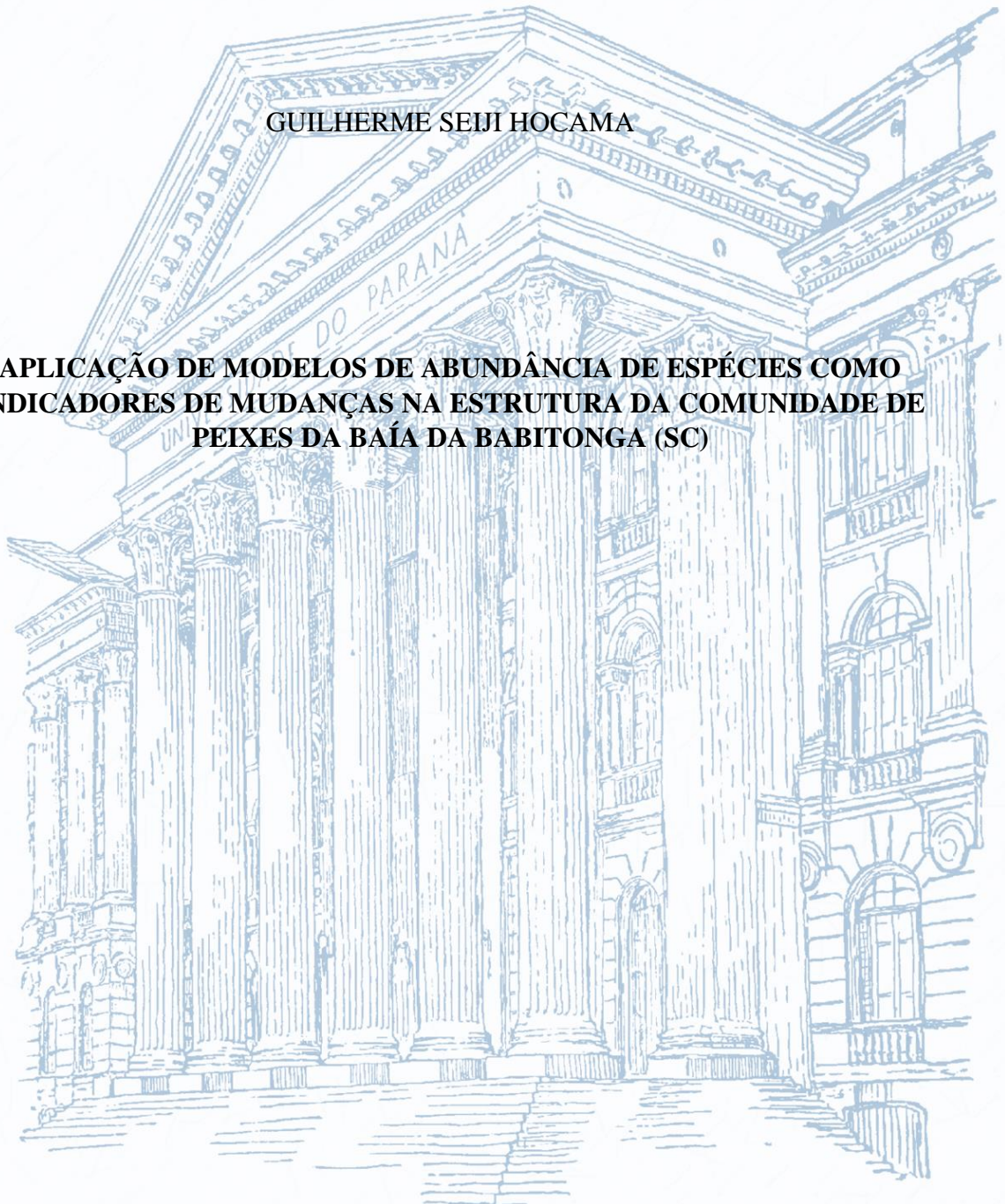


UNIVERSIDADE FEDERAL DO PARANÁ
CENTRO DE ESTUDOS DO MAR
PÓS-GRADUAÇÃO EM SISTEMAS COSTEIROS E OCEÂNICOS

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**APLICAÇÃO DE MODELOS DE ABUNDÂNCIA DE ESPÉCIES COMO
INDICADORES DE MUDANÇAS NA ESTRUTURA DA COMUNIDADE DE
PEIXES DA BAÍA DA BABITONGA (SC)**



PONTAL DO PARANÁ
2015

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Orientador: Maurício G. de Camargo.

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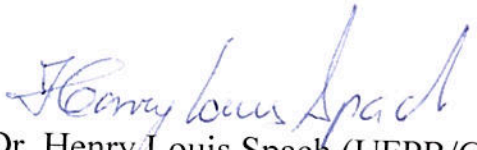
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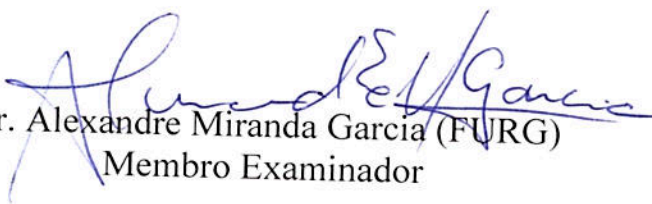
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Pontal do Paraná, 23/03/2015.

*Most people say that it is the intellect which makes a great scientist.
They are wrong: it is character.*
Albert Einstein

Words, in my humble opinion, are the most inexhaustible source of magic we have.
J.K. Rowling

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Aos meus pais.

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Aos *Amiégos* e os *Bando de à toas*.

#pgsicolifestyle

RESUMO

Um dos principais objetivos da ecologia é entender como as espécies se distribuem, tanto espacialmente quanto temporalmente. Descobrir os padrões de distribuição da riqueza e abundância é um passo essencial para esse entendimento. A observação de espécies raras e comuns dentro de um mesmo ambiente é um dos padrões mais recorrente encontrado na ecologia. Conhecer-las e entender o porquê desse padrão é um passo fundamental para a proteção ambiental. Os modelos de Distribuição de Abundância de Espécies aparecem como ferramenta indispensável, uma vez que são capazes de descrever matematicamente a maioria das nuances intrínsecas das comunidades, demonstradas numa curva. A tentativa de explicar essas curvas tem sido um tema central em ecologia teórica, mas ainda sem consenso formal entre pesquisadores. Coletas foram realizadas entre os anos de 2005 a 2008 ao longo de todo o gradiente ambiental da Baía da Babitonga, litoral norte de Santa Catarina, Sul do Brasil. Foram utilizadas seis tipos de rede que foram capazes de amostrar com sucesso a ictiofauna da Baía, como mostrado pela curva de rarefação. Para a modelagem, foram utilizados quatro diferentes modelos, buscando encontrar qual seria o responsável por ilustrar a distribuição da comunidade de peixes de forma mais eficaz. Foram eles: o modelo normal-logarítmico, a série-logarítmica, o de metacomunidade e o de vara-quebrada. Foram realizadas análises de agrupamento e discriminantes para auxiliar nas inferências. Todas as análises foram realizadas no *ambiente R*, com os pacotes *sads* e *vegan*. Para as análises espaciais, o modelo normal-logarítmico foi o elencado, para todas as áreas. Para a análise temporal, novamente o modelo normal-logarítmico foi o elencado, porém, em 2006, o modelo de série-logarítmica e o de metacomunidade também foram escolhidos. Para as análises de guildas, os estuarinos residentes e zooplânctívoros mostraram distribuição metacomunidade e séries-logarítmica; migrantes marinhos, piscívoros e zoobentívoros apresentaram distribuição normal-logarítmica e os marinhos-visitantes distribuição normal-logarítmica, série-logarítmica e metacomunidade. O resultado mostrou que a Baía da Babitonga possui uma comunidade em equilíbrio e pouco impactada, com grande abundância de espécies marinhas, quase igual ao número de espécies estuarinas. O resultado das guildas indica que processos diferentes atuam dentro de escalas menores, como corroborado pelas análises multivariadas, onde os índices ecológicos estavam relacionadas às guildas mais abundantes e com mais espécies. Estudos que avaliem a variação da biomassa são necessários, assim como análises dos parâmetros dos modelos elencados.

Palavras-chave: Estuário subtropical, ictiofauna, normal-logarítmico, ecologia estuarina

ABSTRACT

One of the main goal on ecology is to understand how species are distributed, both spatially and temporally. Unveil the distribution patterns of richness and abundances are essential steps to achieve it. Observation of rare and common species within an ecosystem is one of the most recurrent pattern found on natural communities, and understand why this pattern occurs, is essential for preservation. Species Abundance Distributions (SAD) models are a fundamental tool, once they are able to describe mathematically almost all nuances of each community, showed on a distribution curve. Attempts to explain these curves has been a central theme of theoretical ecology, but with no formal agreement between researcher ecologists. Surveys occurred between years 2005 and 2008, along an environmental gradient of Babitonga Bay, north littoral of Santa Catarina state, South of Brazil. Six different seine nets were utilized, being able to success capture the Bay's diversity, as showed on rarefaction curve. Four different models get tested, trying to identify which is the responsible for accurate representation of fish community distribution, following: lognormal, logseries, matacommunity and broken-stick models. Cluster and discriminant analysis were used to help on inferences. All analyzes were performed on *R Program* with packages *sads* and *vegan*. For spatial analysis, the lognormal model was the chose for all areas. For temporal analysis, lognormal model was also the chosen one, however for year 2006, logseries and metacommunity models were also chosen. For the analysis of guilds, residents, estuarine and zooplanktivore showed metacommunity and logseries distribution; marine-migrants, piscivore and zoobenthivore had lognormal distribution and marine-stragglers lognormal, logseries and metacommunity distribution. The results showed that Babitonga Bay has a balanced community and little anthropogenic affected, with large numbers of marine species, almost equal to the number of estuarine ones. The result of guilds indicates that different processes act in smaller scales, as evidenced by the multivariate analysis, where the ecological indices were related to more abundant and richer guilds. Studies assessing the change in biomass are required, as well as analysis of the parameters of chose guilds models.

Key-words: Babitonga Bay, ichtyofauna, lognormal

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PREFÁCIO

Esta dissertação é requisito parcial para a obtenção do Título de Mestre em Sistemas Costeiros e Oceânicos, conforme modelo proposto pela coordenação. Ela está dividida em três partes: A primeira parte é composta por uma introdução geral, com justificativa, hipótese e objetivos, abordando parte teórica sobre os modelos de distribuição de abundância de espécies; A segunda parte, é um capítulo completo, em inglês (ainda sem revisão) sobre a aplicação dos modelos de distribuição de espécies nos dados espaciais e temporais da ictiofauna da Baía da Babitonga (SC), com submissão pretendida à revista *Ecological Modelling* (estrato Qualis: A1, JCR: 2.326). A terceira parte é um capítulo completo, em inglês (sem revisão), sobre a aplicação dos modelos de distribuição de espécies em diferentes guildas ecológicas e o uso de análises multivariadas para o entendimento de padrões ecológicos da ictiofauna da Baía da Babitonga (SC), com submissão pretendida ao periódico *Oecologia* (Qualis: A1, JCR: 3.248)

INTRODUÇÃO GERAL

Um dos objetivos centrais da ecologia é entender as regras que governam as assembleias ecológicas, tanto em escala global quanto regional (ZHOU; ZHANG, 2008). Compreender como a diversidade, distribuição e abundâncias das espécies alocam-se no ambiente é um passo essencial para tal entendimento, porém ainda há muito a ser elucidado (RICKLEFS; SCHLUTER, 1993).

Os processos determinantes por alocar as espécies criam diferentes nichos e, conseqüentemente, resultam na observação de espécies raras ou comuns, especialistas ou generalistas (BELL, 2001). Esses processos que geram e mantêm a diversidade biológica são complexos e variados – desde processos genéticos, a geológicos globais - tornando inviável sua mensuração e análise direta. Conseqüentemente, resumir-los facilita o entendimento da diversidade (MAURER; MCGILL, 2004) e sua observação permite compreender e prever a natureza dos padrões, respeitando as peculiaridades de cada ambiente (CASSEMIRO; PADIAL, 2008; DEVAUR; GRASS, 2011). Conhecer os reais padrões de distribuição e de abundância das espécies (ARAÚJO; WILLIAMS, 2000; GASTON; BLACKBURN, 2000) e como e por que elas variam no tempo e no espaço (MacARTHUR, 1965; PURVIS; HECTOR, 2000) são ferramentas indispensáveis para

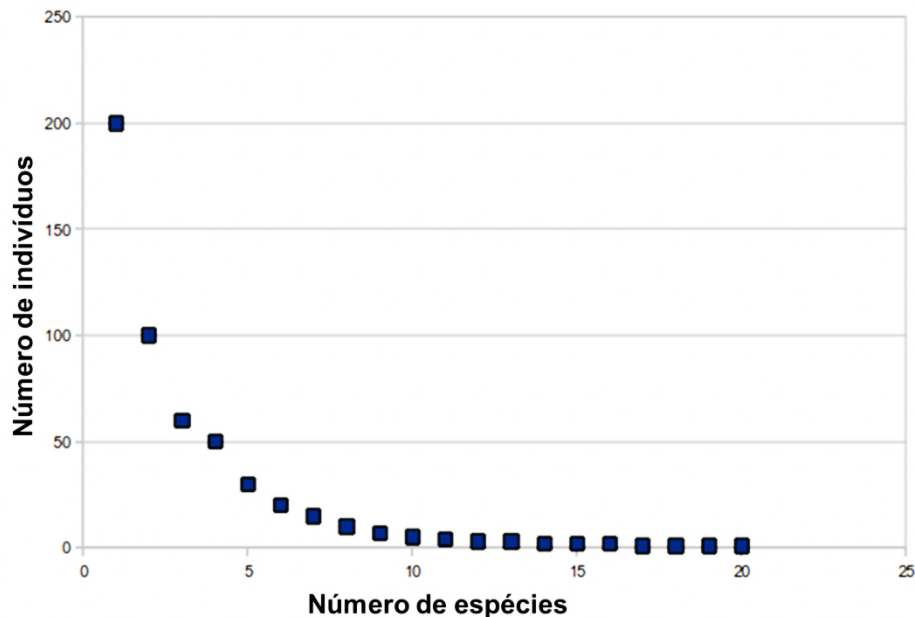
35 ações de preservação. No entanto, frequentemente as informações disponíveis são
36 imprecisas e fragmentadas (JIMENEZ-VALVERDE *et al.*, 2008).

37 Um dos principais teoremas da macroecologia é a relação entre a distribuição e a
38 abundância das espécies, que prega que as espécies comuns e abundantes possuem maior
39 dispersão espacial, enquanto espécies raras são restritas espacialmente (VERBERK,
40 2012), apesar de ambos os grupos serem encontrados em todos os ambientes (MACE *et*
41 *al.*, 2008). Além disso, identificar as espécies raras – predominantes na maioria das
42 comunidades (FISHER; CORBET; WILLIAMS, 1943; PRESTON, 1948) – é de especial
43 interesse, pois elas requerem maiores cuidados (devido ao maior risco de extinção;
44 GASTON, 1994) - e sua inclusão ou exclusão no ambiente pode diminuir a capacidade
45 de detectar e medir as mudanças ecológicas (CAO; WILLIAMS; WILLIAMS, 1998;
46 HESSEN; WALSENG, 2008).

47 A diversidade biológica pode ser analisada de diversas formas, a partir dos índices
48 de univariados, modelos de distribuição de espécies ou análises multivariadas. A
49 utilização dos índices univariados - como diversidade (α – entre locais, β – entre
50 comunidades e γ – entre ecossistemas), riqueza (número de espécies numa determinada
51 região ou período) ou a equitabilidade (relação entre a abundância e o número de
52 espécies) – são os mais recorrentes na literatura (HUBÁLEK, 2000), no entanto foram
53 propostos para medir um dos parâmetros por vez, o que pode acarretar em vieses
54 consideráveis das inferências a partir deles (PURVIS; HECTOR, 2000) devido à alta
55 perda de informações, frequentemente não fornecendo respostas ecológicas plausíveis
56 depois de calculados (DIAS, 2004). As análises multivariadas são mais complexas e
57 servem para encontrar a principal direção de variação dos dados, efetuar correlações entre
58 matrizes ou ainda encontrar diferenças entre grupos (BORCARD; GILLET;
59 LEGENDRE, 2011).

60 Já os modelos de distribuição de abundância das espécies (DAE – ou SAD, do
61 inglês “*species abundance distribution*”) buscam prever matematicamente o
62 comportamento das comunidades a partir do número de indivíduos de cada espécie do
63 ambiente, dado facilmente obtido (GREEN; PLOTKIN, 2007), representados por um
64 gráfico de dispersão que apresenta uma curva côncava (ou “*hollow curve*”, Figura 1),
65 mostrando que poucas espécies são muito abundantes, e muitas espécies são raras. A
66 tentativa de explicar o formato dessa curva tem sido um tema central da ecologia teórica
67 desde a década de 30 (MOTOMURA, 1932; FISHER; CORBET; WILLIAMS, 1943) e

68 tem gerado diversas propostas (ver MARQUET *et al.*, 2004; MCGILL *et al.*, 2007 para
69 detalhes).



70

71 Figura 1: Distribuição de abundância de espécies, mostrando o padrão geral encontrado em
72 comunidades ecológicas, onde é perceptível a dominância numérica de poucas espécies ("espécies
73 comuns") e a grande frequência de espécies raras, com baixas abundâncias. Modificado de Zachary, 2013.

74

75 Mesmo possuindo um formato geral semelhante, estas curvas apresentam
76 diferentes nuances para cada comunidade – como respostas às alterações bióticas e
77 abióticas (BELLIER *et al.*, 2013) – tornando a modelagem estatística delas importante
78 (LIMA *et al.*, 2012), uma vez que algumas teorias estatísticas podem ser convertidas em
79 suposições ecológicas (MCGILL, 2010). Isso representa uma inestimável, porém
80 negligenciada, ferramenta de gestão, uma vez que as alterações podem ser detectadas na
81 comunidade como um todo, tornando o método independente da identificação de espécies
82 indicadoras ou sensíveis a impactos, tornando as comparações independentes da
83 composição taxonômica das comunidades (GRAY *et al.*, 2006).

84

85 Tradicionalmente, duas famílias de modelos têm sido utilizados para a
86 modelagem das abundâncias: biológicos e estatísticos. Enquanto os biológicos
87 manipulam a curva a partir do ambiente, os estatísticos inferem conclusões a partir da
88 curva (MAGURRAN, 2004). Modelos estatísticos, inicialmente criados para outras áreas,
89 vêm se tornando cada vez mais comuns devido a capacidade de prever padrões
90 macroecológicos (NEKOLA; BROWN, 2007), teorias de distribuição (MCGILL;
NEKOLA, 2010) e por sua capacidade de transformação em pressupostos ecológicos

91 (McGILL, 2010), permitindo que as inferências das DAE não sejam divergentes da
92 biologia (GASTON; BLACKBURN, 2008).

93 A partir desses modelos, é possível identificar alterações na estruturação das
94 populações comparando diferentes guildas e faixas etárias (MAGURRAN;
95 HENDERSON, 2012), taxas de natalidade e mortalidade (BOWLER, KELLY, 2012),
96 relações como predação e competição (VERBECK, 2012) relacionando as distribuições
97 com variáveis abióticas (RODRIGUES, 2011), comparando as distribuições com
98 diferentes esforços de amostragem (GREEN; PLOTKIN, 2007), permitindo fazer
99 inferências sobre processos de perturbação antrópico (HILL; HAMER, 1998) e variações
100 climáticas (MAC NALLY, 2007), analisando as respostas das distribuições ao longo de
101 gradiente ambiental (PIELOU, 1977).

102 Apesar de existirem mais de 40 diferentes modelos propostos na literatura
103 (McGILL *et al.*, 2007), ainda não há consenso sobre qual o modelo ideal para explicar
104 um mesmo padrão ecológico (TOKESHI, 1999; MAGURRAN, 2004). A utilização de
105 mais de um modelo concorrente é essencial para a adequada identificação do modelo
106 correto (MAGURRAN, 2004). Neste estudo foram testados quatro modelos concorrentes:
107 normal-logarítmico, série-logarítmica, vara quebrada e de metacomunidade (Figura 2).
108 Para o modelo série logarítmica, a probabilidade de a espécie ocorrer dentro da amostra
109 será dada por:

$$110 \quad f(r|\alpha) = \frac{N^r}{r(N+\alpha)^r \log\left(\frac{N+\alpha}{N}\right)}$$

111 Onde, $f(r|\alpha)$ é a probabilidade da espécie ocorrer na comunidade, dado o parâmetro α
112 (que é proporcional ao número de indivíduos da espécie na amostra e o total de indivíduos
113 N (PRADO, 2010), sendo frequentemente elencado em ambientes de baixa
114 equitatividade, com dominância de espécies raras.

115 Para o modelo normal-logarítmico, a função de probabilidade de abundância da
116 amostra será dado por:

$$117 \quad f(r|\mu, \sigma) = \frac{1}{r\sigma\sqrt{2\pi}} e^{-\frac{(-\ln(r)-\mu)^2}{2\sigma^2}}$$

118 Onde, $f(r|\mu, \sigma)$ é a probabilidade de uma espécie ter abundância r na comunidade, dados
119 os valores μ e σ , que são parâmetros de escala e forma, respectivamente (MANDAI,
120 2010). Esse modelo baseia-se no teorema do limite central, onde a maioria das espécies
121 possuem distribuições intermediárias, com maior equitabilidade.

122 Outros modelos, como o de vara quebrada não utiliza parâmetros
 123 (MACARTHUR, 1957), com a modelagem feita a partir da riqueza e da abundância direta
 124 das espécies. A probabilidade deste modelo é dada por:

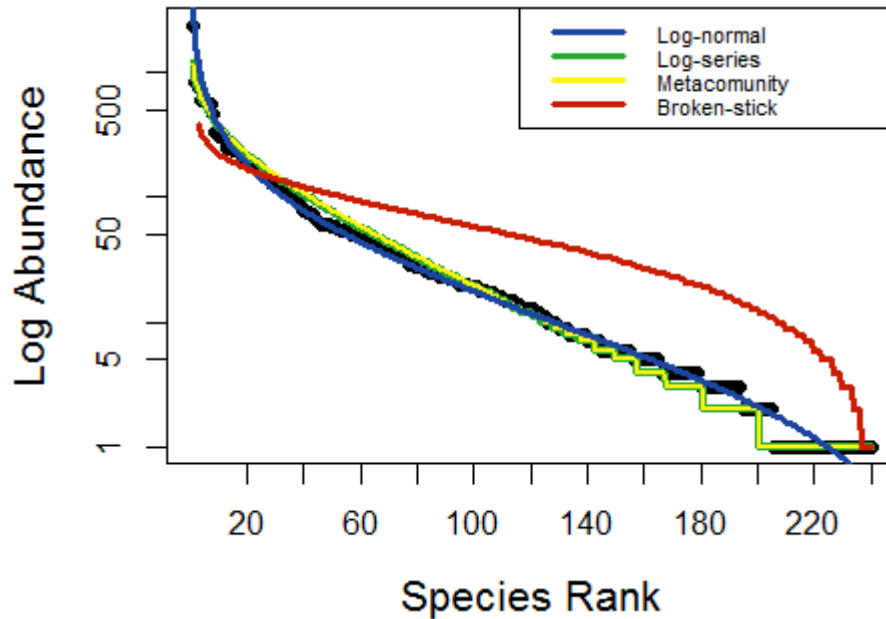
$$125 \quad S(n) = \frac{S(S-1)}{N} \left(\frac{1-n}{N} \right)^{S-2}$$

126 Onde, $S(n)$ é o número de espécies na classe de abundância com n indivíduos; S é o
 127 número total de espécies dentro da comunidade e; N é o número total de indivíduos
 128 (MARTINS; SANTOS, 1999). Para este modelo, as abundâncias são distribuídas
 129 aleatoriamente e de modo desigual, com a comunidade respondendo a um fator principal.

130 O modelo de metacomunidade considera que as espécies possuem iguais
 131 capacidades de ocupação de nichos, tornando-as todas competitivas pelos recursos
 132 dispostos no meio ambientes (HUBBEL, 2001; modificado por ALONSO; MCKANE,
 133 2004). Para esse modelo, a probabilidade de distribuição é dado por:

$$134 \quad S(n) = \theta \int_0^1 P_s(n; J, m, x) \frac{(1-x)^{\theta-1}}{x} dx$$

135 Onde: $S(n)$ é o número de espécies com n indivíduos; θ é o número fundamental da
 136 biodiversidade e $P_s(n; J, m, x)$ é a probabilidade de encontrar uma espécie com n
 137 indivíduos numa assembleia de tamanho J com abundancia relativa x com taxas de
 138 imigração m , onde a distribuição apresenta relação tanto com a heterogeneidade
 139 ambiental quanto com a capacidade de movimentação das espécies.



140

141 Figura 2: Simulação realizada com os dados de abundância de espécies de mariposas (Fisher et al.,
142 1943; pontos pretos) para os modelos de distribuição de espécies normal logarítmico, série-logarítmica,
143 metacomunidade e de vara-quebrada.

144

145 Inicialmente, é realizada a escolha dos parâmetros responsáveis por determinar a
146 aderência do modelos em relação aos dados amostrados, feita a partir dos estimadores de
147 verossimilhança (MANDAI, 2010). Os parâmetros passam a ser responsáveis pela
148 escolha de modelos concorrentes, indicação dos padrões das comunidades e comparações
149 entre áreas (PIELOU, 1977).

150 Dentre os modelos concorrentes, aquele mais plausível será escolhido através do
151 Critério de Informação Akaike (AIC). Os parâmetros de cada modelo são utilizados para
152 melhor ajustar os dados à curva. Uma vez testados os modelos, o AIC calcula o peso dos
153 parâmetros, resultando no melhor ajuste das abundâncias a cada modelo, através da
154 fórmula:

155

$$AIC = 2k - 2L$$

156 Onde: k é o número de parâmetros do modelo e L é o valor da Log-verossimilhança (log
157 da probabilidade) (PRADO, 2010).

158

159

160

JUSTIFICATIVA

161

162 A utilização de novos métodos para a análise de dados são de importância
163 fundamental para a identificação de padrões e entendimento dos diversos fatores
164 responsáveis pela alocação das espécies no meio ambiente. Trabalhos de modelagem
165 estatística de comunidades marinhas aparecem como ferramentas indispensáveis e
166 possuem aplicação prática para a gestão dos recursos marinhos.

167

168

169 **HIPÓTESE**

170

- 171 • Se a distribuição de abundância de espécies responde diretamente às diferenças de
172 abundâncias, então haverá diferentes modelos elencados quando: maior equitabilidade
173 (lognormal), menor equitabilidade (logseries), dominância de processos ecológicos
174 (metacomunidade/vara-quebrada), apresentados de acordo com os conjuntos de dados
175 testados (espacial/temporal/guildas)

176

177

178 **OBJETIVOS**

179

180 *Objetivo geral*

181

- 182 • Aplicar os modelos de distribuição de abundância em dados ictiológicos
183 da Baía da Babitonga.

184

185 *Objetivos específicos*

186

- 187 • Testar a eficiência dos modelos de distribuição de abundância em dados
188 ictiológicos marinhos;
- 189 • Comparar as respostas dos modelos de distribuição de abundância contra
190 análises multivariadas;
- 191 • Identificar alteração do padrão de distribuição de abundância das espécies
192 entre ambientes da Baía da Babitonga;

193

194

195

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1 **CAPÍTULO 1: HOW IS GIVEN THE ABUNDANCE**
2 **DISTRIBUTION OF FISHES IN A SOUTHWESTERN ATLANTIC**
3 **ESTUARY?**

4
5
6 **Introduction**

7
8 Abundances of species within ecological communities are not uniformly
9 distributed and usually presents numerical dominance of few species (Fisher *et al.* 1943;
10 Verbeek 2011). This is one of the most common pattern in ecology: the hollow curve
11 (McGill *et al.* 2007). Attempts to discover the process underlying this pattern, some
12 theories were proposed – such as the niche partitioning (complaining that each species
13 occupies the environment with available resources), neutral theory (assuming that each
14 species have equally capacity of occupying the environment) or the maximum entropy
15 (where each specie is uniformly distributed) (McGill 2010).

16 Some models were created to explain this pattern, trying to undercover the the
17 process responsible for differences in abundances os species in each ecological
18 community, the so called Species Ambundance Distribution (SAD). Since the first
19 model proposed from Motomura (Doi & Mori 2013), more than 30 different distribution
20 were elaborated, still without accordance about their accuracy (McGill *et al.*, 2007, for
21 details). Despite mathematically containing most of ecological information, the
22 existence of this amount of models makes clear that identify all dynamics responsible
23 for community structure are manifold and hardly measurable (Magurran 2004; Bowler
24 & Kelly 2010).

25 Even identifying a recurrent pattern and their self-informative feature (Yen *et*
26 *al.* 2013), few attention has been given to these models (McGill *et al.* 2007), due tolack
27 of tests with empirical data and, being necessary studies capable to define precisely the
28 inferences from each model (Ulrich *et al.* 2010).

29
30 Babitonga Bay is located in South Brazil, in a transitional zone between tropical
31 and temperate Southern Atlantic (Spalding *et al.* 2007). It is a homogeneous estuary,
32 with well demarcated seasons and semi-diurnal tide with 6 m maximum amplitude
33 (Cremer *et al.* 2006). Directly influenced by continental drainage and from Atlantic

34 Ocean, having mangrove and rain forest fringe. Reaching 28 m maximum depth on
35 main channel and exhibits large sandbanks on low-tide (Mazzer & Gonçalves 2011).
36 Shelter two harbors (São Francisco do Sul and Itapóia – suffering extent anthropic
37 pressure from six cities surrounding (Ibama & Cepsul 1998), being considered priority
38 area for conservation (MMA 2007).

39 Utilization of both univariate and multivariate analyzes are broadly utilized for
40 ecological studies in estuaries, but SADs are neglected. Thereby, this work aimed to
41 identify the best fitted SAD model for ichtyofauna in a Brazilian estuary and its
42 inferences, testing the hypothesis: if there is significant alteration in species abundance
43 through areas, then different SAD models will be chosen.

44

45

46 **METHODS**

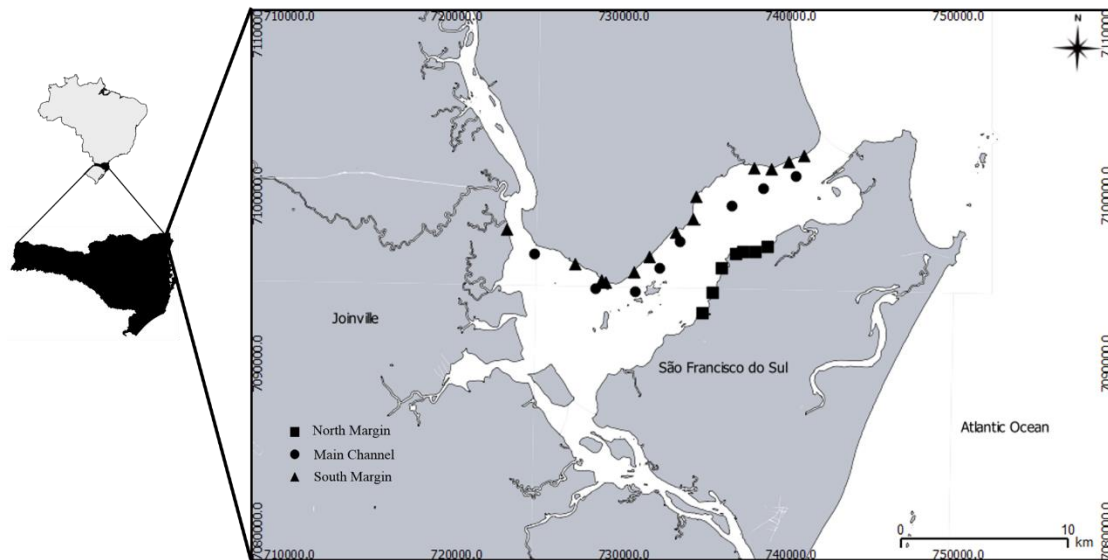
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48 *Data Collection*

49 Abundance data were obtained from three different surveys. On north margin,
50 thirteen sand beaches along the estuarine gradient was sampled in eight months (October
51 and November / 2007, January, February, April, May, July and August / 2008) totaling
52 208 samples. Every months, two hauls per site were made. For the first haul, a beach
53 seine net with 6 m long, 21.6 m height and 1.0mm mesh size was dragged along 10m
54 parallel to the coast. The second haul, the beach seine net had dimensions of 15 m long,
55 2 m height and 2.5 mm mesh, dragged 30 m along the coast.

56 To south margin, three hauls were made through seven sites of polyhaline sector
57 of the bay, between August 2005 to July 2006., totaling 252 samples. First haul was
58 made with a beach seine net with 15 m long, 1.6 m height and 5 mm mesh. For second
59 haul, the seine net had 15 m long, 1.6 m height and 2.5 mm mesh, both over 20 m path
60 parallel to the coast. The third haul, the beach seine net used was 6 m long, 1.6 m high
61 and 1 mm mesh over 6 m parallel to the coast, to minimize net clogging.

62 For channel, the collections were performed on eight months (October and
63 November / 2007, January, February, April, May, July and August / 2008) in 9 sites
64 along the main channel of Babitonga Bay. In each sampling site, two bottom trawls
65 were dragged for minimum of 5 minutes, in a total of 144 samples (Figure 1).



66
67 Figure 1: Babitonga Bay, north littoral of Santa Catarina, Brazil. Indications of three surveys
68 made through years 2006 to 2008.
69

70 All fishes captures were frozen and carried to the laboratory, where they were
71 identified (following the (Figueiredo & Menezes 1978, 1980, 2000; Menezes &
72 Figueiredo 1980, 1985; Barletta & Corrêa 1992).
73

74 *Modelling*

75 The abundance data of the estuary was categorized in three conjuntos analysis:
76 General – considering all species abundance sampled within the Babitonga Bay;
77 Channel – considering all abundances sampled through the main channel of the bay; and
78 Margins – where abundance of both north and south margins were summed up. As for
79 temporal analyses, the collected data was divided accordingly years (2005, 2006, 2007
80 and 2008).
81

82 Incomplete sampling areas can cause serious problems in identifying the best
83 fitted model, leading to biases in modeling due to sampling method (Dewdney 2000).
84 The nd out if the samples were sufficient for accurate inferences from the models, we
85 calculated the rarefaction of species (Hurlbert 1971) based on the abundances found and
86 tested using the non-parametric Mann-Whitney (considering the significance level of
87 0.05). The rarefaction curve (Hurlbert 1971) demonstrates the efficiency of capture,
88 considering the 29 sites analyzed in this study.

89 Four different models were tested: the logseries (Fisher *et al.* 1943), lognormal
90 (Preston 1948), broken-stick (MacArthur 1960) and metacommunity (Hubbell, 2001,
modified by Alonso & Mckane, 2004). Both logseries and lognormal models are the

91 most utilized and elected for heterogeneous communities, when logseries normally
 92 elected where there is incomplete sampling and many singletons. The broken-stick
 93 model is based on sequential partitioning of resources and high evenness (Baczkowski
 94 2000) and the metacommunity says that species has equally distribution, occupying pre-
 95 determined niches and resources available distributed equally between them (Magurran
 96 2005). The lognormal model was 0.05 truncated to model only the real abundances.

97 Model selection was through Akaike Information Criteria – AIC (Akaike
 98 1973), that calculates the best adjustment of model, where the best fitted model has the
 99 lowest values (Johnson & Omland 2004). All analysis were performance in R (R Core
 100 Team 2014), with available packages *sads* (Prado & Miranda 2014) and *vegan*
 101 (Oksanen *et al.* 2013).

102

103

104 **RESULTS**

105

106 *Richness*

107 Rarefaction curve showed that the richness of all spatial categories and years
 108 analyzed was successfully represented in surveys.

109

110



111

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114 *Abundance*

115 For Babitonga Bay as a whole, 253.189 individuals were sampled, distributed
 116 among 141 taxon. Only one specie – *Steliffer rastrifer* – was responsible for numerical
 117 dominance, accounting for 34.23 % of total captures. Opposite to that, there were 17
 118 singletons collected (Figure 2).

119

120 Figure 2: Dispersion of abundances of species found in three surveys performance on Babitonga
 121 Bay (SC)

122

123 As for margins of the Bay, 130.265 individuals were sampled, distributed among
 124 111 taxon. The numerical dominance was accounted for *Mugil sp* (17.29%),
 125 *Engraulidae sp.* (16.45%) and *Atherinella brasiliensis* (16.45%) that accounted for
 126 50.20% of total abundance. Despite having the lowest abundance of only one specie
 127 (*Mugil sp.* - 22.529 individuals), was the area that showed the higher richness and the
 128 higher number species with one individual (14 singletons).

129 The channel presented 122.924 individuals, distributed among 73 species.
 130 *Stellifer rastrifer* was responsible for numerical dominance, accounting for 70.21% of
 131 individuals sampled. This area presented a higher abundance of one specie, but
 132 presented the smaller richness (73 species) and lowest number of singletons (10
 133 species).

134

135 *Model Selection*

136 Both for the general abundance and for spatial categories, lognormal model had
 137 the best fit for all scenarios studied ($\Delta AIC = 0$), and had at minimum 9.6 of different for
 138 the second best model (Table 1). The lognormal is the only tested model that has two
 139 parameters (σ and μ), meaning that, even with punishment of AIC, it is the strongest
 140 explaining the collected data, opposed to the broken-stick model, that don't have
 141 parameters but showed the worst fit to the data.

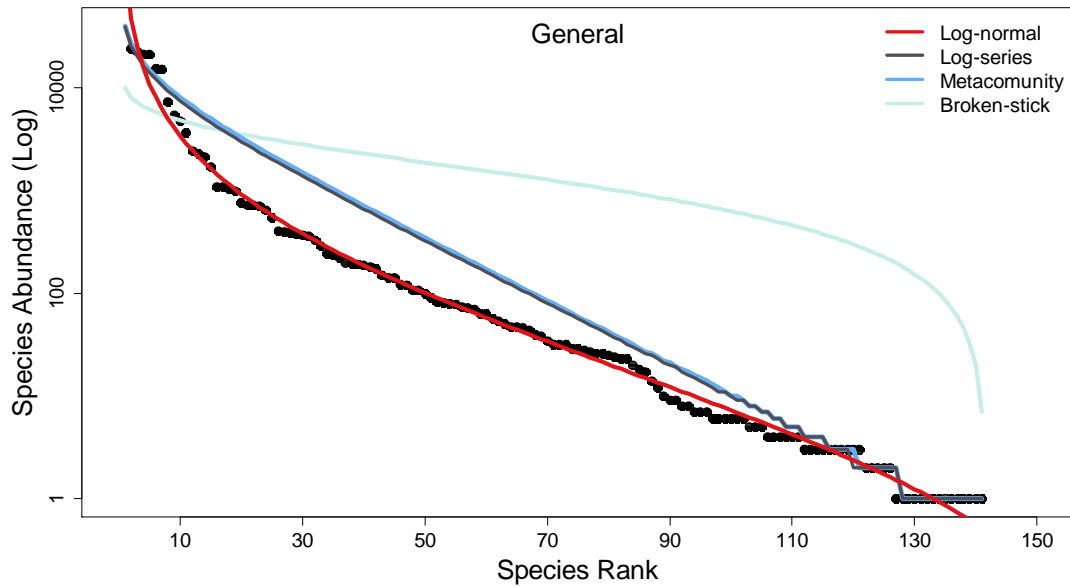
142

143 Table 1: Model selection to the three surveyed areas in Babitonga Bay. AIC -
 144 Akaike Information Criteria results; ΔAIC - the difference between AICs.

MODELO	GENERAL		CHANNEL		MARGINS	
	AIC	ΔAIC	AIC	ΔAIC	AIC	ΔAIC
LOGNORMAL	1717.48	0.00	812.92	0.00	1270.59	0.00
LOGSERIES	1731.79	14.31	830.58	17.66	1279.76	9.17
METACOMUNITY	1733.38	15.9	835.29	22.37	1280.2	9.61
BROKEN-STICK	2420.47	702.99	1304.21	491.29	1789.26	518.67

145

146 The graphical selection shows clearly the lognormal adherence to the data
 147 collected, with all three other models showing a weak explanation of data. The
 148 lognormal had best fit specially for intermediate abundance, which comprised most of
 149 species abundances (Figure 3)



150

151

Figure 3: Graphical selection of the four tested models over Babbitonga Bay fish fauna.

152

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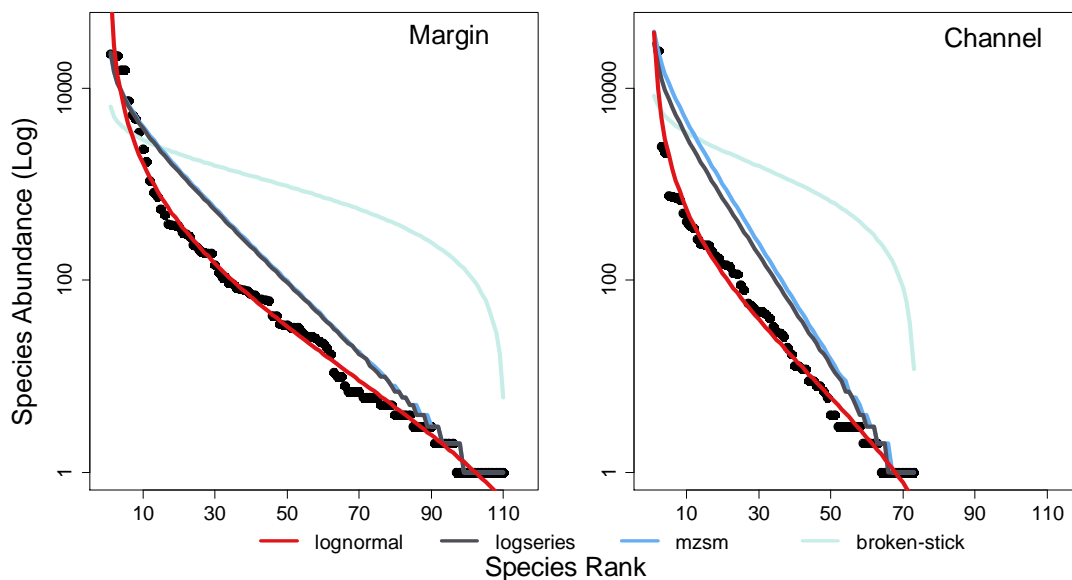
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Graphical analysis shows that the channel had the worst fit of models, what might be correlated to the smaller abundance found in this area. However, the lognormal still is the best model explaining the data collected. For margins, the visual selection makes clear that, among the studied models, only the lognormal had adherence to the data (Figure 4).



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Figure 4: Graphical selection of two sampled areas - Margins and Channel - over Babbitonga Bay fish fauna

Comparing the variation trough years, the abundances varied substantially, probably reflecting the sampling effort among the years. Years that presented higher

164 abundances also showed the best AIC values, indicating that the models are better
 165 represented when the abundances increases. Instead of this, the lognormal was the best
 166 explaining all years, despite other two models had significantly ΔAIC for 2006
 167 (logseries and metacommunity) (Table 2).

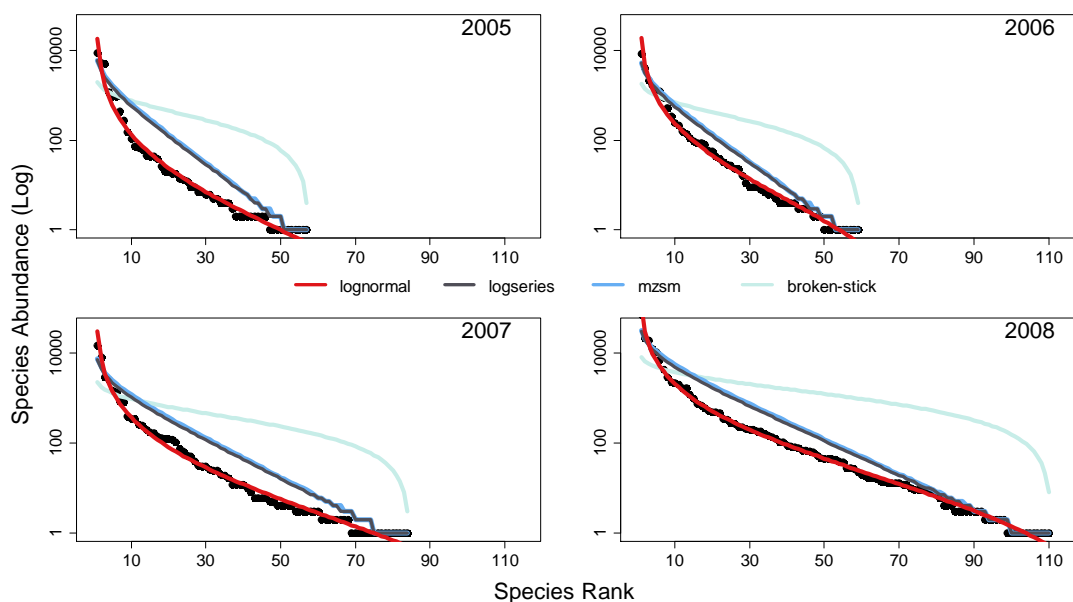
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169 Table 2: Model selection to the four years analyzed to Babitonga Bay fish fauna.
 170 Results of Akaike Criteria Information (AIC), and the values of ΔAIC .

MODELO	2005		2006		2007		2008	
	AIC	ΔAIC	AIC	ΔAIC	AIC	ΔAIC	AIC	ΔAIC
LOGNORMAL	533.9	0.00*	611.51	0.00*	822.13	0.00*	1331.35	0.00*
LOGSERIES	545.41	11.51	612.67	1.16*	834.32	12.19	1341.03	9.68
METACOMUNITY	546.2	12.3	613.32	1.81*	836.07	13.94	1342.99	11.64
BROKEN-STICK	816.37	282.47	830.29	218.78	1212.77	390.64	1865.98	534.63

171

172 Graphical selection makes clear the variation in richness found between the
 173 years analyzed, where 2005 showed the lower values and 2008 the higher values. The
 174 lognormal curve is adjusted to the to all years, but to 2006, the other curves (logseries
 175 and metacommunity) also showed fit, specially in the extreme values of abundance
 176 (Figure 5).



177

178 Figure 5: Graphical selection showing the fit of four curve models adjusted to the fish fauna
 179 abundance of Babitonga Bay (SC).

180

181

DISCUSSION

This study tested four different species abundance distribution models on ichthyofauna of Babitonga Bay attempting to find a pattern capable to explain the dynamics and structure of abundance and richness within the estuary, along the spatial gradient and years.

Studies related to abundance of species have shown that the success of predictions is related to the success on sampling the community analyzed, that depends on sampling effort and techniques utilized (Ulrich *et al.* 2010). Use of different nets and techniques is the most adequate to catch fish fauna (Clement *et al.* 2014) as did in this study, where six different nets were utilized, with different seize nets, length and time of sampling, besides the long time – 20 months – allowing the accurate estimate of species of Babitonga Bay, confirmed by rarefaction test.

Within the Bay, 141 species were collected. Accordingly with a recent bibliographic study, the estuary shelters 152 fish species (Vilar *et al.* 2011a), but in our study, some specific habitats wasn't sampled – such as oyster farming and the Canal do Linguado. Accordingly with Reis-Filho *et al.* (2010) all East Atlantic estuaries presents a very similar fish fauna, wich is also similar to the one found here, with specific composition of temperate and tropical species, related to the oceanographic conditions (Blaber 2008; Vilar *et al.* 2011a) and harbor activity (Freitas & Velastin 2010).

Our study found the lognormal model as the best one on explaining the abundances distributions within the bay. Despite of being a statistical model, current literature cites it as the best for heterogeneous, but ecologically equilibrated areas that were adequate surveyed (Preston 1948; Magurran 1988; Unterseher *et al.* 2011). Connolly *et al.*, (2005) and Hercos *et al.*, (2013) also elected the same model for fish fauna modeling, but the fist author only found this pattern over large scales (above of km). The Babitonga Bay presents elevated levels of organic and metal contaminants (Cremer *et al.* 2006), especially nearby of the emissary (Martins *et al.* 2010) but, apparently, not directly influencing ichthyofauna abundance, maintaining this population in a equilibrated status.

Such as the estuary studied here, lognormal model has also showed success describing the abundances distribution on locations with both rare and common species (Connolly *et al.* 2009). Abundance of common species had a greater abundance than the rare ones (accounting for over 132 thousand individuals). The presence of these

216 species being numeric significant and biologically associated to estuaries might
217 camouflage a recurrent pattern on smaller areas: the logseries pattern of rare species
218 (Correa *et al.* 2006; Magurran & Henderson 2012), where few species have a
219 dominance competitively (Martins & Santos 1999), sharing the resources in
220 distinguished ways (Henderson & Magurran 2010). Such higher abundances might be
221 determined by resources partitioning (Magurran & Henderson 2003), once they are
222 responsible for dominance of area use (Gotelli & Graves 1996), but not on a sequential
223 recruitment normal on some environments, as proposed by broken-stick (Magurran
224 1988).

225 Lognormal choice suggests yet the dispersion of species as result of ecological
226 process – such as random niche portioning (Fesl 2002), biological characteristics
227 (Gaston & Blackburn 2008) and that the central limit theorem is important of
228 community dynamics, when mostly of species presents the intermediate abundances
229 (Connolly *et al.* 2005; Ulrich *et al.* 2010; Locey & White 2013). The lack of fit of
230 metacommunity model indicates yet that the neutral theory might not have important
231 influence on these data, corroborating that the niche partitioning of resources is
232 prevailing, being drove by random events, therefore being important on understanding
233 for community structure (Arakaki & Tokeshi 2011).

234 Another significant side revealed for the chosen models is the residency of
235 mostly of individuals (Magurran & Henderson 2003; Ulrich & Ollik 2004). Our study
236 found higher abundances in estuarine species – e.g. *Stellifer*, *Cathorops* and *Atherinella*
237 (Barletta *et al.* 2008; Reis-Filho *et al.* 2010), that might indicate that the estuary is also
238 an important ecosystem for development e reproduction of species, and not just for
239 larvae and juveniles of marine species, with predominance of core species (Henderson
240 & Magurran 2014). For instance, if the abundances of stranglers species were dominant,
241 the model selected should be the logseries (Ulrich *et al.* 2010)./

242 On tropical and temperate estuaries, authors assigns the fish communities
243 dynamics to abiotic variability, mainly salinity, but also to temperature, tides and
244 dissolved oxygen and substratum (Andrade-Tubino *et al.* 2008; Blaber 2008; Paiva *et*
245 *al.* 2008; Xavier *et al.* 2012). Our study did not find significant differences between the
246 areas (channel and margin), what might indicate that the structure of community also
247 respond to biotic interactions, such as feeding, migration and competition inter and intra
248 specifics. This patters was also found by (Maes *et al.* 2004) that discuss the lack of

249 explanation by abiotic factors, that might be attributed to migration patterns (Thiel &
250 Potter 2001).

251 Due to high number of factors responsible for temporal variation of fish fauna,
252 there is no agreement of how the patterns of variance in structure of community occurs
253 within years (Shimadzu *et al.* 2013), needing extra regard (Rosenzweig 1995). In our
254 study, there was no variation in total abundance between years, but there was variation
255 of species composition entre years, but it might be attributed to the samples surveys.
256 This lack of variation might be due to the time, not pointed as determinant to fish
257 structure (Villarroel 1994; Barletta *et al.* 2003).

258

259

260 CONCLUSION

261

262 Our study did not find differences of model chosen between the areas studied,
263 despite of specific composition considerable different. Through the models, that might
264 indicate that community studied are in balance, with alternation only in diversity, not in
265 abundances (Shimadzu *et al.* 2013). It mean that, even with spatial and temporal
266 alteration of species, the ichtyofauna is capable to respond of these alterations and
267 maintain the dynamics within the bay.

268 All results found in these work are compatible to the scales analyzed. Others
269 scales, such as samples or guilds might respond to specific factors (such as inter-
270 specific relation or abiotic attributes) and presenting different distributions. Despite of
271 not presenting losses on fish fauna or alteration on community structure, the protection
272 of Babitonga bay is necessary due to high levels of contaminants described to the water,
273 leading to structural modification of community and, the surveys being done before the
274 implementation of Itapoá harbor that has great chances of impact the subjacent area.

275

276

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436

1 **CAPÍTULO 2: DOES SADS DISTINGUISHED OVER**
2 **DIFFERENT FISH GUILDS? A STUDY CASE FROM**
3 **SOUTHWESTERN ATLANTIC ESTUARY**

4
5
6 **INTRODUCTION**

7
8 A abundance distribution tries to describes all abundances of species recorded
9 within an ecological community, which is an universal law that, generally, have many
10 species with few individuals and few species have greater abundances (Magurran 1988;
11 Matthews & Whittaker 2014). This general law is responsible to create the so called
12 hollow curve, which is the most common ecological pattern (McGill *et al.* 2007).
13 Several attempts where proposed to explain it, started in 1932 with Motomura
14 proposing a mathematical solution – the geometric distribution (Doi & Mori 2013).

15 Were created models to predict how the abundances are distributed between
16 species through mathematical equations: the species abundance distributions – SAD.
17 These equations are transformed in a distribution, with parameters responsible for the
18 adjustment of the model on the empirical community curve. Although the similarity
19 between them, each curve has nuances responsible to predict the biotic and abiotic
20 influences on the distribution (Bellier *et al.* 2012).

21 The statistical modelling of these models are important since some statistical
22 theories may be converted in ecological assumptions (McGill 2010; de Lima *et al.*
23 2012) allowing the inferences from statistical modelling not being divergent from
24 ecology (Gaston & Blackburn 2008). The modelling is capable of identify patterns in a
25 community such as born/death rates; predation and competition interaction, sampling
26 effort and different guilds (Green & Plotkin 2007; Bowler & Kelly 2012; Magurran &
27 Henderson 2012).

28 The use of guilds of estuarine fish have been identified groups and dynamics,
29 providing understanding of relations, patterns and similarities (Barletta & Blaber 2007;
30 Elliott *et al.* 2007). Different species make use of the estuary accordingly with
31 individual tolerance to disturbance of abiotic factors and the resources availability. This
32 differences may directly influence the way each species use the estuary (Henderson &
33 Magurran 2010), therefore modifying the abundance distribution. Understanding how

34 and why this alteration occurs is an essential step for comprising the ecological
35 biogeography (McGill *et al.* 2007; Matthews & Whittaker 2014).

36 The Babitonga Bay is located on north coast of Santa Catarina state, South of
37 Brazil. Having approximated 23 km of extent, seasons well defined and semi-diurnal
38 tide (Cremer *et al.* 2006). Presents a 6 m of mean depth, with major areas with less than
39 2 m (Mazzer & Gonçalves 2011), being directly influenced by continental drainage and
40 hydrodynamic from adjacent sea currents (Barros Grace *et al.* 2008). Holds two harbors
41 (São Francisco and Itapoá Harbors), being directly impacted from all 6 cities it is
42 surrounded (IBAMA 1998), therefore regarded as proprietary area for conservation
43 (MMA 2007).

44 The aim of this study was identify if the separation of fish fauna in different
45 estuarine use and food guilds are capable of influencing the abundance curve and,
46 therefore, the chosen SAD model. Further multivariate analysis performed to
47 understand the relation of the guilds with some ecological descriptors. The hypothesis
48 tested is if there are different number of species within each guild, different SAD
49 models will be choosen.

50

51

52 **METHODS**

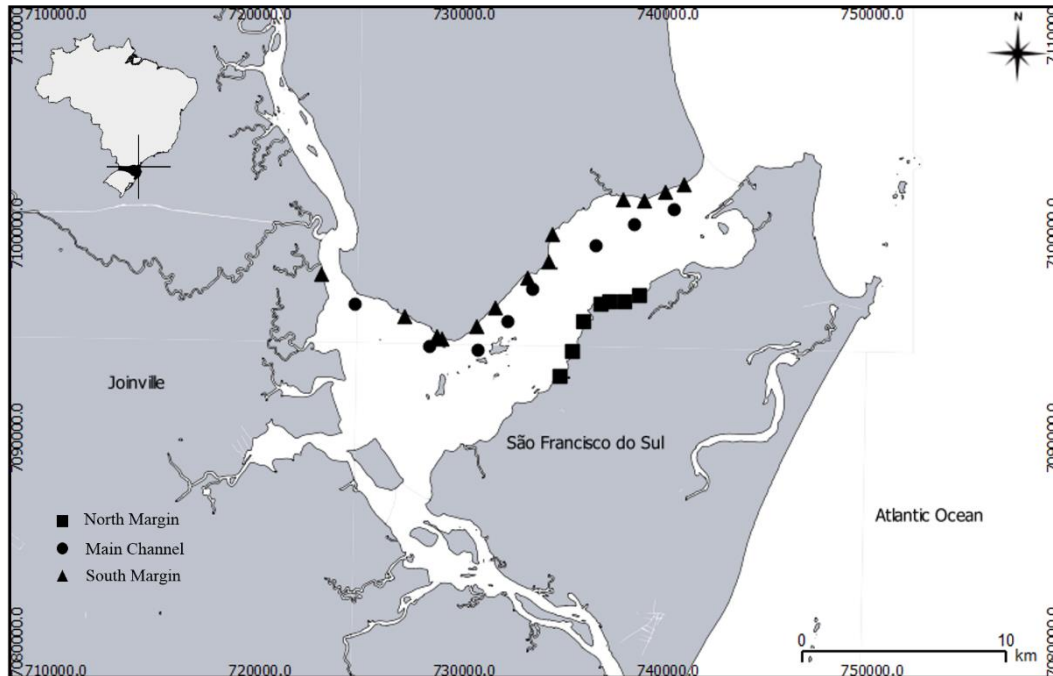
53

54 *Data collection*

55 Samples taken by Laboratório de Ecologia de Peixes (CEM/UFPR) in three
56 different occasions. At south margin, from August/2005 to July/2006, three monthly
57 single tows parallel to the coast carried out in the margin of seven sites. First tow had
58 15m x 1.6m (5mm mesh size); second tow had 15m x 1.6m (2.5mm mesh size), both
59 dragged over 20m; third tow had 6m x 1.6 (1mm mesh size) carried by 6 meters to
60 minimize mesh clogging, totalizing 252 samples.

61 At north margin, samples taken over eight months (October and
62 November/2007, January, February, April, May, July and August 2008) at thirteen
63 different sites throughout the estuarine gradient, totalizing 208 samples. At each survey,
64 three seine nets were used. One net with 6m x 1.6m (1.0mm mesh size) thought 10m
65 parallel to the coast, and one net with 15m x 2m (2,5mm mesh size) thought 30m
66 parallel to the coast.

67 At the main channel, sampling were collected at same eight months of north
 68 margin, but at nine different sites within estuarine gradient. At each sampling occasion,
 69 two bottom trawling with Wing Trawl nets over 5 minutes, totaling 144 samples (Figure
 70 6).



71 Figure 6: Babitonga Bay (SC), Brazil

72
 73
 74 All specimens were frozen and taken to the laboratory, identified to the least
 75 taxonomic level possible, accordingly with specialized keys (Figueiredo & Menezes
 76 1978, 1980, 2000; Menezes & Figueiredo 1980, 1985; Barletta & Corrêa 1992). All
 77 taxons identified, were classified following the proposed guilds by (Elliott *et al.* 2007),
 78 based on previously literature (Kawakami & Amaral 983; Bergesen 1982; Juras &
 79 Yamaguti 1985; Vasconcelos Filho & Oliveira 1999; Chaves & Vendel 2001; Santos &
 80 Castro 2003; Spach *et al.* 2004; Chaves & Bouchereau 2004; Fischer *et al.* 2004;
 81 Barletta & Blaber 2007; Barletta *et al.* 2008; Morais 2008; Silva *et al.* 2008; Reis-Filho
 82 *et al.* 2010; Bornatowski & Costa 2010; Espinosa *et al.* 2010; Hackradt *et al.* 2011;
 83 Medeiros 2011; Derisio *et al.* 2011; Moraes *et al.* 2012; Denadai *et al.* 2012; Koenig &
 84 Coleman 2013; Muto *et al.* 2014; Froese & Pauly 2015). The use of estuary guilds:
 85 marine stragglers (MS), marine migrants (MM), estuarine species (ES), anadromous
 86 (AN), catradomous (CA), amphidromous (AM) and freshwater migrants (FM). The
 87 feeding guilds are: zooplanktivore (ZP), detritivore (DV;), herbivore (HV), omnivore
 88 (OV), piscivore (PV), zoobenthivore (ZB) and opportunist (OP).

89

90 *Modelling*

91 Incomplete surveyed areas may lead to infamous problems over choice of
92 correct model, taking biases over inferences based only due incorrect sampling
93 (Dewdney 2000). Testing the success of sampling, was calculated from rarefaction
94 curve, and based on richness found in all sampling together.

95 For SADs analyses, were used only the guilds with more than twenty species,
96 due to inefficiency of choosing correct SAD model from lower richness, being used
97 only in multivariate analysis. Four different models were utilized in this study:
98 Logseries (Fisher *et al.* 1943); Lognormal (Preston 1948), Broken-stick (MacArthur
99 1960) and Metacommunity (Hubbell 2001; modified by Alonso & Mckane 2004).
100 Logseries and Lognormal are both the most used models explaining heterogeneous
101 communities, often with proper sampling and higher singletons. Broken-stick is based
102 on sequential partitioned of available resources, where the occupied niche is determined
103 by resources availability (Baczkowski 2000). Metacommunity proposes the equality of
104 species, where they occupy pre-determined niches (Magurran 2005). The lognormal
105 model where truncated at 0.05 to exclude species under sampled.

106 Selection model were based on Akaike Information Criteria – AIC (Akaike
107 1973), which calculates the best fit of collected data on tested models, given the ΔAIC ,
108 where the minimum values represents the best predictions (Johnson & Omland 2004).
109 Multivariate analyses based on Bray-Curtis dissimilarity matrix, made from
110 untransformed data, both for nMDS (Nonmetric Multidimensional Scaling) and RDA
111 (Redundancy Analysis). Ecological indicators used were: richness, Shannon Index (H),
112 Simpson Index (D) and Inverse Simpson (D.inv). All statistics analyses were
113 performance with R (R Core Team 2014), and available packages sads (Prado &
114 Miranda 2014) and vegan (Oksanen *et al.* 2013)

115

116

117 **RESULTS**

118

119 Sampling of ichthyofauna on Babitonga Bay collected 253.189 individuals,
120 classified within 140 taxon, belonging to 49 different families. The sampling effort was
121 considered successfully, since the calculated asymptote of rarefaction curve were
122 stabilized through the sites sampled (Figure 7).

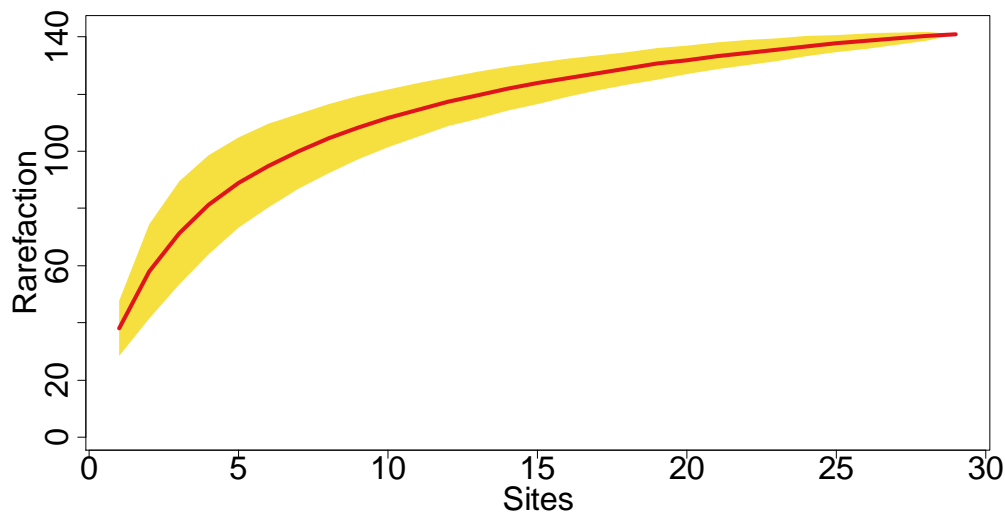


Figure 7: Rarefaction curve with 95% confidence interval (shaded area)

123

124

125

126 *Estuary Use*

127 Classification of species accordingly with estuarine use found eight different
 128 classes. The higher number of species was within marine stragglers (MS – 40 species),
 129 followed by estuarine residents (ES - 43 species) and marine migrants (MM – 38
 130 species). As expected, the abundances were consistently with the number of species,
 131 presenting higher abundance on guilds with higher richness.

132 The AIC from model selection pointed different models to each of guilds (Table
 133 3). For estuarine residents and marine stragglers three of tested models were choose as
 134 efficient on explaining the distribution, all of them with ΔAIC under 2. Concerning
 135 marine migrants, only one model – lognormal – was selected as efficient on describing
 136 the abundance distribution.

137

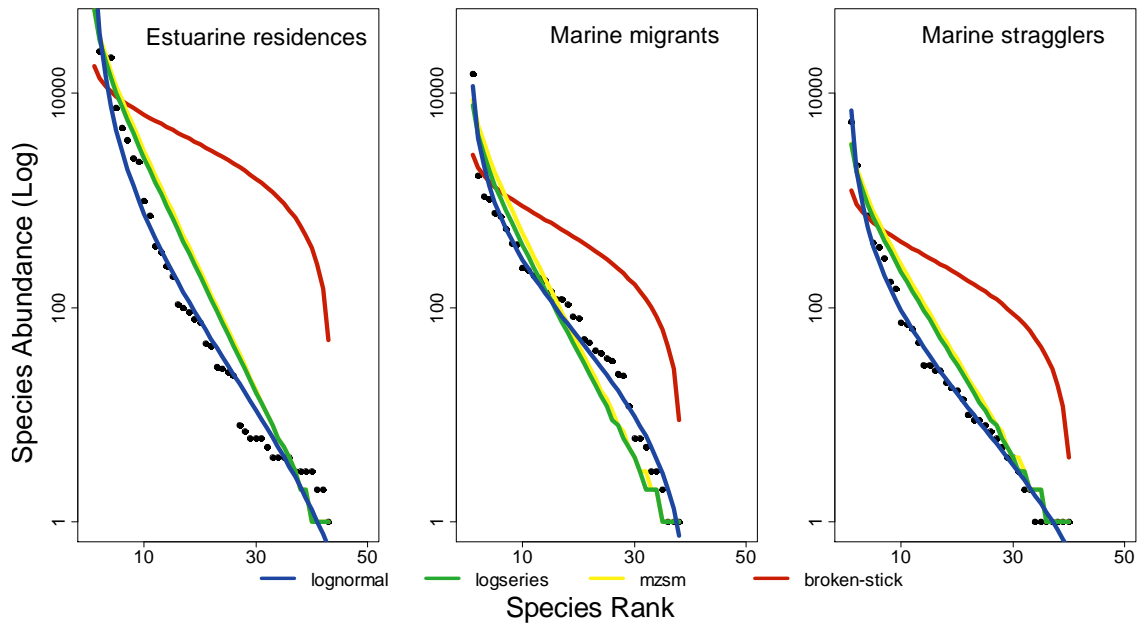
138 Table 3: Model selection to the three estuarine use guilds with higher abundances
 139 in Babitonga Bay. AIC - Akaike Information Criteria results; ΔAIC the difference
 140 between AICs.

MODEL	ER		MM		MS	
	AIC	ΔAIC	AIC	ΔAIC	AIC	ΔAIC
LOGNORMAL	582.61	1.72	484.25	0*	411.78	0.04*
LOGSERIES	581.52	0.63*	486.38	2.13	411.74	0*
METACOMMUNITY	580.89	0*	487.78	3.53	412.44	0.7*
BROKEN-STICK	817.39	236.5	591.46	107.21	545.09	133.35

141

142 Graphical selection showed that matacommunity and logseries models best fitted
 143 the extreme abundances, meanwhile the lognormal explained better the intermediated
 144 ones. Despite the graphics showing that are three models explaining the distribution for
 145 marine migrants, the ΔAIC value should overlap the decision of model selection (Figure
 146 8).

147



148

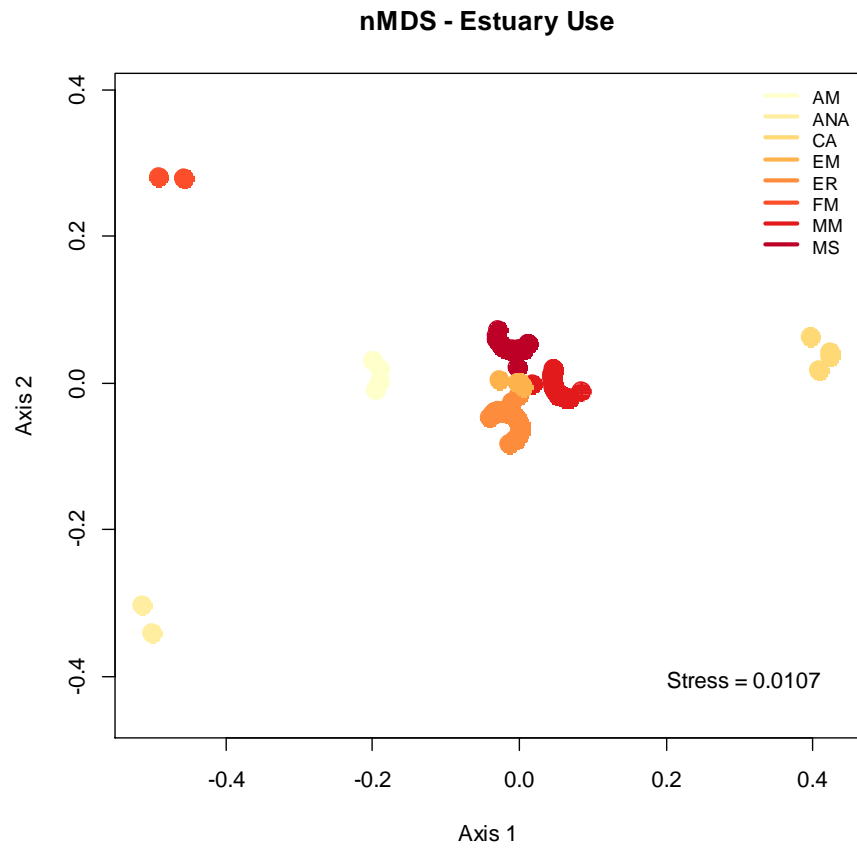
149

Figure 8: Graphical selection of the four tested models over fish guilds of Babitonga Bay

150

151 The nMDS for estuarine use successfully separated all guilds, gathering all three
 152 richest guilds. RDA showed that, the dominance parameters (evenness and diversity)
 153 were grouped and positively correlated with the guilds studied, due to the higher
 154 number of richness and abundance of these guilds (Figure 9). Marine stragglers was the
 155 principal guild showed on RDA, probably due to dynamics of all species. The opposite
 156 was also observed, with gathered of less representative guilds, because that minimum
 157 record of species difficulties ecological calculates (Figure 10).

158

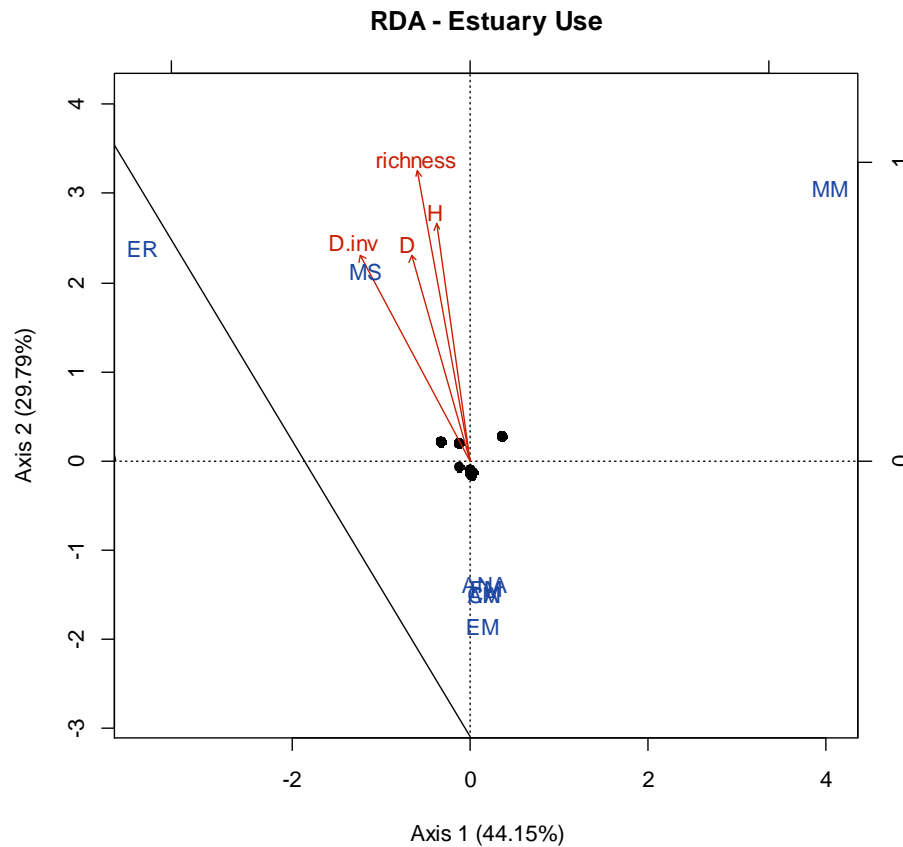


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160

161

Figure 9: nMDS for estuarine use guilds within Babitonga Bay. For legend abbreviations see the Methods



162

163

Figure 10: RDA for estuarine use guilds of fishes within Babitonga Bay. For abbreviations, see the methods

164

165

166 *Trophic Guilds*

167

168 Guilds classification accordingly the feeding habits has also found eight
 169 categories. The ones that presented the bigger number of species were: zoobenthivore
 170 (ZB – 78 species), piscivorous (PV - 22 species) and zooplanktivore (ZP – 21 species).

171 In the analysis of the competing models tested, both piscivorous and zoobenthivore, the
 172 chosen model that showed the best fit was the lognormal. For zooplanktivore species
 173 were chosen two models, the logseries and the metacommunity (Table 4).

173

174

175

176

Table 4: Model selection to the three trophic guilds with higher abundances Babitonga Bay. AIC - Akaike Information Criteria results; Δ AIC the difference between AICs.

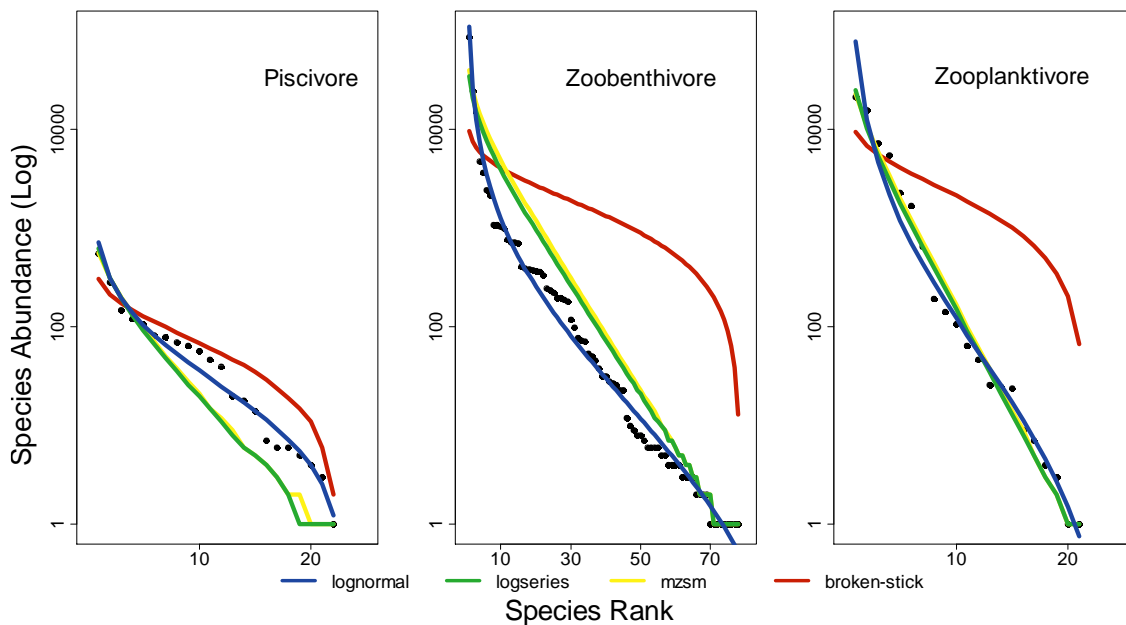
MODEL	PV		ZB		ZP	
	AIC	Δ AIC	AIC	Δ AIC	AIC	Δ AIC
LOGNORMAL	233.47	0.00*	954.94	0.00*	303.64	4.64
LOGSERIES	236.06	2.59	961.38	6.44	299.58	0.58*

METACOMMUNITY	235.56	2.09	964.12	9.18	299	0.00*
BROKEN-STICK	237.93	4.46	1380.54	425.6	377.16	78.16

177

178 The graphics of model selection makes clear the difference in richness between
 179 the categories analyzed, which apparently did not influence directly in the listed models.
 180 Thought the graphics, it is clear the lognormal selection for piscivore and
 181 zoobenthivores categories, and the logseries and metacommunity to Zooplanktivores
 182 (Figure 11).

183

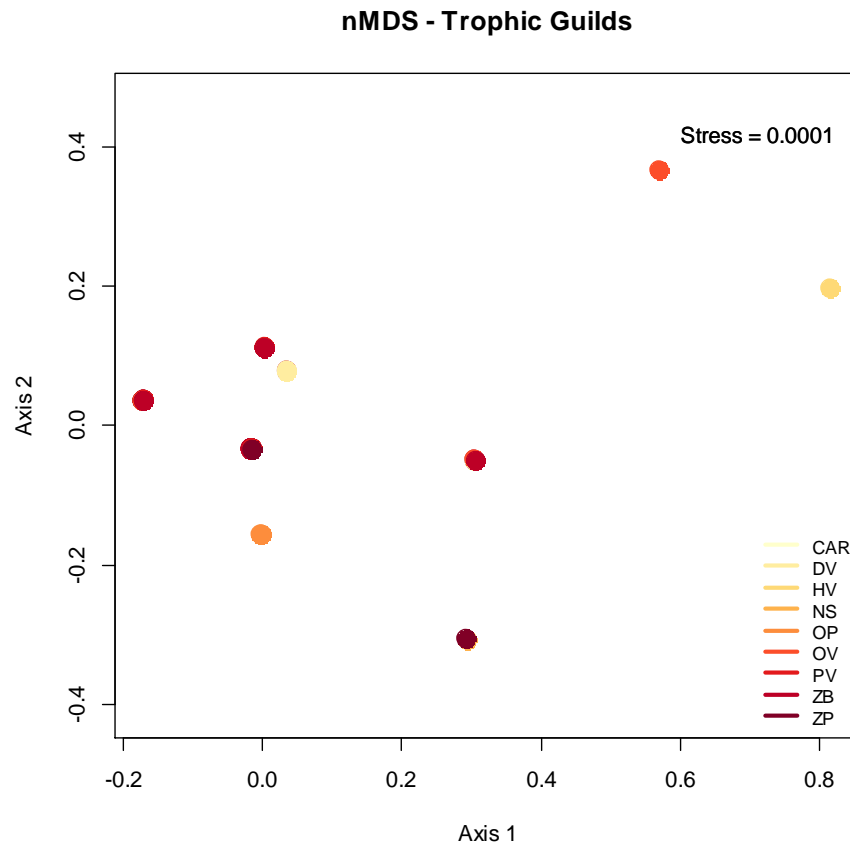


184

185 Figure 11: Graphical selection of the four tested models over trophic fish guilds of Babitonga
 186 Bay

187

188 Concerning trophic categories, nMDS was not efficient over species separation,
 189 as long mostly of them were overlapped, except by omnivorous, herbivorous and
 190 opportunist ones (Figure 12). As for RDA, piscivorous guild were positively correlated
 191 with Dinv, while zoobenthivorous with richness. All others guilds were inversely
 192 correlated with the ecological descriptors (Figure 13).

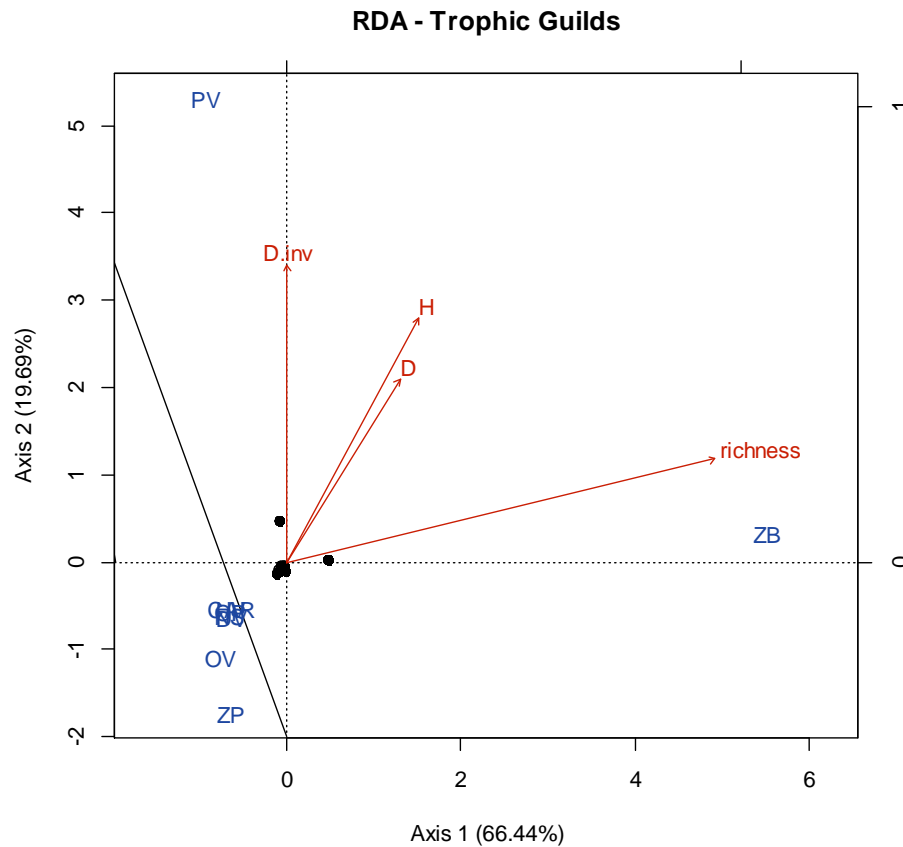


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Figure 12: nMDS for trophic guilds within Babitonga Bay. For legend abbreviations see the Methods



196

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Figure 13: RDA for trophic guilds of fishes within Babitonga Bay. For abbreviations, see the methods

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200

201 DISCUSSION

202

203 Correctly sampling on ichthyofauna community are essential for inferences about
 204 the ecology (Clement *et al.* 2014). On this study, we used six different mesh and two
 205 sampling methods, which were effective to sample the richness of community, as shown
 206 on rarefaction curve. Although VILAR *et al.* (2011) had found more species on his
 207 literature review about Babitonga's fish fauna (153 species total), this study didn't
 208 sampled specific environments (such as bivalve farming and headlands), making all
 209 analysis trustable.

210

211

212

All guilds classified – both of estuarine guild and feeding habits – were similar to others Brazilian estuarine systems (Barletta & Blaber 2007; Xavier *et al.* 2012; Passos *et al.* 2013). The guilds used on ecological modelling showed that, in some

213 scales, each species might utilize the resources available in a specific way, since that
214 more than one model was selected.

215 Accordingly with Andrade-Tubino *et al.* (2008), most of species that use
216 Brazilian estuaries are estuarine-opportunistic, represented by marine stranglers and
217 marine-migrants in this paper, which present mostly of species classified. They use
218 highly developed capability of osmoregulation to get in the estuaries and use it as
219 feeding areas, protection and reproduction habitats (Whitfield 1999; Barletta-Bergan *et*
220 *al.* 2002; Barletta *et al.* 2005). All canivorous species were dominating in this study,
221 which is a regular pattern found on estuarine systems, where predators (mainly over
222 invertebrates) is documented (Chaves & Bouchereau 2004; Blaber 2008; Paiva *et al.*
223 2008).

224 In species abundance distributions analysis, different models were elected. For
225 estuarine resident and zooplanktivora species, two models were selected:
226 metacommunity and logseries. Accordingly with these models, the use of available
227 resources – such as food or space – are used in a specific way for each specie
228 (Henderson & Magurran 2010), belonging to a heterogeneous community (Dornelas *et*
229 *al.* 2009; Ulrich *et al.* 2010) and dominance of singletons, mostly related to alternation
230 of species along of time (Thiel & Potter 2001; Ulrich *et al.* 2010).

231 For marine stragglers, three of the tested models were selected by AIC
232 explaining the distribution. Choosing three models are frequently related to
233 heterogeneity of guild, what means that are lots of factors operating within it (such as
234 environmental responses and biological drivers) (Shimadzu *et al.* 2013). As shown by
235 RDA, all ecological descriptors are positively correlated with this guild, indicating that,
236 within it, there is a highly dynamics driving the community interactions, but not
237 influencing significantly the trophic dynamics of estuary (Correa *et al.* 2006; Magurran
238 & Henderson 2012). The species turnover may be another factor influencing the choose
239 of multimodal, once they use of the estuary may not be enough to change these
240 dynamics (Henderson & Magurran 2014).

241 Elliott *et al.* (2007) states that the use of estuary by species might differ
242 significantly within the estuary, where some species are allocated accordingly with the
243 physical characteristics of environment (Andrade-Tubino *et al.* 2008; Parsons *et al.*
244 2014). This characteristics might influenced the choose of models, since them implies
245 the resource split on abundances distributions (Henderson & Magurran 2010).

246 For marine migrants, piscivorous and zoobenthivorous, the elected model was
247 lognormal. The input of marine species inside estuaries is frequently registered, despite
248 that mostly of the literature cites it as seasonal (Whitfield 1999; Barletta *et al.* 2003;
249 Spach *et al.* 2003), this study did not find variation of abundances, mainly due to
250 entrance of the species along all year. The variations of these guilds were low, due to
251 the available food resources in Bay (Elliott *et al.* 2007). We might believe that, this
252 species are very well adapted to estuaries, due to the model selection (Unterseher *et al.*
253 2011)

254 Chapter 1 showed that the model for the Babitonga Bay as all, is the lognormal.
255 The fact that different models were selected for the specific guilds analysis can be due
256 to biases caused for modelling a minor number of species, that might decrease the
257 accuracy, or by the fact that they use of resources occurs differently (McGill *et al.*
258 2007). However, the community dynamics in different scales are capable to reveal
259 different patterns within the community, affecting smaller scales (Henderson &
260 Magurran 2010), but not disrupt the community as a whole (Sheaves *et al.* 2014). This
261 general pattern was also found on the coast of Australia, where the smaller scales
262 presented a logseries standard and larger scales (kilometer) showed a lognormal
263 distribution (Connolly *et al.* 2005).

264 An another side that should be considered is that there is no identification of
265 species, only abundances, what means, the turnover of species does not influences the
266 community, since there's other species that can be used as food resource available on
267 trophic dynamics (Magurran & Henderson 2012). According to (Vance *et al.* 1996),
268 estuaries are important areas of recruitment of species, where larvae and juveniles may
269 use this ecotone for ontogenetic development. This way, changes of abundance are not
270 the best choice for conducting studies about ecological changes, should being used
271 biomass or age of individuals (Vance *et al.* 1996; Ulrich *et al.* 2010).

272 This study revealed that, despite having a equilibrated ichtyofauna, Babitonga
273 Bay presents couple of other sectors with dissimilarities concerning the space use and,
274 therefore, on structure for each classification (guild). The use of empiric data for model
275 validation of SADs are very necessary and scarce. This work comes to complement the
276 understanding of environment from theories that explain abundance variation successes
277 in categorize the knowledge of space and enable effective acts of environment
278 preservation.

279

280

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Diferenciação com as diferentes categorias

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588

589 A Modelagem ecológica dos dados de peixes da Baía da Babitonga mostrou que,
590 dependendo da escala analisada, diferentes modelos são elencados e, conseqüentemente,
591 são diferentes processos internos que guiam a distribuição das abundâncias.

592

593 Apesar do modelo elencado para a comunidade de peixes como um todo (Normal-
594 Logarítmico), mostrar que a Baía ainda apresenta um estágio com baixo grau de impacto,
595 esse resultado deve ser considerado com cuidado, uma vez que os dados foram coletados
antes da implantação do Porto de Itapoá.

596

597 A falta de estudos com dados empíricos na aplicação dos modelos ainda é uma
598 lacuna grande nos estudos da área, assim, este trabalho vem no intuito de ajudar a entender
599 a aplicabilidade e inferências possíveis a partir da utilização das DAEs em comunidades
600 naturais. Como nenhuma inferência encontrado neste trabalho divergiu das inferências
601 propostas por cada um dos modelos, acreditamos que a utilização desse método é eficaz
no entendimento e desenvolvimento de planos de pesquisa.

602

603 Para futuros estudo, acredito que a comparação entre os modelos das curvas, e a
604 aplicação de dados de biomassa nos modelos são caminhos promissores para a
complementação do entendimento tanto de comunidades, quanto dos próprios modelos.