *Z. jahu* during almost the entire period of simulations, under scenarios 7 and 8. When the estimated F_{MSY} full compensation were applied, catches were near or even higher than MSY for *P. lineatus*, *S. brasiliensis*, and *Z. jahu*, in the last years of simulation, contrasting with catch levels of *P. corruscans* which did not increased at all. The only stock that produced MSY under F_{MSY} scenarios (scenario 7 and 8) was *P. pirinampu*. Catches of *P. squamosissimus* increased at certain level under F_{MSY} full compensation, but stabilized before reaching the MSY, with its biomass levels decreasing until the biomass limit.

The F_{MSY} and MSY obtained by the full compensation mode were higher than the ones estimated when considering food availability and predation impacts constant (stationary approach). This output was expected, because the full compensation approach includes indirect compensatory responses through the ecosystem to changes in abundance of target species (Walters *et al*. 2005). In this way, the ability of the ecosystem models to account for losses due to predation, require higher fishing mortality to achieve the MSY reference point (Mackinson *et al*. 2009b).

The F_{MSY} estimates for both stationary and full compensation modes were the same for *P. pirinampu* probably because its estimated low vulnerability value (v=1; low influence of predator on it), so the effects of indirect compensatory responses could be negligible, leading to equal F_{MSY} estimates for both stationary and full compensation mode. Ecosim can overestimates F_{MSY} when the species had the vulnerability estimated as v=2, and biomass levels far below the unfished biomass in the Ecopath base scenario (Christensen *et al*. 2008), like *Z. jahu*, which is a migratory species with low abundance after the construction of Itaipu reservoir (Hoeinghaus *et al*. 2009).

According to the estimated biomass until 2011, the only stock being overfished during all the time period was *P. lineatus*, although overfishing was not occurring, and catches were far below the MSY. These results indicate that besides the fishing impacts, other factors are influencing its population dynamics. Environmental effects are known to affect fisheries yield, and regarding freshwater fisheries, productivity of stocks are known to be affected negatively by impoundment and by water level oscillation, due to dam operation, especially the stocks of migratory species, such as *P. lineatus* and other species (Hoeinghaus *et al*. 2009; Oliveira *et al*. 2015). Even though our ecosystem model did not include environmental anomalies, there is sound scientific knowledge, and also fishers' knowledge about the negative impacts of impoundment, and dam operation on fishery yields (Agostinho *et al*. 2016; Philippsen *et al*. 2016).

Another possibility is that the outputs of our model could be overestimated for F_{MSY}. So, considering that F_{MSY} was overestimated, our conclusion that overfishing was not occurring for *P. lineatus*, could be wrong, and besides environmental effects, there was high fishing mortality upon this stock. It is not an easy task to disentangle fishing and environmental effects on fish populations. Moreover, there are uncertainties in model outputs, mainly in data-poor fisheries, where usually the only data available is fishery-dependent. An alternative to account for uncertainties in model outputs could be the adoption of a buffer value, for the reference points obtained with models, as is done by the Pacific Fishery Management Council in the United States, for fisheries where only catch data is available (Wetzel and Punt 2015).

The simulations results showed little increase in catches with increased fishing effort for *P. corruscans* and *Z. jahu*, and higher biomass estimates in those scenarios. These results can be an indicative that the biomass levels for these species are currently too low to afford higher fishing pressure. Also, these species have low and very low resilience, respectively (Froese and Pauly 2016), which is also a factor that influences the stocks' productivity (Musick 1999). The fishing mortality was high in the beginning of the time series upon stocks of *P. corruscans* and *Z. jahu*, which added to the negative effects of habitat alteration, and their low resilience, resulted in low biomass levels. In this way, increased fishing effort upon these species is not advisable. On the contrary, *P. pirinampu* which also has low resilience seems to be a stock that can afford higher fishing efforts.

The concept of a F_{MSY} estimate that accounts compensatory responses is still a new idea in fisheries science, and careful is needed if implementing it in real situations. In our case, simulations showed that for some species (*P. lineatus*, *P. corruscans* and *Z. jahu*) the predicted biomass declined after applying F_{MSY}, both stationary and full compensation, and these stocks did not produced the maximum sustainable yield. These results are in accordance with the discussed above, and highlight that even the theoretical MSY approach is not suitable for them, considering all the elements involved in stock productivity (environmental effects, resilience, population biomass). On the contrary, the stocks of *P. squamosissimus* and *P. pirinampu* produced the MSY under F_{MSY} scenarios, and biomass levels were at or above the biomass target. Although fishing mortality at MSY did not produce the expected yield for *S. brasiliensis*, its predicted biomass level was above the biomass limit. Considering that this species is migratory, and is under the same negative effects caused by impoundment, as *P. corruscans* and *Z. jahu*, its medium resilience can be an explanation for the more optimistic outputs obtained for this species. At the same time, if we compare *S. brasiliensis* with *P. lineatus*, which is also a migratory species, and has medium resilience, although the results were different. An explanation could be that along the years, fishers reduced their effort upon *S. brasiliensis* because the costs were too high to continue to fish this species (fishers information), which did not happen to *P. lineatus*.

4.5 CONCLUDING REMARKS

Ecological models are increasingly being adopted to evaluate alternative fisheries management scenarios (Coll *et al*. 2009; Forrest *et al*. 2015). Models are known to be a simple representation of the systems, and to have uncertainties, but even this way, they are useful to understand ecosystem and fisheries dynamics (Hill *et al*. 2007). When dealing with data-poor fisheries, usually there is lack of data, and so the uncertainties increase, and more caution is needed to interpret the outputs and apply them in real situations. We acknowledge that our model is just a hypothesis representing the complex dynamics of the ecosystem and fisheries in Itaipu reservoir, even though, our findings are important because they allowed a more holistic evaluation of the local fishery, putting it in an ecosystem context.

In terms of management advice, our results indicate that fishing effort should not increase upon *P. lineatus*, *P. corruscans* and *Z. jahu*. The enforcement of the law to protect mainly *Z. jahu* is very advisable, because it was identified as a keystone species in Itaipu reservoir. The severe decline of this species will result not just in loss to fishery yields but also can impact the structure and functioning of the ecosystem. The species that the model did not reproduce the temporal trends of catches, *H. edentatus* and *P. granulosus*, should be investigated further to understand their dynamics, and to find a model that could represent their dynamics better than in this study.

The management of a multispecies fishery is not an easy task, especially in fisheries that are developed in reservoirs, which are constantly under environmental variation. Species and ecosystem conservation, appropriate income and food source are dimensions that should be taken into account under the ecosystem approach to fisheries management. Our study fulfilled the ecological dimension analysis, providing scientific knowledge to understand the Itaipu fisheries in an ecosystem context. Although, there is still a need to investigate the uncertainties related to the ecosystem model through a sensitivity analysis, which will allow evaluating how sensitive biomass estimates are, for example, to changes in input parameters. Also, assessment of the value chain of Itaipu fishery, will allow the investigation of the socio-economic impacts of different fishing management strategies, and complement the EAF for Itaipu fishery.

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APÊNDICE C – Food-web modeling approach to assess the stock status of a reservoir fishery

Section 1: Balancing the Itaipu model (Ecopath component)

After the setup of initial parameters for the Itaipu reservoir model, the EwE software proceeds to estimate the missing parameters and to achieve mass balance. To balance the model it is necessary to (i) estimate ecotrophic efficiency (EE) values for all the functional groups to be less than 1; (ii) the production/consumption ratio (P/Q) has to be between 0.05 and 0.3, for most groups; (iii) the respiration/biomass ratio (R/B) for fish groups must be in the range 1-10 year^{-1}; (iv) net efficiency cannot be lower than gross food conversion efficiency, GE (P/Q) (Christensen *et al*. 2008).

There were eight functional groups with EE higher than 1. To balance the model, changes in diet composition matrix were made to reduce the predation mortality rate on some functional groups (initial diet composition matrix is presented in Supp. Material, Table S1). We also changed some P/Q values, using the standard deviation of Z. For *Serrasalmus* spp. we changed the biomass, using the standard deviation. The only Q/B value changed was for *S. brasiliensis*, we used the value given by Angelini and Agostinho (2005). This was done in attempt to get P/Q value higher than 0.1.

To accomplish the item iii (R/B for fish groups lower than 10) for a balanced model, the unassimilated consumption (in the Basic input) was changed for higher values, because the fish functional groups that showed R/B greater than 10 were detritivores and herbivores. According to Christensen *et al*. (2008), the default value (0.2) for unassimilated consumption often underestimates egestion, especially for detritivores and herbivores species. The unassimilated consumption was changed for *P. lineatus*, *S. borellii*, *R. descalvadensis*, *M. intermedia*, *A. altiparanae*, and *Steindachneria* spp. After changing this parameter value, some species still showed R/B > 10 (Table 3).

Table S1. Input diet composition matrix for Itaipu reservoir model.

Prey \ predator	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**30**
1	0.7	0	0	0.15	0	0.9	0	0	0	0	0	0.4	0.1	0.1	0	0.15	0.1	0.3	0.1	0	0	0	0	0	0.15	0	0.1
2	0	0	0.2	0	0.4	0	0	0	0	0	0	0	0	0	0	0.3	0	0.1	0.25	0.1	0	0	0	0	0	0.04	0
3	0	0.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0.1	0	0	0	0	0	0	0.5	0.05	0	0	0	0	0	0.1	0.1	0	0	0	0	0	0	0.1
5	0	0	0	0.15	0.1	0.05	0	0.05	0	0	0	0	0.05	0.1	0	0.05	0.1	0.3	0	0	0	0	0	0	0.15	0	0.5
6	0	0	0	0	0.4	0.05	0.7	0	0	0	0	0.1	0.2	0.1	0	0.2	0.1	0	0.4	0.8	0	0	0.15	0	0	0.5	0.2
7	0	0	0	0	0	0	0	0	0.37	0.2	0	0	0	0	0	0	0	0	0	0	0.2	0	0	0	0	0	0
8	0	0	0	0	0	0	0	0	0	0.15	0	0	0	0	0	0	0	0	0	0	0.05	0.15	0.12	0	0	0	0
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.23	0.12	0	0	0	0
10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0.05	0.15	0.1	0	0	0.1	0
11	0	0	0	0	0	0	0	0.16	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.4	0	0	0	0	0	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0	0	0	0	0	0	0.05	0	0	0.05	0	0	0	0	0.1	0.15	0.12	0	0	0.2	0
18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05	0	0	0.15	0	0	0
19	0	0	0	0	0	0	0	0.1	0	0.15	0	0	0	0	0	0	0	0	0	0	0	0.15	0.1	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05	0
21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0.24	0	0	0	0	0.1	0	0.09	0.05	0	0	0	0	0.3	0.17	0.12	0.45	0	0.1	0
23	0	0	0	0	0	0	0	0	0	0.35	0	0	0	0	0	0	0	0	0	0	0.1	0	0.1	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0.07	0	0	0	0	0	0	0.41	0	0	0	0	0	0	0	0.07	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0.35	0	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0.01	0
27	0	0	0	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.4	0	0	0
29	0	0	0	0	0	0	0	0.23	0	0	0	0	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0.15	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Detritus	0.3	0.5	0.8	0.55	0	0	0.3	0	0	0	0	0	0	0.7	0	0.2	0.7	0.1	0.15	0	0	0	0	0	0.7	0	0.1
Import	0	0	0	0.15	0	0	0	0	0.15	0.15	0.15	0	0.15	0	0	0	0	0.2	0	0	0.15	0	0	0	0	0	0
Sum	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

Table S2. Diet Composition (DC) matrix after balancing Itaipu reservoir model (for Functional groups number, see Table 1).

Prey \ predator	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**30**
1	0.7	0	0	0.15	0	0.9	0	0	0	0	0	0.4	0.1	0.1	0	0.15	0.1	0.3	0.1	0	0	0	0	0	0.15	0	0.1
2	0	0	0.2	0	0.4	0	0	0	0	0	0	0	0	0	0	0.3	0	0.1	0.25	0.1	0	0	0	0	0	0.04	0
3	0	0.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0.1	0	0	0	0	0	0	0.5	0.05	0	0	0	0	0	0.1	0.1	0	0	0	0	0	0	0.1
5	0	0	0	0.15	0.1	0.05	0	0.05	0	0	0	0	0.05	0.1	0	0.05	0.1	0.3	0	0.2	0	0	0	0	0.15	0	0.5
6	0	0	0	0	0.4	0.05	0.7	0	0	0	0	0.1	0.2	0.1	0.15	0.2	0.1	0	0.4	0.6	0	0	0.15	0	0	0.41	0.2
7	0	0	0	0	0	0	0	0	0.47	0.4	0	0	0	0	0	0	0	0	0	0	0.2	0	0	0	0	0	0
8	0	0	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0.07	0.15	0.12	0	0	0	0
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.23	0.12	0	0	0	0
10	0	0	0	0	0	0	0	0.1	0	0	0.1	0	0.1	0	0.25	0	0	0	0	0	0.05	0.15	0.1	0	0	0.1	0
11	0	0	0	0	0	0	0	0.16	0.23	0	0	0	0	0	0	0	0	0	0	0	0.06	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.3	0	0	0	0	0	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
17	0	0	0	0	0	0	0	0.2	0	0	0	0	0.05	0	0.1	0.05	0	0	0	0	0.1	0.15	0.12	0	0	0.2	0
18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.05	0	0	0.15	0	0	0
19	0	0	0	0	0	0	0	0.05	0	0.13	0	0	0	0	0	0	0	0	0	0	0	0.15	0.1	0	0	0	0
20	0	0	0	0	0	0	0	0	0	0.12	0.01	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0.05	0
21	0	0	0	0	0	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0.18	0	0	0	0	0.1	0	0.1	0.05	0	0	0	0	0.3	0.17	0.12	0.45	0	0.2	0
23	0	0	0	0	0	0	0	0	0	0.1	0	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0	0.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
27	0	0	0	0	0	0	0	0	0	0	0.01	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.07	0.4	0	0	0
29	0	0	0	0	0	0	0	0.15	0	0	0	0	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0
30	0	0	0	0	0	0	0	0.1	0.15	0	0.03	0	0.05	0	0	0	0	0	0	0	0	0	0.1	0	0	0	0
Detritus	0.3	0.5	0.8	0.55	0	0	0.3	0	0	0	0	0	0	0.7	0	0.2	0.7	0.1	0.15	0	0	0	0	0	0.7	0	0.1
Import	0	0	0	0.15	0	0	0	0	0.15	0.15	0.15	0	0.15	0	0	0	0	0.2	0	0	0.16	0	0	0	0	0	0
Sum	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

Section 2: Pre-Bal analysis

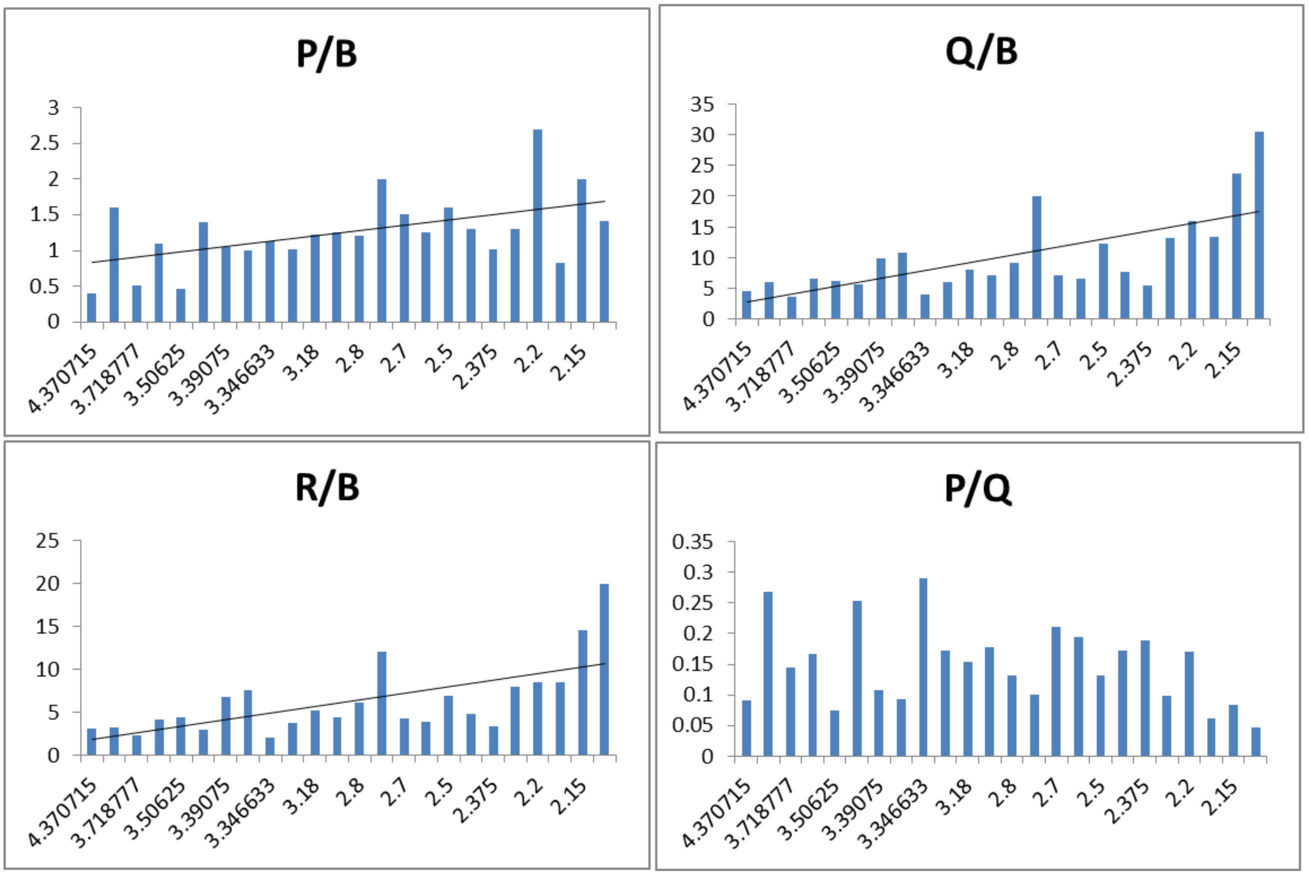

Fig. S1. Pre-Bal results. The plot only shows fish functional groups (x-axis represents parameters values and y-axis represents trophic levels).

Section 3: Ecosim fitting

Table S3. Stepwise fitting results, showing all the combinations of fishing, predator-prey interactions (v for vulnerabilities) and anomaly function (pp). K is number of parameters estimated. NVs is the number of vulnerabilities included in each model. NSpline is the number of spline points in the anomaly search.

Model	K	NVs	NSpline	SS	AIC	AICc
Fishing	0	0	0	383.597	90.85693	90.85693
Fishing and 1v	1	1	0	369.9921	82.90489	82.90489
Fishing and 2v	2	2	0	336.0082	58.34274	58.3574
Fishing and 3v	3	3	0	308.3645	36.69155	36.73566
Fishing and 4v	4	4	0	307.8449	38.28552	38.37408
Fishing and 5v	5	5	0	305.7402	38.46664	38.61479
Fishing and 6v	6	6	0	282.3889	18.6283	18.85135

Fishing and 7v	7	7	0	281.576	19.93838	20.25181
Fishing and 8v	8	8	0	277.6262	18.16077	18.58025
Fishing and 9v	9	9	0	275.355	18.03092	18.57227
Fishing and 10v	10	10	0	272.0812	16.88328	17.56252
Fishing and 11v	11	11	0	259.5235	6.011203	6.844536
Fishing and 2pp	2	0	2	383.5937	94.89847	94.91312
Fishing and 4pp	4	0	4	377.4246	94.52732	94.61588
Fishing and 6pp	6	0	6	369.2812	92.67175	92.89479
Fishing and 8pp	8	0	8	360.6247	90.35192	90.7714
Fishing and 10pp	10	0	10	359.5691	93.83369	94.51294
Fishing and 1v + 2pp	3	1	2	369.9862	86.97416	87.01828
Fishing and 1v + 4pp	5	1	4	364.4148	86.92039	87.06853
Fishing and 1v + 6pp	7	1	6	357.1025	85.52161	85.83504
Fishing and 1v + 8pp	9	1	8	349.8255	84.09794	84.63929
Fishing and 1v + 10pp	11	1	10	349.5686	88.21851	89.05185
Fishing and 2v + 2pp	4	2	2	335.8634	62.32739	62.41595
Fishing and 2v + 4pp	6	2	4	331.5524	62.92653	63.14958
Fishing and 2v + 6pp	8	2	6	325.0739	61.7072	62.12667
Fishing and 2v + 8pp	10	2	8	319.6729	61.37386	62.0531
Fishing and 3v + 2pp	5	3	2	308.0547	40.54815	40.6963
Fishing and 3v + 4pp	7	3	4	303.6968	40.81149	41.12492
Fishing and 3v + 6pp	9	3	6	297.7035	39.56913	40.11048
Fishing and 3v + 8pp	11	3	8	292.3626	38.89597	39.7293
Fishing and 4v + 2pp	6	4	2	305.7061	40.52589	40.74894
Fishing and 4v + 4pp	8	4	4	300.8027	40.29018	40.70966
Fishing and 4v + 6pp	10	4	6	295.3269	39.51046	40.1897
Fishing and 5v + 2pp	7	5	2	304.3647	41.41779	41.73122
Fishing and 5v + 4pp	9	5	4	292.0049	34.23478	34.77613
Fishing and 5v + 6pp	11	5	6	283.0258	29.93782	30.77116
Fishing and 6v + 2pp	8	6	2	279.7765	20.29018	20.70966
Fishing and 6v + 4pp	10	6	4	278.1171	22.93921	23.61845
Fishing and 7v + 2pp	9	7	2	279.334	21.9907	22.53205
Fishing and 7v + 4pp	11	7	4	275.7298	22.72967	23.563
Fishing and 8v + 2pp	10	8	2	275.6056	20.43547	21.11471
Fishing and 9v + 2pp	11	9	2	274.2803	21.27495	22.10829
Baseline	0	0	0	676.709	247.528	247.528
Baseline and 1v	1	1	0	676.6689	249.5262	249.5262
Baseline and 2v	2	2	0	676.709	251.5719	251.5866
Baseline and 3v	3	3	0	676.709	253.6162	253.6603
Baseline and 4v	4	4	0	676.7081	255.6752	255.7637
Baseline and 5v	5	5	0	676.7064	257.7491	257.8973
Baseline and 6v	6	6	0	676.6922	259.8334	260.0564

Baseline and 7v	7	7	0	676.7033	261.9435	262.257
Baseline and 8v	8	8	0	676.625	264.0331	264.4525
Baseline and 9v	9	9	0	676.6144	266.1661	266.7074
Baseline and 10v	10	10	0	676.6642	268.3399	269.0191
Baseline and 11v	11	11	0	676.694	270.5219	271.3552
Baseline and 2pp	2	0	2	676.6898	251.5641	251.5788
Baseline and 4pp	4	0	4	640.2698	240.3985	240.487
Baseline and 6pp	6	0	6	605.3824	229.0991	229.3221
Baseline and 8pp	8	0	8	577.5507	220.3364	220.7559
Baseline and 10pp	10	0	10	571.2963	221.6222	222.3014
Baseline and 1v + 2pp	3	1	2	676.2858	253.4435	253.4877
Baseline and 1v + 4pp	5	1	4	586.4203	218.2258	218.3739
Baseline and 1v + 6pp	7	1	6	554.8329	207.1394	207.4528
Baseline and 1v + 8pp	9	1	8	551.871	209.9208	210.4622
Baseline and 1v + 10pp	11	1	10	537.7328	207.0812	207.9145
Baseline and 2v + 2pp	4	2	2	662.0671	249.6382	249.7268
Baseline and 2v + 4pp	6	2	4	576.668	215.6873	215.9103
Baseline and 2v + 6pp	8	2	6	544.2227	203.9316	204.3511
Baseline and 2v + 8pp	10	2	8	538.8729	205.4959	206.1752
Baseline and 3v + 2pp	5	3	2	676.709	257.7502	257.8983
Baseline and 3v + 4pp	7	3	4	616.933	236.4211	236.7346
Baseline and 3v + 6pp	9	3	6	492.3828	178.4409	178.9822
Baseline and 3v + 8pp	11	3	8	487.6151	180.0786	180.9119
Baseline and 4v + 2pp	6	4	2	676.709	259.8402	260.0633
Baseline and 4v + 4pp	8	4	4	598.4352	230.1405	230.56
Baseline and 4v + 6pp	10	4	6	460.3358	162.0195	162.6987
Baseline and 5v + 2pp	7	5	2	676.709	261.9459	262.2593
Baseline and 5v + 4pp	9	5	4	613.4469	239.1159	239.6573
Baseline and 5v + 6pp	11	5	6	415.1031	135.6428	136.4761
Baseline and 6v + 2pp	8	6	2	676.709	264.0673	264.4868
Baseline and 6v + 4pp	10	6	4	586.6159	228.9258	229.605
Baseline and 7v + 2pp	9	7	2	676.709	266.2047	266.746
Baseline and 7v + 4pp	11	7	4	574.2659	225.2229	226.0562
Baseline and 8v + 2pp	10	8	2	676.709	268.3582	269.0374
Baseline and 9v + 2pp	11	9	2	676.709	270.528	271.3613

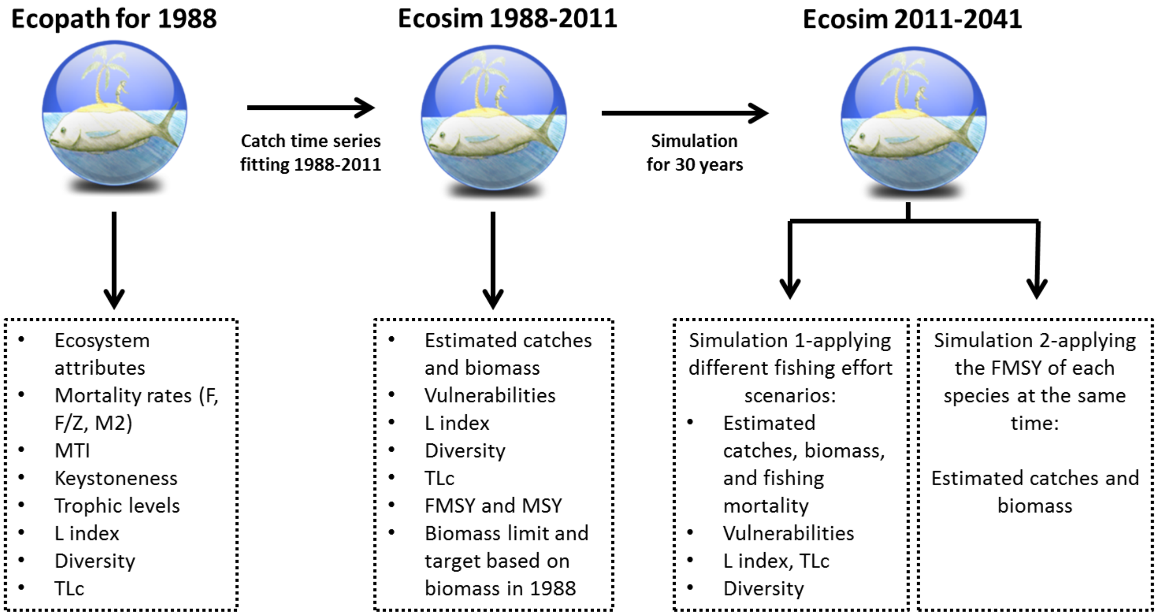

Fig. S2. Schematic diagram of the EwE modeling approach adopted in this study. Boxes with dot lines are showing the outputs analyzed in each step of the modeling procedure. F: fishing mortality; F/Z: fishing mortality relative to total mortality; M2: predation mortality; MTI: mixed trophic impact; TLc: mean trophic level of the catch.

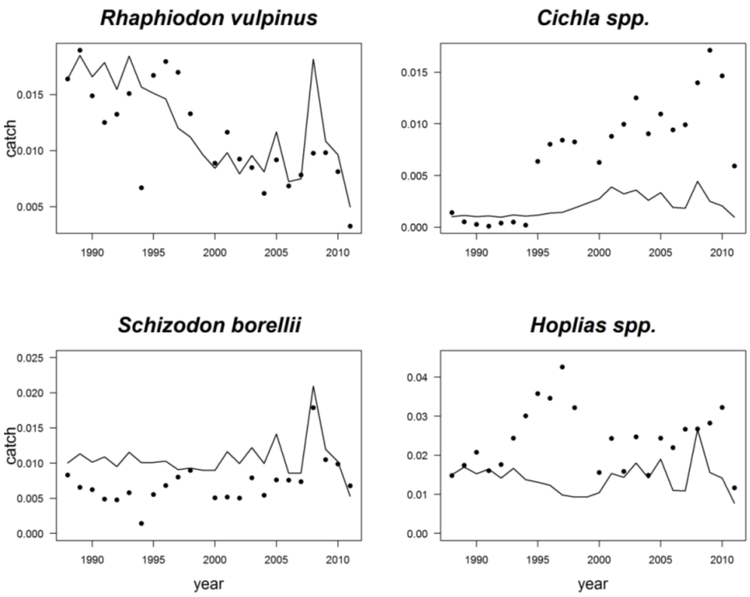

Fig. S3. Observed and predicted catches. Full circles are observed data and line is the model prediction.

Section 4: References used for input parameters and diet data.

Table S4. References for biomass, P/B and Q/B parameters. The numbers indicate the references used: 1: Angelini *et al*. 2006; 2: Froese and Pauly 2016; 3: Gubiani *et al*. 2012; 4: Froese and Binohlan (2000); 5: Angelini and Agostinho 2005; 6: $L_{\infty} = L_{max} * 1.05$; 7: Santana (2014); 8: Okada *et al*. 2012; 9: Petrere Junior and Angelini (2009); 10: Ambrósio *et al*. (2003); 11: Feitosa *et al*. (2004); 12: Dei Tos *et al*. (2009); 14: mean from the values of Angelini and Agostinho (2005), and Castro (1998); 15: Palomares and Pauly (1980); 16: Z from Beverton-Holt estimator in Quinn and Deriso (1999); 17: measured at Ichthyological Collection/Nupélia/UEM.

Group name	**biomass**	**QB**	**PB**	**K**	**Linf**	**Lmat**	**Winf**	**Ar**
Phytoplankton	1		1					
Macrophytes	1		1					
Periphyton	1		1					
Benthos	1	1	1					
Insects	ecopath	1	1					
Zooplankton	ecopath	1	1					
Leporinus elongatus	COM-SIR	15	16	9	6	8	2	17
Schizodon borelii	COM-SIR	15	16	5	5	4	3	5
Prochilodus lineatus	COM-SIR	15	16	7	7	8	2	5
Hypophthalmus edentatus	COM-SIR	15	16	0	10	8	2	5
Leporinus friderici	COM-SIR	15	16	5	6	4	2	5
Pterodoras granulosus	COM-SIR	15	16	5	6	8	2	5
Astyanax altiparanae	ecopath	5	5					
Roeboides descalvadensis	ecopath	15	3					
Raphiodon vulpinus	COM-SIR	15	16	5	6	4	2	5
Salminus brasiliensis	COM-SIR	5	16	11	6	12	2	5
Plagioscion squamosissimus	COM-SIR	15	16	14	6	8	2	5
Hoplias spp.	COM-SIR	15	16	5	6	6	2	5
Pinirampus pirinampu	COM-SIR	15	16	5	6	8	2	5
Moenkhausia intermedia	ecopath	5	5					
Hypostomus spp.	COM-SIR	15	16					
Cichla spp.	COM-SIR	15	16	4	6	4	2	3
P. corruscans	COM-SIR	15	16	5	6	4	2	5
Hemisorubim platyrhynchos	COM-SIR	15	16	5	6	4	2	5
Acestrorhynchus lacustris	1	15	16	5	6	4	2	5
Steindachnerina spp.	ecopath	5	5					
Gymnotus spp.	ecopath	3	3	3	6	4	**2**	3
Hoplosternum littorale	Ecopath	5	5					

Serrassalmus spp.	COM-SIR	15	16	5	6	4	2	5
Zungaro jahu	COM-SIR	15	16	5	6	4	2	5

Table S5. References used to obtain the diet information.

Functional group	**Reference**
Benthos	Angelini *et al*. 2006
Insects	Angelini *et al*. 2006
Zooplakton	Angelini *et al*. 2006
Leporinus elongatus	Hahn *et al*. (1998)
Schizodon borelli	Hahn *et al*. (1998)
Prochilodus lineatus	Hahn *et al*. (1998)
Hypophthalmus edentatus	Hahn *et al*. (1998)
Leporinus friderici	Hahn *et al*. (1998)
Pterodoras granulosus	Hahn *et al*. (1992)
Astyanax altiparanae	Hahn *et al*. (1998)
Pimelodus maculatus	Hahn *et al*. (1998)
Roeboides descalvadensis	Hahn *et al*. (1998)
Raphiodon vulpinus	Hahn *et al*. (1998); Luz-Agostinho *et al*. (2008)
Salminus brasiliensis	Bozza and Hahn (2010)
Plagioscion squamosissimus	Hahn *et al*. (1997); Bozza e Hahn (2010)
Hypostomus spp.	Hahn *et al*. (1998)
Hoplias spp.	Hahn *et al*. (1998); Bozza e Hahn (2010)
Pinirampus pirinampu	Hahn *et al*. (1998)
Moenkhausia intermedia	Hahn *et al*. (1998)
Cichla spp.	Hahn *et al*. (1998); Luiz *et al*. (2011)
Pseudoplatystoma corruscans	Bozza and Hahn (2010)
Hemisorubim platyrhynchos	Bozza and Hahn (2010)
Acestrorhynchus lacustris	Bozza and Hahn (2010); Hahn *et al*. (1998)
Steindachnerina spp.	Hahn *et al*. (1998)
Gymnotus spp.	Vidotto-Magnoni and Carvalho (2009); Pereira and Resende (2006)
Zungaro jahu	fishers' knowledge
Serrasalmus spp.	Hahn *et al*. (1998)

Section 5. Ecosystem attributes from Itaipu reservoir model.

Table S6. Ecosystem metrics of Itaipu reservoir model. TE: transfer efficiency (calculated as geometric mean for TL II-IV).

Attributes (unit)	Value
Sum of all consumption (t/km^2/year)	1241.32
Sum of all exports (t/km^2/year)	2857.1
Sum of all respiratory flows (t/km^2/year)	829.71
Sum of all flows into detritus (t/km^2/year)	3686.43
Sum of all production (t/km^2/year)	3845.35
Gross efficiency (catch/net p.p.)	0.0003
PPR/catch (total)	350.2
PPR/TotalPP (%)	0.532
Calculated total net primary production (t/km^2/year)	3682
Net system production (t/km^2/year)	2852.3
Total primary production/total biomass	26.25
Total biomass/total throughput (/year)	0.016
Total biomass (excluding detritus) (t/km^2)	140.27
Total catch (t/km^2/year)	1.08
Ecopath pedigree index (dimensionless)	0.182
TE from primary producers (%)	7.44
TE from detritus (%)	7.33
Throughput cycled (excluding detritus) (t/km^2/year)	0.325
Predatory cycling index (%)	0.026
Throughput cycled (including detritus) (t/km^2/year)	264.2
Overhead total (%)	57.26

Section 6. Results – Ecosim simulations.

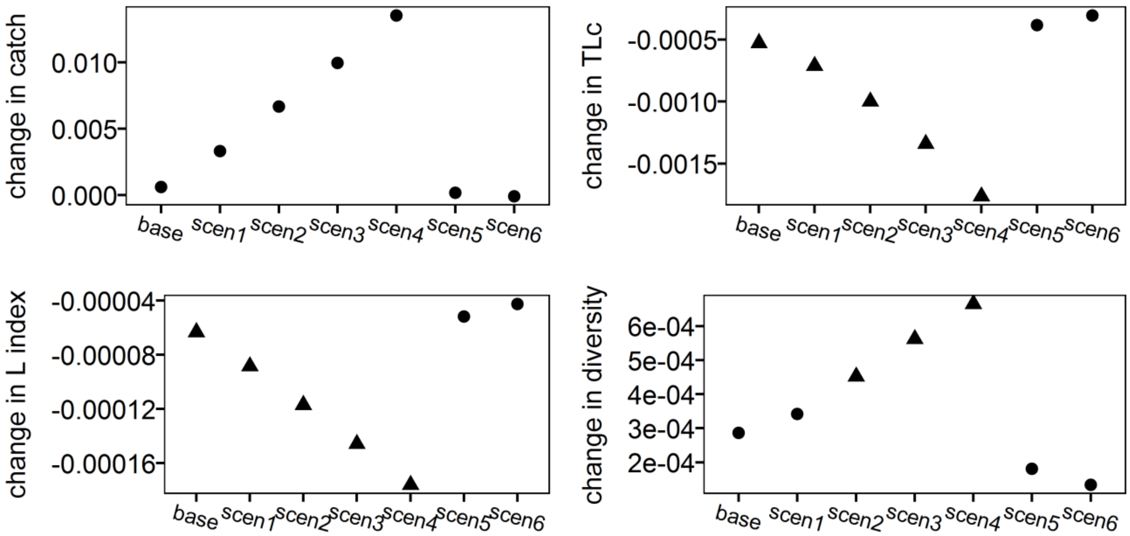

Fig. S4. Rates of change (year^{-1}) of the ecosystem indicators, obtained from the food web model of Itaipu reservoir, under different scenarios of fishing effort. Triangles indicate significant slopes (p-value < 0.05) and filled circles indicate no significant slopes. Scen1: scenario 1 (+25%), Scen2: scenario 2 (+50%), Scen3: scenario 3 (+75%), Scen4: scenario 4 (+100%), Scen5: scenario 5 (-10%), Scen6: Scenario 6 (-20%), Base: baseline (fishing effort in 2011).

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5 AVALIAÇÃO E CONCLUSÃO GERAIS

A gestão eficaz de recursos pesqueiros depende, entre outros fatores, de informações disponíveis a cerca do estado dos estoques e do esforço realizado. Modelos uni-específicos formam a base da abordagem tradicional de avaliação dos estoques pesqueiros. Nos últimos anos, a comunidade científica tem percebido a necessidade de considerar: a) os efeitos da pesca, não só nas populações alvo, mas também no ecossistema e b) os efeitos de outros impactos (mudanças climáticas, alterações no habitat, por exemplo) tanto no ecossistema, como na atividade pesqueira.

Este estudo investigou o estado dos estoques pesqueiros de um dos principais reservatórios brasileiros, utilizando diferentes abordagens: modelos uni-específicos e indicadores baseados no tamanho e um modelo ecossistêmico.

Dentre os modelos uni-específicos, os métodos limitados em dados, têm sido a alternativa para avaliar os estoques que possuem somente dados de captura disponíveis. A comparação de dois modelos baseados em dados de captura, evidenciou que as conclusões obtidas de diferentes modelos podem ser também bastante diferentes. Devido à falta de dados disponíveis, alguns pressupostos são necessários, porém muitas vezes, estes não correspondem à realidade. Uma alternativa para a gestão nestes casos seria adotar medidas conservativas, baseadas em pontos de referência limites ao invés de alvo.

Os ndicadores baseados no comprimento e um modelo baseado em capturas (COM-SIR), evidenciaram que alguns estoques no reservatório de Itaipu não são sustentáveis, pois há grande proporção de indivíduos abaixo do tamanho de primeira maturação na captura pesqueira do reservatório de Itaipu. Medidas de gestão devem ser tomadas para evitar a captura de indivíduos abaixo de Lm, e inclusive, implementar um limite para o tamanho máximo de captura a fim de proteger os indivíduos maiores e mais velhos.

O método baseado em capturas revelou que a mortalidade por pesca foi alta durante a maior parte da série temporal analisada, para quase todos os estoques, mas especialmente para *Z. jahu* (jaú) e *P. squamosissimus* (corvina) que apresentaram biomassa abaixo do recomendado e elevada proporção de captura de indivíduos jovens. A espécie *Z. jahu* possui resiliência muito baixa e sua população sofreu impactos negativos devido a construção do reservatório de Itaipu. Este fato destaca a delicada situação da gestão de recursos pesqueiros em reservatórios, uma vez que a prioridade é a produção de energia elétrica, independente da conservação dos recursos naturais e da sobrevivência das famílias que necessitam destes recursos.

A adoção de modelos ecossistêmicos para avaliar medidas de gestão está sendo cada vez mais priorizada. Embora seja uma abordagem que requer uma grande quantidade de dados e informações, que usualmente não estão disponíveis para pescarias limitadas em dados, ela permite avaliar o que aconteceria além da população que está sendo explorada. O modelo ecossistêmico do reservatório de Itaipu evidenciou a importância ecológica de determinadas espécies, como também que o efeito da pesca no ecossistema, não é tão negativamente impactante quanto se esperava. Em relação às estimativas de MSY e F_{MSY} obtidas com o modelo ecossistêmico, elas foram maiores que os valores obtidos com os modelos uni-específicos. Nem mesmo as estimativas calculadas com o modo estacionário, que deveriam ser semelhantes aos resultados dos modelos uni-específicos, foram maiores, com exceção de F_{MSY} para *P. corruscans* (pintado).

A classificação dos estoques em relação à mortalidade por pesca diferiu entre as abordagens ecossistêmica e uni-específica. Considerando os níveis de biomassa no ano de 2011, foi observado o mesmo padrão da mortalidade por pesca, com exceção de *Z. jahu*, que também foi classificado como sobrepescado. Embora o modelo ecossistêmico considere as interações tróficas, para estimar a biomassa e os pontos de referência (MSY e F_{MSY}), os resultados obtidos parecem ser muito otimistas. Sabe-se que além da pressão pesqueira, há também os efeitos negativos das variações hidrológicas sobre as populações de peixes no reservatório de Itaipu. Entretanto, as hipóteses testadas incluindo variações abióticas resultaram em ajustes ruins, e não foi possível incluir o efeito hidrológico no nosso modelo. Além disso, as estimativas de F_{MSY} e MSY obtidas com o software EwE são calculadas por meio de uma análise de equilíbrio, o que pode resultar em valores demasiadamente otimistas. A simulação da pesca com a mortalidade por pesca que produz rendimento máximo sustentável (F_{MSY}) mostrou um declínio na biomassa da maioria das espécies analisadas. Ainda, níveis de biomassa acima dos pontos de referência só foram observados nos últimos anos da simulação, assim como o rendimento máximo sustentável. Estes resultados confirmam o uso conservativo das estimativas dos pontos de referência.

Uma possibilidade futura poderia ser a investigação do comportamento da biomassa e da captura no contexto ecossistêmico, com simulações considerando os valores de F_{MSY} estimados com os modelos uni-específicos. Além disso, por se tratar de uma pescaria multiespecífica, ao estabelecer pontos de referência limite para a mortalidade por pesca, deve-se levar em consideração que diferentes espécies são capturadas com o mesmo aparato de pesca, o que dificulta ainda mais a operacionalização dos pontos de referência. Por fim, ainda é necessário incluir o valor econômico dos recursos pesqueiros de Itaipu, e o impacto que diferentes medidas de gestão terão na renda dos pescadores, dessa maneira, a abordagem da gestão da pesca baseada no ecossistema incluirá as dimensões social e econômica.