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ABSTRACT

Summary of objectives, methods and results...

RÉSUMÉ

Usually the french version of the abstract goes here, but it is included here to show how accents might be added to text and how non-numbered sections work.

1 INTRODUCTION

Hecate Strait and Queen Charlotte Sound contain some of the most productive fishing grounds in British Columbia (BC), providing key habitat for many commercially important groundfish species. This project will employ multivariate statistics and geostatistical approaches to analyse relationships between environmental factors and distribution and productivity of key groundfish populations in Hecate Strait and Queen Charlotte Sound. The project will improve advice for management of Pacific groundfish stocks by: (i) improving understanding of environmental drivers of groundfish distribution and productivity needed for ecosystem-based management; (ii) improved estimates of abundance for key species; (iii) identification of juvenile habitats; (iv) provision of a baseline for understanding impacts of environmental change on species distribution; and (v) identification of species that could indicate ecosystem change through shifts in distribution and productivity.

Distribution and abundance of groundfish species is associated with invariant (e.g., depth, bottom-type) and variable (e.g., temperature, salinity) environmental factors [1][2][3]. Measuring relationships between these factors and distribution and abundance is the first step in understanding drivers of productivity (recruitment, growth, mortality), which is a critical component of ecosystem-based management. This project will employ statistical and hierarchical Bayesian geostatistical models ([4][5][2][3]) to analyse relationships between environmental factors and distribution, abundance and size structure of a set of key, commercially harvested groundfish species in Hecate Strait and Queen Charlotte Sound. Models will utilize data from commercial trawl logbooks and fishery independent surveys. Temperature and salinity data from the Regional Oceanographic Model System (ROMS) [6] will provide key model inputs.

Results for each species will include maps of predicted distribution and abundance of adults and juveniles; Bayesian predictive probability distributions of the relationships between habitat and environmental factors and abundance; and plots of the distribution of adults and juveniles along environmental gradients. Species most likely to be impacted by large environmental changes (e.g., ocean temperature) will be identified. Working with our external collaborator, results for a subset of species will be compared to results from Alaska to test generality of results and identify key differences. The project will provide updated estimates of abundance for the species of interest and will identify locations that may represent critical juvenile habitat. Results will be published in the primary literature, and in a CSAS Research Document reviewed through the Centre for Science Advice Pacific.

In the long-term, the project will provide important baseline data for understanding potential future impacts of environmental change. Some species (e.g., Pacific Cod) are known to vary their habitat with depth to maintain a limited temperature range [1], indicating that their distribution could be strongly affected by long-term changes in ocean temperature. Published studies have shown that large-scale redistribution of north Pacific fish populations may occur under future climate scenarios, with the potential for large impacts on ecosystem structure and function [7][8]. Groundfish indicator species most likely to be affected by environmental change will be identified in this project. Finally, ecosystem-based fishery management is based on principles of understanding the structure and function of the living components of marine ecosystems. In the US, NOAA is mandated to identify habitats essential for every managed fish species and identify those habitats that contribute most to survival, growth and productivity [9]. The analyses in this project will form an important component of this understanding for central and northern BC

waters. Through partnership with our external collaborator, comparative analyses will test generality of results and identify differences between BC and Alaska.

2 METHODS

2.1 MODELS

The project will apply a mix of established and recently-published statistical approaches to achieve the deliverables of the project. An earlier study [1] applied a set of multivariate statistical models to classify groundfish species in Hecate Strait according to their relationships with invariant and variable environmental factors. Recent studies have further developed these types of approaches for Alaskan groundfish species (e.g., [2][3]). A problem with spatial datasets for many marine species is the high proportion of zero observations, which can bias results. One approach to solving this problem is to use a two-stage model to first predict presence and absence, then analyse relationships between environmental variables and abundance [10]. More recently, the problem has been addressed using an elegant new Bayesian hierarchical model developed by co-investigator Dr. Lecomte, which estimates both the probability of zero observations and abundance in a hierarchical framework [4][5]. Within this framework, a geostatistical approximation, consisting of a linear model with spatially-correlated errors, is used to efficiently predict spatial abundance as a function of environmental factors [5]. The model outputs spatial predictions of abundance, and predictive probability distributions of the effects of each environmental factor on abundance for each species. Models are calibrated with spatial abundance observations. Analyses can be done on different size-classes of the population to better understand differences in adult and juvenile distribution and improve understanding of productivity. Dr Jean-Baptiste Lecomte is the primary author of the hierarchical Bayesian model, and is currently a post-doctoral fellow at the Pacific Biological Station. This work is highly relevant to current ecosystem management needs, and the project represents an excellent opportunity for Dr Lecomte to transfer his knowledge to Canadian scientists in the Pacific Region. This project will extend Dr Lecomte's current post-doctoral fellowship by six months. Dr Lecomte's co-author, Dr Marie Etienne (UMR 518 AgroParisTech), is also an expert in this methodology and will collaborate on the project through contract (Year 1, Task 8). In addition to the hierarchical model, the datasets will be used in simpler, multivariate statistical analyses (e.g., [1][3]), and to model distribution of adults and juveniles along environmental gradients, using methods developed by our external collaborator, Dr Christopher Rooper [2].

2.2 DATA

The project will utilize spatial data from DFO's Groundfish Synoptic Bottom Trawl Surveys in Hecate Strait and Queen Charlotte Sound. These biennial surveys have been operating since 2003 and employ a random, stratified sampling design. Spatially-resolved catch weight of more than 100 species is recorded from each tow. Length, weight, sex, maturity and age data are collected, according to a prioritized sampling protocol. Temperature, dissolved oxygen and salinity and depth data are also recorded. Highly spatially-resolved, commercial logbook data are available from BC's 100%-observed groundfish bottom trawl fishery. All these data are held in

Oracle databases, co-managed by the Pacific Groundfish Statistics Program. Spatially-gridded predictions of temperature and salinity data for Hecate Strait and Queen Charlotte Sound, will be output from the Regional Oceanographic Model System by Dr Masson at the Institute of Ocean Sciences. Spatial bottom-type data at 100m and 20m resolution are available at the Pacific Biological Station. Scientists at NOAA's Alaska Fisheries Science Center are currently engaged in developing distribution maps for all commercially-fished species in Alaska. Some of these data will be available, via our external collaborator Dr Rooper, in the second year of the project. Software: A version of the hierarchical Bayesian model has already been written using the OpenBUGS programming language. Dr Lecomte will provide this code, which will be customized and refined for this project, by the PI and Dr Etienne in Year 1 (Contract 2) and by Dr Lecomte in Year 2. All other statistical models and graphic outputs will be developed using the R-programming language, building, where possible, on existing code. Species abundance and data distribution maps will be made using ArcGIS or a similar, open source mapping software (e.g., QGIS, PBSMapping). Several members of the project team are expert in these softwares.

2.3 DATA MANAGEMENT

Spatially-gridded Canadian datasets and gridded predictions of distribution and abundance will be transferred to a database managed by the Pacific Groundfish Statistics program. They will be available internally to Pacific stock assessment scientists, and by request externally. Maps will be incorporated into an intranet-based tool, making them available to Pacific scientists and managers. Methods, statistical results and graphic outputs will be published in a CSAS Research Document that will be publicly available through CSAS. Key results will also be published in the primary literature.

Open the file `example.Rnw`. Look at the first R code chunk, starting on line 191. This is where the R environment is loaded so that the figures and tables can be made, and values can be referenced later in the document. There are two choices: source the R file, or load a binary R environment. Sourcing the file works fine, but if there is a lot of loading of data or calculations that have to happen during the sourcing the build will take a long time. A much quicker way is to open an R session, and source the `example.r` manually, then save the R environment to a file called `.RData` in the `r` directory. If this method is used, make sure to set `use.binary.envir <- TRUE` on line 209 of `example.Rnw`.

To build this document, open a command line and enter **buildtex.bat**. When you run `buildtex.bat` two things happen:

1. Rscript calls knitr which goes through and *knits* your *example.Rnw* file, which means it runs all the R code it finds, stores figures in the *knitr-cache* directory, and creates a \LaTeX file which \LaTeX can then understand. It also creates a file called `knitrOutput.log` which contains all output and errors encountered during the knitting procedure. That is where to first look when there are problems compiling your document. Here is the line in `buildtex.bat` that does this:

```
Rscript -e "library(knitr);knit('./example.Rnw')" 1> knitrOutput.log 2>&1
```

2. \LaTeX runs through the newly-created \TeX file (*example.tex*) and calls *bibtex* to find the

references and make the bibliography. There are three output formats of the document: .ps, .dvi, and .pdf. The .ps and .dvi formats require special viewers (Yap and GhostView respectively) and do not incorporate the reference links that are so convenient in the .pdf file. During development of very complex documents, you can leave the last part of this call out to avoid PDF generation, and put it back in when ready to complete the document.

```
@latex -synctex=1 "example.tex" && bibtex "example" && latex "example.tex"
&& latex "example.tex" && dvips "example.dvi" && ps2pdf "example.ps"
```

Some \LaTeX packages may have to be installed. If so, the package manager dialog will open. You must choose to install from internet, then make sure to select *ctan* using *HTTP* protocol from *BC*. The default settings will most likely not work.

2.4 THE KNITTING PROCESS

When *knitr* is called, it parses the *example.Rnw* file, looking for special parenthesis characters which are called *R code chunks*. The chunks begin with a set of parentheses and equals sign `<< >>=` and end with the *at* symbol `@`. Anything between them is an R code chunk which will be evaluated by *knitr*. Inside the beginning parentheses, you can define many *chunk options*. The official page listing these options is here: [Knitr chunk options](#). In this document the file *example.Rnw* holds one chunk which loads the R environment, and *maindoc.Rnw* holds the figure chunks (one for each figure) which each hold simple commands to plot some examples. For example, figure 3 is called like this:

```
<<fig.height=9, fig.width=8>>=
half.torus()
@
```

2.4.1 Running R code directly in text

One should always write calculated values or data by using a reference to the R objects instead of typing the numbers in as text. This way, if something changes you don't have to read and verify every number in your document, they will be updated automatically by *knitr*.

Here's how you write some values by reference from your R environment inside \LaTeX text block: For example to get the mean of *x* you would use the command: `\Sexpr{mean(x)}` which in this case evaluates to 19.8623508. The `\Sexpr{}` construct represents an S-expression, where S was the predecessor to R. For some reason it hasn't yet been changed to `\Rexpr{}`. In this example, the values for the *x* vector were read in from *example.r* at the beginning of the knitting process and is accessible throughout the document. You can call simple R commands using the `\Sexpr{}` command inside \LaTeX . You can do more than one command by separating with a semicolon, for example the command `\Sexpr{z=x+y;mean(z)}` evaluates to 68.3410075 for the *x* and *y* values loaded from *example.r*.

2.5 WHAT TO DO IF THERE'S AN ERROR

If there's an error, the first thing to do is check the *knitrOutput.log* file. This will contain all messages both regular and error which *knitr* outputs. If there was an error during the knitting process, you will find it there. The last lines of the file should say:

```
output file: example.tex
```

```
[1] "example.tex"
```

If you see this message and the file *example.tex* exists then the *knitr* part has worked but the \LaTeX part of the compilation has failed. The message in the case that \LaTeX has failed will be something like *l.132...error message*. In that case, the error happened on line 132 of the *example.tex* file. You will have to look at this file first to see where the error is, then go back to your *example.Rnw* file and fix it. Sometimes errors earlier on can trigger something later to fail, which makes it very hard to debug. The best advice is to compile after every change to make sure it is still working. A lot of time can be wasted tracking down errors if you haven't compiled in a long time and made many changes, where more than one error may have been introduced. Matching parenthesis errors can be particular insidious.

If there is an error stating:

```
**** Could not open the file example.pdf
```

it means that you still have the PDF open and you need to close it and re-compile. If you have the GhostView viewer, you can keep the postscript (*example.ps*) file open instead while developing. You won't get an error even if it stays open.

3 EQUATIONS IN \LaTeX

Equations are fairly straightforward, and if organized using the same label prefix (**eq:**), they will be numbered automatically. Here are some example equations from the 2015 Arrowtooth Flounder assessment with added margins for captions:

$$B_y = \sum_{i=1}^k C_{y_i} A_i = \sum_{i=1}^k B_{y_i} \quad (1)$$

where C_{y_i} is the mean CPUE density (kg/km^2) for species s in stratum i , A_i is the area of stratum i , B_{y_i} is the biomass of Arrowtooth Flounder in stratum i for year y , and k is the number of strata.

CPUE (C_{y_i}) for Arrowtooth Flounder in stratum i for year y was calculated as a density in kg/km^2 by:

$$C_{y_i} = \frac{\sum_{j=1}^{n_{y_i}} \left[\frac{W_{y_i,j}}{D_{y_i,j} w_{y_i,j}} \right]}{n_{y_i}} \quad (2)$$

where $W_{y_i,j}$ is the catch weight in kg for Arrowtooth Flounder in stratum i , year y , and tow j , $D_{y_i,j}$ is the distance travelled in km for tow j in stratum i and year y , $w_{y_i,j}$ is the net opening in km by tow j , stratum i , and year y , and n_{y_i} is the number of tows in stratum i .

The variance of the survey biomass estimate V_y for Arrowtooth Flounder in year y is calculated in kg^2 as follows:

$$V_y = \sum_{i=1}^k \left[\frac{\sigma_{y_i}^2 A_i^2}{n_{y_i}} \right] = \sum_{i=1}^k V_{y_i} \quad (3)$$

where $\sigma_{y_i}^2$ is the variance of the CPUE in kg^2/km^4 for year y in stratum i , V_{y_i} is the variance of Arrowtooth Flounder in stratum i for year y , where $\sigma_{y_i}^2$ was obtained from bootstrapped samples (see below).

The CV for Arrowtooth Flounder for each year y was calculated as follows:

$$CV_y = \frac{\sqrt{V_y}}{B_y} \quad (4)$$

where CV_y is the CV for year y .

3.0.1 A few more equation tidbits

Here is an example of overline usage: \overline{R}_{init} .

Double dashes can be used to make a longer solid line to show value ranges: $0.308y^{-1} - 0.406y^{-1}$.

Here's how you show a fraction inline: $\frac{B_{2016}}{B_{ReferencePoint}} < 1$.

4 HOW REFERENCES WORK

4.1 HOW THE BIBLIOGRAPHY WORKS

The bibliography is automatically generated by \LaTeX . The file `all.bib` contains thousands of references and is added to on an ongoing basis. The format of that file is simple and self-explanatory. When you cite a document, you use a `citet` command to get a reference to a paper. For example, `\citet{arf2001}` = ?. You can also click the reference to go to its entry in the bibliography. Press Alt-left arrow to come back to where you were after. The `bibtex` program, which is called up by \LaTeX , searches `all.bib` for this and inserts the correct reference in a file

called *example.bbl* which is then used to generate the bibliography. The bibliography is generated at the end of the process, and only those references included in the document by you (and in *example.bbl*) are included in the bibliography. Here are a bunch more references: **?**, **??**, **??**. Check the bibliography to see that they are all there. You can use these references anywhere in the document, including in child documents like *maindoc.Rnw* and any appendices.

4.2 HOW THE FIGURE AND TABLE REFERENCES WORK

See Figures 1, 2, 3, and 4. Note that these numbers are clickable and you can go directly to the figure. These are referenced figures.

A figure/table reference works by adding a reference name to a figure/table, then remembering what it was and using a `\ref` command to reference the figure/table. For example in Figure 1, the figure reference code has a label tag like this `\label{fig:example-random-stuff}`. The figure can be referenced anywhere in the latex document by using this syntax: `\ref{fig:example-random-stuff}`. The numbering is taken care of for you and is separate for each type of reference. Here is a list of suggested prefixes to use for different reference types:

1. **sec**: - section
2. **subsec**: - subsection
3. **fig**: - figure
4. **tab**: - table
5. **eq**: - equation
6. **lst**: - code listing
7. **itm**: - enumerated list item (like this list)
8. **chap**: - appendix

4.3 HOW APPENDIX REFERENCES WORK

Appendix references are much like chapters of a book. They can be added or commented out easily at the bottom of *example.Rnw*. This helps with the incremental form of development where you make sure the main document is compiling and then when ready, uncomment the appendix inclusion code and the appendix will be included in the document. Once included, any appendix references will be resolved.

The code which adds an appendix is *knitr* code because you want the appendix added before the knitting process so that any figures or R expressions are resolved, just like in the main document. This is an example of how appendix code is added:

```
\rfoot{Appendix A -- Example appendix 1}  
  
<<appendix-1, child='appendix-1/appendix-1.Rnw'>>=  
@
```

To reference this appendix, use this syntax: `\ref{chap:example.1}` which resolves to appendix

A. This is also clickable and will take you directly to the appendix. The reference must be defined at the beginning of *appendix-1.Rnw* like this: `\label{chap:example.1}`. This method is repeated for all appendices. They will be lettered in the order in which they appear in *example.Rnw*, so it is very easy to change the order of appendices and rebuild the document.

5 SUMMARY

Here's a reference to an appendix:

sectionREFERENCES bibliography../../all

6 TABLES

Table 1. Estimated and fixed parameters and prior probability distributions used in the Reference Case.

Parameter	Number estimated	Bounds [low,high]	Prior (Mean, SD) (single value=fixed)
Log recruitment ($\ln(R_0)$)	1	[-2,6]	Uniform
Steepness (h)	1	[0.2,1]	Beta($\alpha = 13.4, \beta = 2.40$)
Log natural mortality ($\ln(M)$)	1	[-5,0]	Normal($\ln(0.2), 0.2$)
Log mean recruitment ($\ln(\bar{R})$)	1	[-2,6]	Uniform
Log initial recruitment ($\ln(\bar{R}_{init})$)	1	[-2,6]	Uniform
Variance ratio (ρ)	0	Fixed	0.059
Inverse total variance (ϑ^2)	0	Fixed	1.471
Survey age at 50% selectivity (\hat{a}_k)	3	[0,1]	None
Fishery age at 50% selectivity (\hat{a}_k)	1	[0,1]	None
Survey SD of logistic selectivity ($\hat{\gamma}_k$)	3	[0,Inf]	None
Fishery SD of logistic selectivity ($\hat{\gamma}_k$)	1	[0,Inf]	None
Survey catchability (q_k)	4	None	Normal(0.5,1.0)
Log fishing mortality values ($\Gamma_{k,t}$)	19	[-30,3]	[-30,3]
Log recruitment deviations (ω_t)	19	None	Normal(0, τ)
Initial log recruitment deviations ($\omega_{init,t}$)	19	None	Normal(0, τ)

Table 2. Example using xtable with some pseudo-random seeded numbers. The function get.align makes the left column justified left and the rest justified right which is how most tables giving values are shown.

ID	$R_{s=1}$	$R_{s=2}$	$R_{s=3}$	$R_{s=4}$	\bar{R}	σ
1	1.52	11.57	12.54	16.04	10.42	6.23
2	5.19	12.18	5.18	6.16	7.18	3.37
3	11.12	16.99	11.56	19.04	14.68	3.94
4	5.87	7.55	1.58	19.49	8.62	7.67
5	14.75	8.27	15.46	5.33	10.95	4.96
6	1.58	6.21	2.02	15.79	6.40	6.60
7	15.16	3.91	3.79	8.43	7.82	5.35
8	13.65	6.07	5.13	1.70	6.64	5.04
9	19.58	14.46	10.44	13.04	14.38	3.85
10	16.18	3.30	15.46	4.54	9.87	6.89
11	12.75	8.52	8.08	18.19	11.88	4.70
12	10.49	7.17	16.04	5.64	9.83	4.60
13	5.80	17.18	11.04	13.30	11.83	4.75
14	4.09	13.79	16.24	2.37	9.12	6.91
15	6.30	9.46	4.25	17.04	9.26	5.61
16	17.23	3.48	12.21	12.05	11.24	5.71
17	3.71	1.65	2.14	9.24	4.18	3.48
18	4.15	4.07	16.51	1.54	6.57	6.74
19	19.46	16.45	18.98	5.80	15.17	6.39
20	18.94	3.53	19.74	19.90	15.53	8.01

Table 3. Sensitivity cases and their parameters.

Scenario	Description	Parameters
1	Reference Case	See Table 1
2	Decrease σ to 0.1	$\vartheta^2 = 1.538; \rho = 0.015$
3	Estimate Total Variance	ϑ^2 estimated; $\rho = 0.059$
4	Increase τ to 1.0	$\vartheta^2 = 0.962; \rho = 0.038$
5	Decrease τ to 0.6	$\vartheta^2 = 2.500; \rho = 0.100$
6	Decrease mean of h prior to 0.72	$h = \text{Beta}(\alpha = 12.7, \beta = 5.0)$
7	Decrease SD of $\ln(M)$ prior to 0.05	$\ln(M) = \text{Normal}(\ln(0.2), 0.05)$
8	Increase SD of $\ln(M)$ prior to 0.25	$\ln(M) = \text{Normal}(\ln(0.2), 0.25)$
9	Increase mean of $\ln(M)$ prior to $\ln(1.0)$	$\ln(M) = \text{Normal}(\ln(0.3), 0.20)$
10	Increase mean of $\ln(q_k)$ prior to $\ln(1.0)$	$\ln(q_k) = \text{Normal}(\ln(1.0), 1.0)$
11	Increase SD of $\ln(q_k)$ prior to 1.5	$\ln(q_k) = \text{Normal}(\ln(0.5), 1.5)$
12	Selectivity Ogive = Maturity Ogive	$\hat{a} = 4.99 \text{ yrs}; \hat{\gamma} = 1.27 \text{ yrs}$
13	Age-at-50%-harvest set to 6 yrs	$\hat{a} = 6.00 \text{ yrs}; \hat{\gamma} = 1.00 \text{ yrs}$

Table 4. Sensitivity cases for q_k ; posterior quantiles.

Index	Sensitivity 10			Sensitivity 11		
q_k	2.5%	50%	97.5%	2.5%	50%	97.5%
QCSSS	0.081	0.158	0.508	0.029	0.083	0.226
HSMAS	0.079	0.121	0.155	0.035	0.081	0.136
HSSS	0.070	0.118	0.200	0.027	0.067	0.136
WCVISS	0.061	0.104	0.172	0.022	0.059	0.118

7 FIGURES

Random Stuff

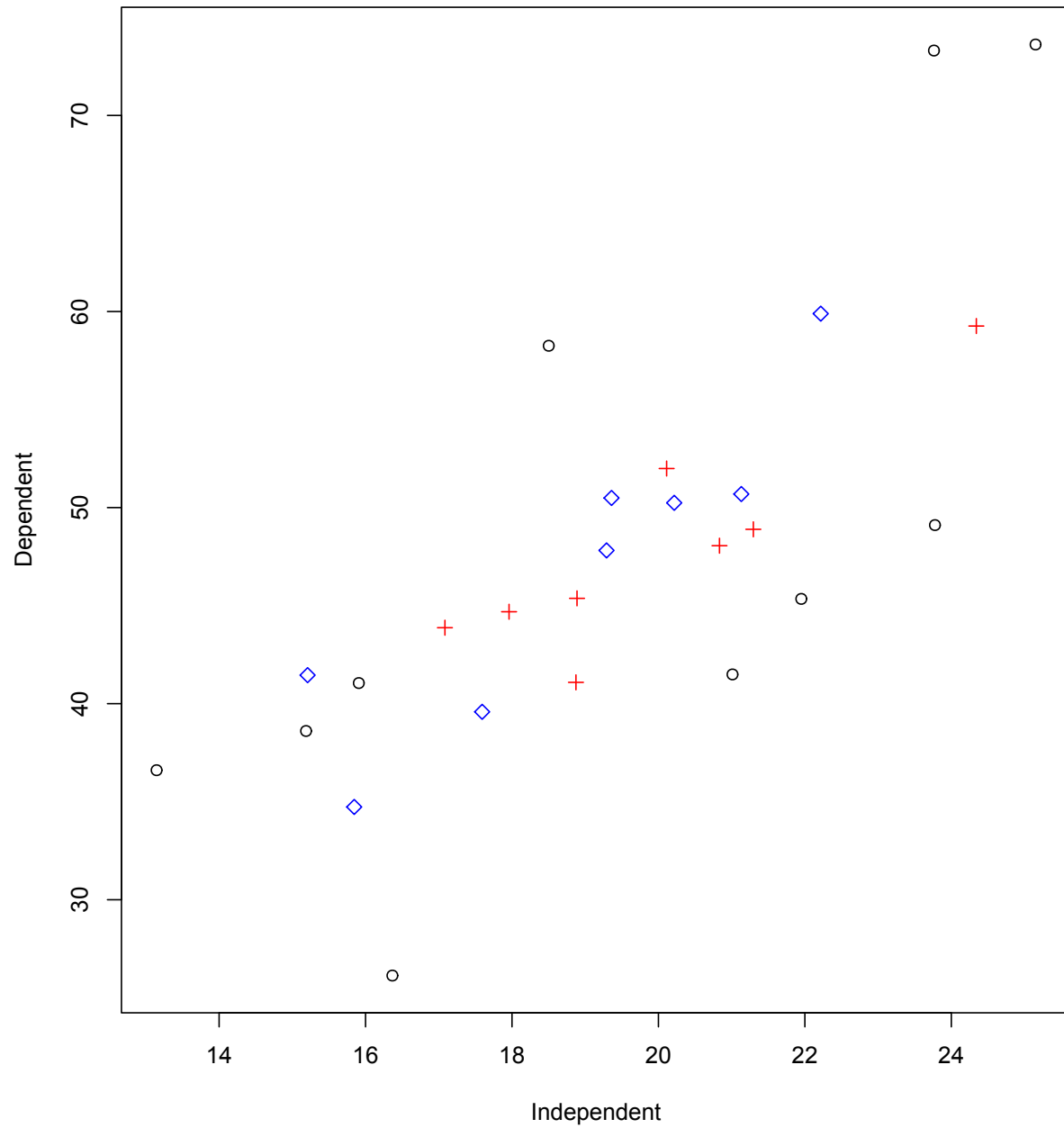


Figure 1. Random points example... Degrees are represented in \LaTeX like this 0.1° and superscript like this km^2)

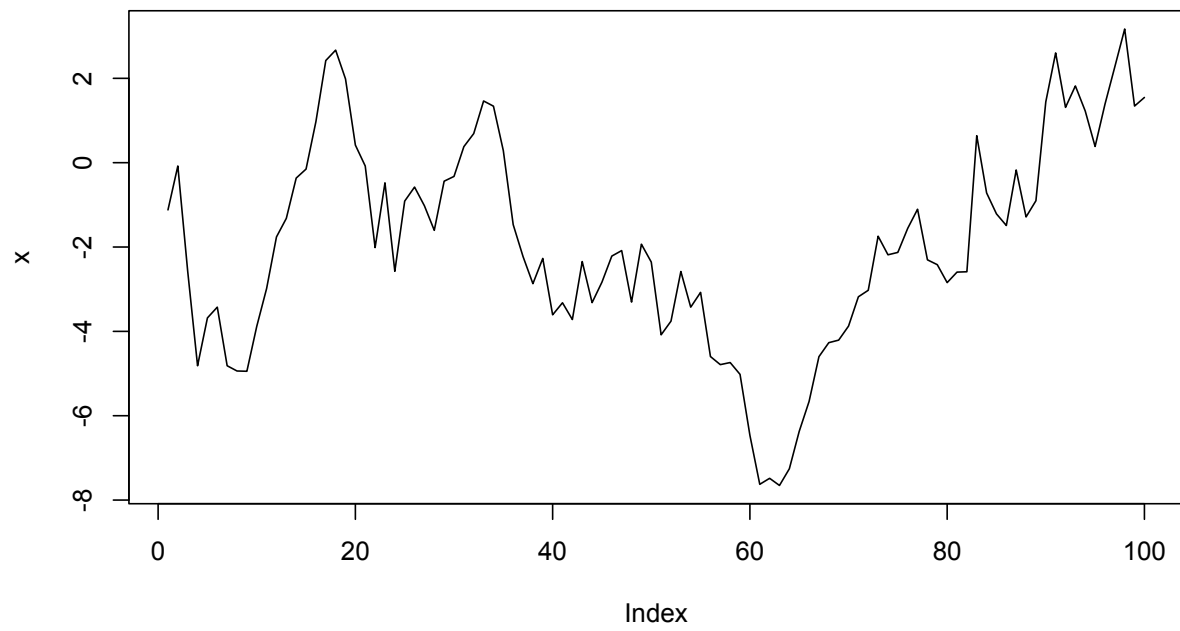


Figure 2. Brownian motion example..

Half of a Torus

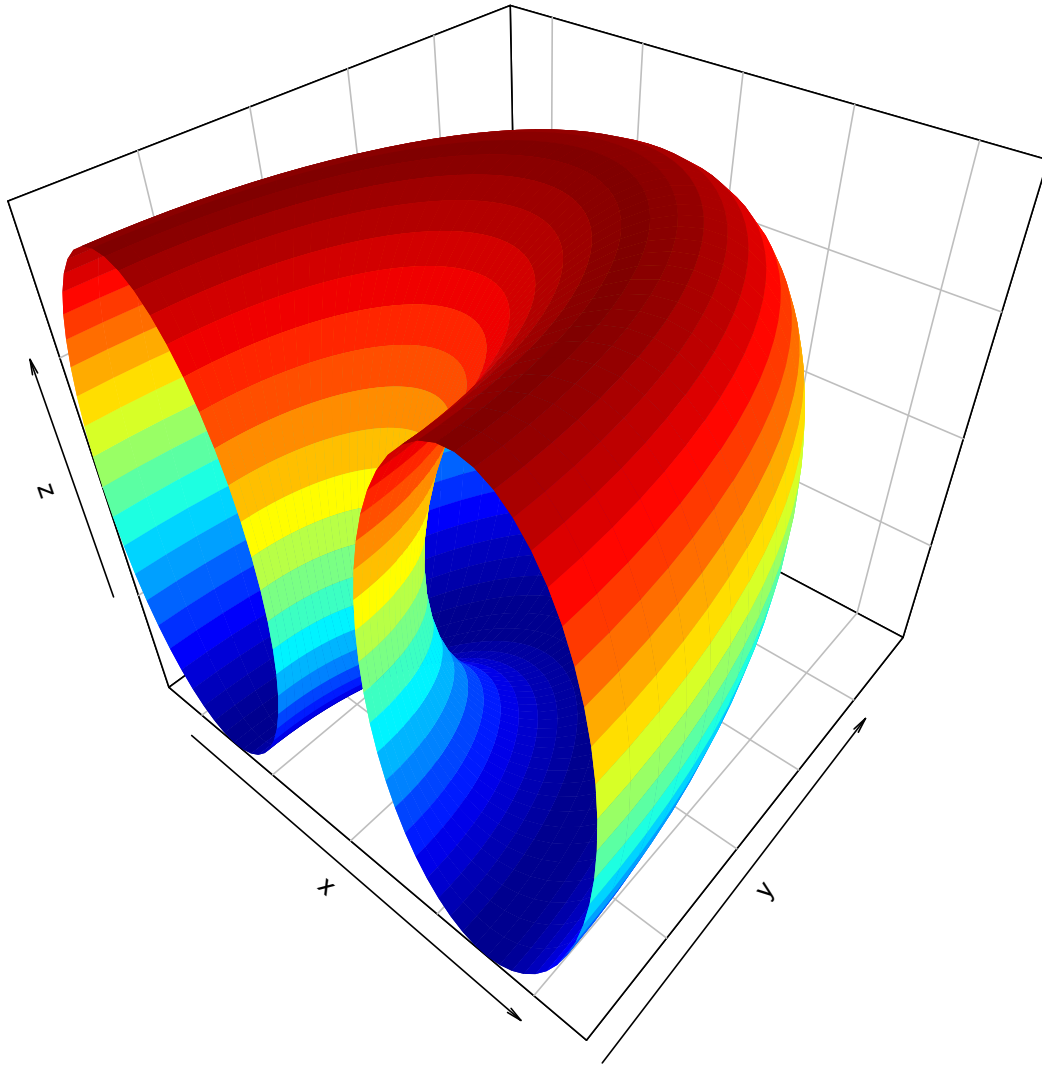


Figure 3. Half torus example..

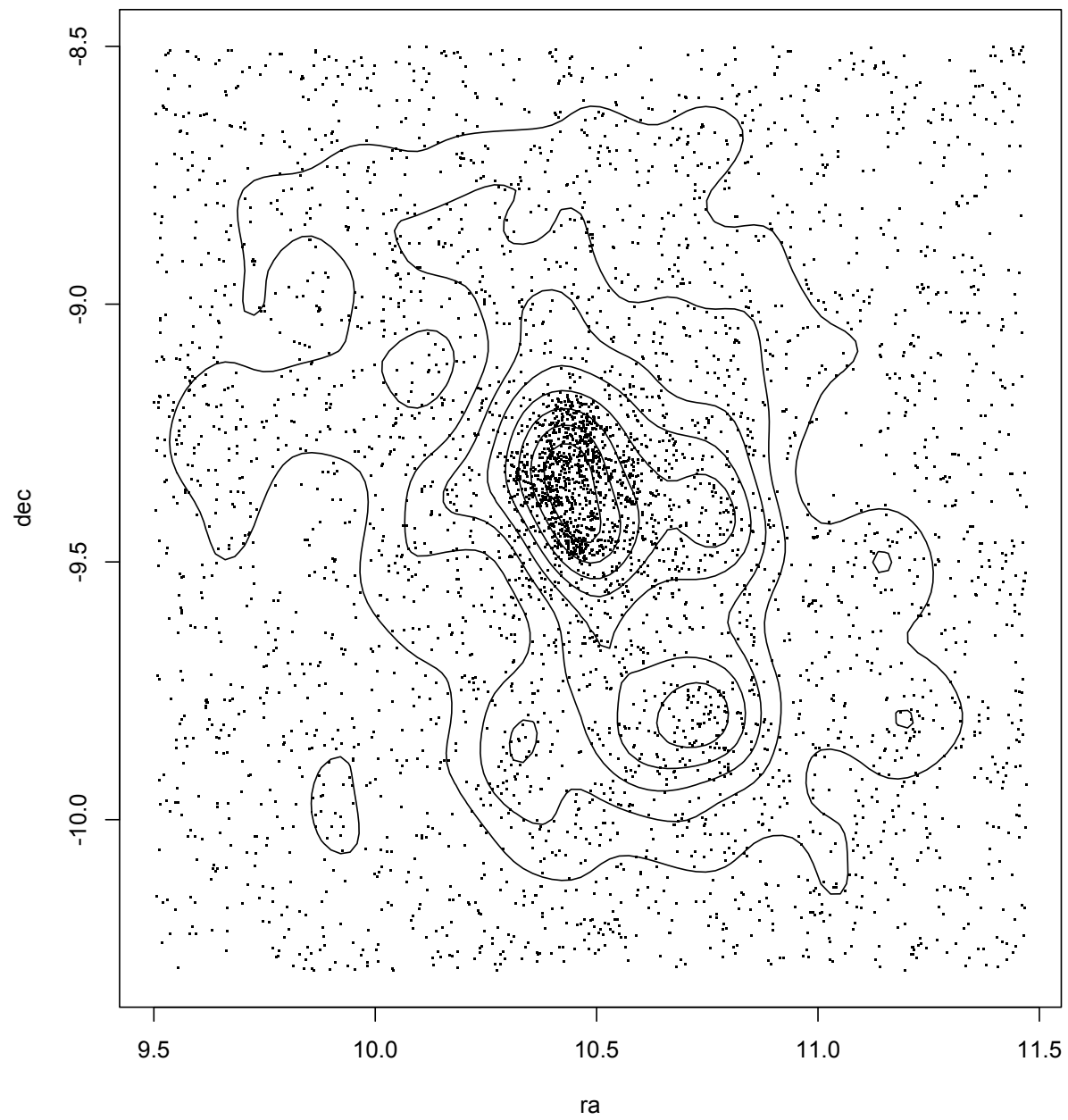


Figure 4. Galaxy example

A EXAMPLE APPENDIX 1

A.1 INTRODUCTION

Stock Assessment modelling was done using the Integrated Statistical Catch Age Model (iSCAM), developed by S. Martell (?). iSCAM is written in AD Model Builder and the source code and documentation for the original iSCAM is available at <https://github.com/smartell/iSCAM>. Code for the version used in this assessment can be found at <https://github.com/cgrandin/iSCAM>. iSCAM uses a statistical catch-at-age model implemented in a Bayesian estimation framework.

Running of iSCAM and compilation of results figures was streamlined using the `iscam-gui` software package developed at the Pacific Biological Station by C. Grandin (<https://github.com/cgrandin/iscam-gui>). `iscam-gui` is written in the statistical language R, and provides a graphical user interface that allows users to run and show output of multiple iSCAM model scenarios in a comparative fashion.

A.2 MODEL DESCRIPTION

Note we can reference tables in the main document by using the `ref` keyword. Here we reference the table with random numbers in it: Table 2. Note that this reference `tab:example-table` was given to the R function `make.xtable` as an argument. See `maindoc.Rnw`.

We can also reference any equation found anywhere, such as 1 which is referenced by the tag `eq:sweptareaindex` or 2 which is referenced by `eq:cpuecalc`.

A.3 ANALYTIC METHODS: EQUILIBRIUM CONSIDERATIONS

A.3.1 A STEADY-STATE AGE-STRUCTURED MODEL

Here is another equation written in a slightly different way than in the `maindoc`. Latex allows for lots of different ways to do things:

$$s_o = \frac{\kappa}{\phi_E},$$

and the density-dependent term is given by:

$$\beta = \frac{\kappa - 1}{R_o \phi_E}$$

Here is an example of an inline fraction: $s_o = \frac{\kappa}{\phi_E}$.

A.4 RESIDUALS, LIKELIHOODS, AND OBJECTIVE FUNCTION VALUE COMPONENTS

This is an example of nested lists using enumeration.. The objective function contains five major components:

1. The negative log-likelihood for the catch data
2. The negative log-likelihood for the relative abundance data
3. The negative log-likelihood for the age composition data
4. The prior distributions for model parameters
5. Three penalty functions that are invoked to regularize the solution during intermediate phases of the non-linear parameter estimation. The penalty functions:
 - (a) constrain the estimates of annual recruitment to conform to a Beverton-Holt stock-recruit function
 - (b) weakly constrain the log recruitment deviations to a normal distribution
 - (c) weakly constrain estimates of log fishing mortality to a normal distribution ($\sim N(\ln(0.2), 4.0)$) to prevent estimates of catch from exceeding estimated biomass.

This example shows the use of some other special functions such as *widehat* both inline and in equation form: The residuals between the observed ($p_{t,a}$) and predicted proportions ($\widehat{p}_{t,a}$) is given by:

$$\eta_{t,a} = \ln(p_{t,a}) - \ln(\widehat{p}_{t,a}) - \frac{1}{A} \sum_{a=1}^A [\ln(p_{t,a}) - \ln(\widehat{p}_{t,a})] \quad (\text{A.1})$$

B WEIGHTING OF AGE PROPORTIONS

This appendix summarizes a method for representing commercial and survey age structures for a given species through weighting observed age frequencies x_a or proportions x'_a by catch||density in defined strata. The methodology presented in this appendix is based on that presented by ? for Rock Sole.

Ideally, sampling effort would be proportional to the amount of the species caught, but this is not usually the case. Therefore, the stratified weighting scheme presented below attempts to adjust for unequal sampling effort among strata. For commercial samples, strata comprise quarterly periods within a year, while for survey samples, the strata are defined by longitude, latitude, and depth. Within each stratum, commercial ages are weighted by the catch weight (kg) of the species in tows that were sampled, and survey ages are weighted by the catch density (kg/km²) of the species in sampled tows. A second weighting is then applied: quarterly commercial ages are weighted by the commercial catch weight of the species from all tows within each quarter; stratum survey ages are weighted by stratum areas (km²) in the survey. Throughout this section, we use the symbol '||' to delimit parallel values for commercial and survey analyses, respectively, as the mechanics of the weighting procedure are similar for both.

For simplicity we illustrate the weighting of age frequencies x_a , unless otherwise specified. The weighting occurs at two levels: h (quarters for commercial ages, strata for survey ages) and i (years if commercial, surveys in series if survey). Notation is summarised in Table B.1.

Table B.1. Equations for weighting age frequencies or proportions for Arrowtooth Flounder.
(c) = commercial, (s) = survey

Symbol	Description
Indices	
a	age class (1 to A , where A is an accumulator age-class)
d	(c) trip IDs as sample units (s) sample IDs as sample units
h	(c) quarters (1 to 4), 91.5 days each (s) strata (area-depth combinations)
i	(c) calendar years (1977 to present) (s) survey IDs in survey series (e.g., QCS Synoptic)
Data	
x_{adhi}	observations-at-age a for sample unit d in quarter stratum h of year survey i
x'_{adhi}	proportion-at-age a for sample unit d in quarter stratum h of year survey i
C_{dhi}	(c) commercial catch (kg) of a given species for sample unit d in quarter h of year i (s) density (kg/km ²) of a given species for sample unit d in stratum h of survey i
C'_{dhi}	C_{dhi} as a proportion of total catch density $C_{hi} = \sum_d C_{dhi}$
y_{ahi}	weighted age frequencies at age a in quarter stratum h of year survey i
K_{hi}	(c) total commercial catch (kg) of species in quarter h of year i (s) stratum area (km ²) of stratum h in survey i
K'_{hi}	K_{hi} as a proportion of total catch area $K_i = \sum_h K_{hi}$
p_{ai}	weighted frequencies at age a in year survey i
p'_{ai}	weighted proportions at age a in year survey i

For each quarter||stratum h we weight sample unit frequencies x_{ad} by sample unit catch||density of the assessment species. For commercial ages, we use trip as the sample unit, though at times

one trip may contain multiple samples. In these instances, multiple samples from a single trip will be merged into a single sample unit. Within any quarter||stratum h and year||survey i there is a set of sample catches||densities C_{dhi} that can be transformed into a set of proportions:

$$C'_{dhi} = \frac{C_{dhi}}{\sum_d C_{dhi}} . \quad (\text{B.1})$$

The proportion C'_{dhi} is used to weight the age frequencies x_{adhi} summed over d , which yields weighted age frequencies by quarter||stratum for each year||survey:

$$y_{ahi} = \sum_d (C'_{dhi} x_{adhi}) . \quad (\text{B.2})$$

This transformation reduces the frequencies x from the originals, and so we rescale (multiply) y_{ahi} by the factor

$$\frac{\sum_a x_{ahi}}{\sum_a y_{ahi}} \quad (\text{B.3})$$

to retain the original number of observations.

At the second level of stratification by year||survey i , we calculate the the annual proportion of quarterly catch (t) for commercial ages or the survey proportion of stratum areas (km²) for survey ages

$$K'_{hi} = \frac{K_{hi}}{\sum_h K_{hi}} \quad (\text{B.4})$$

to weight y_{ahi} and derive weighted age frequencies by year||survey:

$$p_{ai} = \sum_h (K'_{hi} y_{ahi}) . \quad (\text{B.5})$$

Again, if this transformation is applied to frequencies, it reduces them from the original, and so we rescale (multiply) p_{ai} by the factor

$$\frac{\sum_a y_{ai}}{\sum_a p_{ai}} . \quad (\text{B.6})$$

to retain the original number of observations.

Finally, we standardise the weighted frequencies to represent proportions-at-age:

$$p'_{ai} = \frac{p_{ai}}{\sum_a p_{ai}} . \quad (\text{B.7})$$

If initially we had used proportions x'_{adhi} instead of frequencies x_{adhi} , the final standardisation would not be necessary. However, its application does not affect the outcome.

The choice of data input (frequencies x vs. proportions x') can sometimes matter: the numeric outcome can be very different, especially if the input samples comprise few observations. Theoretically, weighting frequencies emphasises our belief in individual observations at specific ages while weighting proportions emphasises our belief in sampled age distributions. Neither method yields inherently better results. However, if the original sampling methodology favoured sampling few fish from many tows rather than sampling many fish from few tows, then weighting frequencies probably makes more sense than weighting proportions. In this assessment, we weight age frequencies x .