GMACS Overview

June 29, 2015

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GMACS

- Project Objectives
- Software overview
  - Assessment Model
  - R-Packages & Simulation Tools
  - Code Repository
  - Documentation
- Working examples and issues

Project Objectives

- Develop a generalized size-structured assessment model for Alaskan crab stocks.

```
DATA_SECTION

  // |---------------------|
  // | SIMULATION CONTROLS |
  // |---------------------|
  int simflag;
  int rseed
  LOC_CALCS
    simflag = 0;
    rseed   = 0;
    int opt,on;
    if((on=option_match(ad_comm::argc,ad_comm::argv,"-sim",opt))>-1)
    {
      simflag = 1;
      rseed   = atoi(ad_comm::argv[on+1]);
    }
  END_CALCS

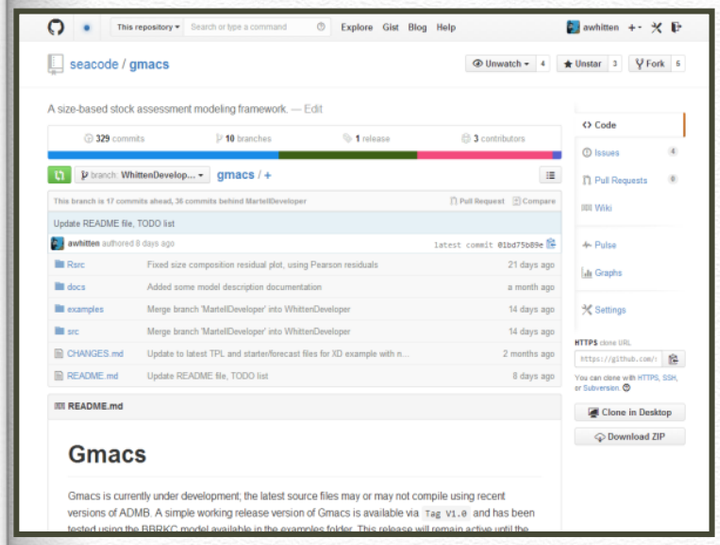
  // |------------------------|
  // | DATA AND CONTROL FILES |
  // |------------------------|
  init_adstring datafile;
  init_adstring controlfile;

  !! ad_comm::change_datafile_name(datafile); ECHO(datafile);ECHO(controlfile);

  // |-----------------|
  // | MODEL DIMENSIONS |
  // |-----------------|
  init_int syr;       ///> initial year
  init_int nyr;       ///> terminal year
  init_number jstep;  ///> time step (years)
  init_int nfleet;    ///> number of gears
  init_int nsex;      ///> number of sexes
  init_int nshell;    ///> number of shell conditions
  init_int nmature;   ///> number of maturity types
  init_int nclass;    ///> number of size-classes

  init_vector size_breaks(1,nclass+1);
  vector      mid_points(1,nclass);
  !! mid_points = size_breaks(1,nclass) + first_difference(size_breaks);
  !! ECHO(syr); ECHO(nyr); ECHO(nfleet); ECHO(nsex); ECHO(nshell);ECHO(nmature); ECHO(nclass);
```

Git Version Control



Models

BBRKC

NSRKC

PIRKC

Snow

```
DATA_SECTION

  // |---------------------|
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  // |---------------------|
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  int rseed
  LOC_CALCS
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    rseed   = 0;
    int opt,on;
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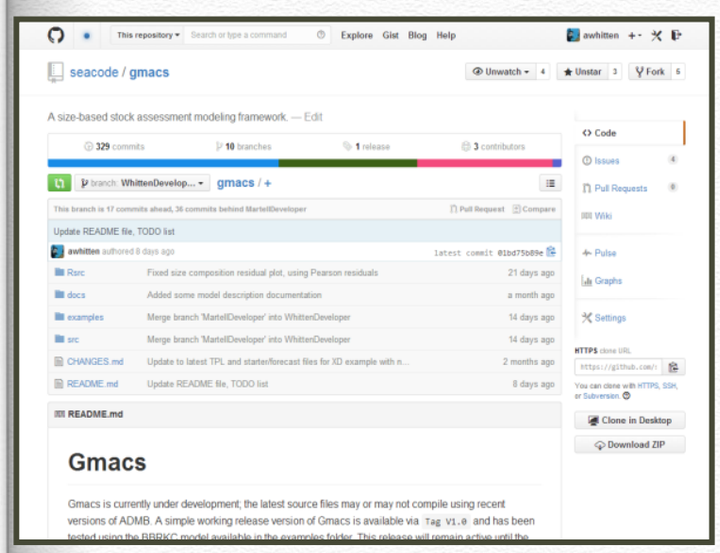
Git Version Control



Models

BBRKC

NSRKC

PIRKC

Snow

GMR (R Package)

Template Report

Imported tables
Imported plots
Results and code

Software Overview

GMACS

- There are four major components to the GMACS package:

1. Assessment model (ADMB & C++)

2. R-packages and Scripts (R & Shell Scripts)

3. Code repository (https://github.com/seacode/gmacs)

4. Documentation

    1. API: http://seacode.github.io/gmacs/index.html

    2. General model description (https://github.com/seacode/gmacs/blob/develop/docs/manuscript/GLBAM.pdf)

    3. User manual (wiki https://github.com/seacode/gmacs/wiki)

Assessment Model

Started fall 2013 (Sep 8, 2013, post-doc)

- Code adopted originally from André's work for crab MSE (i.e., P* etc)
- Major re-write in summer of 2014

Inputs:

- Data file (catch, cpue, composition, etc.)
- Control file (i.e., model specification)

- Outputs:
  - Parameter estimates & uncertainty
  - Derived quantities (abundance, residual fits, reference points, etc.)

Input data

- Model dimensions

```
1953   # Start year
2014   # End year
1      # Time-step (years)
4      # Number of distinct data groups
1      # Number of sexes
2      # Number of shell condition types
1      # Number of maturity types
20     # Number of size-classes in the model
```

Input data

- Length-schedules

```
# size_breaks (a  vector  giving  the b
65  70  75  80  85  90  95  100 105 110
# weight-at-length  allometry W = a*L^b
##  a (male,  female)
4.03E-07
##  b (male,  female)
3.141334
# Male  mature  weight-at-length  (weig
0 0 0 0 0 0 0 0 0 0 0 0 1.432 1.625 1.835
# Proportion  mature  by  sex.
0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1
```

Input data

Catch

```
## ____________________________________________________________________________
##
## CATCH DATA
## Type of catch: 1 = retained, 2 = discard, 3 =
## Units of catch: 1 = biomass, 2 = numbers
## for BBRKC Units are in 1000 mt for landed & million crabs for discards.
## ____________________________________________________________________________
##
## Male Retained 1000
## year seas fleet sex obs      cv     type units mult   effort discard_mortality
  1953 1    1    1   6036.9 0.0316 1    1     0.001 0      0.2
  1954 1    1    1   4870.2 0.0316 1    1     0.001 0      0.2
  1955 1    1    1   4741.9 0.0316 1    1     0.001 0      0.2
  1956 1    1    1   4546.4 0.0316 1    1     0.001 0      0.2
  1957 1    1    1   4057.8 0.0316 1    1     0.001 0      0.2
  1958 1    1    1   3544.8 0.0316 1    1     0.001 0      0.2
  1959 1    1    1   6062.3 0.0316 1    1     0.001 0      0.2
```

Input data

- Relative Abundance

```
## ———————————————————————————————————————————————————————————————— ##
## RELATIVE ABUNDANCE DATA
## Units of Abundance: 1 = biomass, 2 = numbers
## TODO: add column for maturity for terminal molt life-histories
## for BBRKC Units are 1000 t
## ———————————————————————————————————————————————————————————————— ##
## Number of relative abundance indices
2
## Number of rows in each index
40 2
# Survey data (abundance indices, units are tons of crabs)
# Year, Seas, Fleet, Sex, Abundance, CV    units
 1975 1    3     1    146.0280   0.188 1
 1976 1    3     1    200.0830   0.169 1
 1977 1    3     1    237.7770   0.141 1
 1978 1    3     1    203.1600   0.155 1
 1979 1    3     1    160.7790   0.133 1
 1980 1    3     1    164.2590   0.221 1
```

Input data

Size Composition

```
##  SIZE  COMPOSITION DATA  FOR ALL FLEETS
## ____________________________________________________________________________________ ##
##  SIZE  COMP  LEGEND
##  Sex:  1 = male, 2 = female, 0 = both  sexes combined
##  Type  of  composition:  1 = retained, 2 = discard,  0 = total composition
##  Maturity  state:  1 = immature, 2 = mature, 0 = both  states  combined
##  Shell condition:  1 = new shell,  2 = old shell,  0 = both  shell types combined
## ____________________________________________________________________________________ ##
##length  proportions of  retained  males
##Year, Seas, Fleet,  Sex,  Type, Shell,  Maturity, Nsamp,  DataVec
 1975  1 1 1 1 0 0 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0.0071  0.0741  0.1721  0.2239  0.2122  0.1464  0.0858  0.0785
 1976  1 1 1 1 0 0 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0.0016  0.0290  0.1418  0.2316  0.2199  0.1635  0.1071  0.1055
 1977  1 1 1 1 0 0 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0.0017  0.0192  0.1382  0.2442  0.2226  0.1605  0.1040  0.1096
 1978  1 1 1 1 0 0 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0.0012  0.0209  0.1441  0.2588  0.2401  0.1673  0.0966  0.0711
 1979  1 1 1 1 0 0 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0.0013  0.0119  0.0747  0.1649  0.1998  0.2004  0.1556  0.1914
 1980  1 1 1 1 0 0 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0.0008  0.0138  0.0919  0.1771  0.1950  0.1792  0.1404  0.2019
 1981  1 1 1 1 0 0 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0.0006  0.0225  0.1164  0.1743  0.1711  0.1584  0.1284  0.2283
```

Input data

- Molt Increment

```
## ———————————————————————————————————————————————— ##
## Growth data (increment)
# nobs_growth
20
## Note SM used loewss regression for males BBRKC data
## and cubic spine to interpolate 3 sets of female BBRKC data
## ———————————————————————————————————————————————— ##
# MidPoint Sex Increment CV
 67.5     1   16.510674 0.2
 72.5     1   16.454438 0.2
 77.5     1   16.398615 0.2
 82.5     1   16.343118 0.2
 87.5     1   16.287715 0.2
 92.5     1   16.23213  0.2
 97.5     1   16.176368 0.2
```

Control File

- Leading Parameters

```
# ntheta
  9
# ———————————————————————————————————————————————————————————————— #
# ival      lb      ub      phz   prior    p1     p2       # parameter          #
# ———————————————————————————————————————————————————————————————— #
  0.18     0.01      1       4      2   0.18   0.02       # M
  -1.2     -10      20       2      1   -1.2    0.1       # logR0
   5.0     -10      20      -2      1    3.0    5.0       # logR1
   5.0     -10      20      -1      1    3.0    5.0       # logRbar
  72.5      55     100      -4      1   72.5   7.25       # Recruitment EV
  0.55     0.1       5      -3      0    0.1      5       # Recruitment scale
 -0.6931    -10    0.75      -4      0    -10   0.75      # ln(sigma_R)
  0.75    0.20    1.00       2      3    3.0   2.00       # steepness
  0.001   0.00    1.00      -3      3   1.01   1.01       # recruitment AR1
# ———————————————————————————————————————————————————————————————— #
```

Selectivity Controls

```
## ------------------------------------------------------------------------------------------ ##
## SELECTIVITY CONTROLS                                                                       ##
##    -Each gear must have a selectivity and a retention selectivity                          ##
## LEGEND sel_type:1=coefficients,2=logistic,3=logistic95                                     ##
##        Index: use +ve for selectivity, -ve for retention                                   ##
##        sex dep: 0 for sex-independent, 1 for sex-dependent.                                ##
## ------------------------------------------------------------------------------------------ ##
## ivector for number of year blocks or nodes
## POT       TBycatch  NMFS_S   BSFR_S
## Gear-1    Gear-2    Gear-3   Gear-4
  1         1         2        1        #Selectivity blocks
  1         1         1        1        #Retention blocks
  1         0         0        0        #male   retention flag (0 -> no, 1 -> yes)
## ------------------------------------------------------------------------------------------ ##
## sel              sel   sel   sex  size    year    phz                          start  end    ##
## Index  type  mu   sd  dep  nodes  nodes mirror lam1  lam2  lam3 | block  block    ##
## ------------------------------------------------------------------------------------------ ##
## Selectivity P(capture of all sizes)
  1     3   100  120  0   1     1    -1     12.5  12.5  12.5   1975   2014
  2     3   110  130  0   1     1    -2     12.5  12.5  12.5   1975   2014
  3     3    60   65  1   1     1    -3     12.5  12.5  12.5   1975   1981
  3     3    60   65  1   1     1    -4     12.5  12.5  12.5   1982   2014
  4     3    70   90  0   1     1    -5     12.5  12.5  12.5   1975   2014
## ------------------------------------------------------------------------------------------ ##
## Retained
 -1     3   133  137  0   1     1    -1     12.5  12.5  12.5   1975   2014
 -2     2   595   10  0   1     1    -2     12.5  12.5  12.5   1975   2014
 -3     2   590   10  0   1     1    -3     12.5  12.5  12.5   1975   2014
 -4     2   580   20  0   1     1    -4     12.5  12.5  12.5   1975   2014
## ------------------------------------------------------------------------------------------ ##
```

Current Model Controls

Control	Initial value	Bounds	Informative Prior	Penalized likelihood
Leading parameters	Y	Y	Y	NA
Growth parameters	Y	Y	Y	NA
Seletivity parameters	Y	Y*	N	Y
Catchability	N	N	Y	NA
Fishing Mortality	N	Y	Y*	Y
Time varying M	Y	Y	Y*	Y

Other Controls

```
## ———————————————————————————————————————————————————————————————————————— #
## OTHER CONTROLS
## ———————————————————————————————————————————————————————————————————————— #
 3        # Estimated rec_dev phase
 0        # VERBOSE FLAG (0 = off, 1 = on, 2 = objective func)
 1        # INITIALIZE MODEL AT UNFISHED RECRUITS (0=FALSE, 1=TRUE)
 1984     # First year for average recruitment for Bspr calculation.
 2014     # Last year for average recruitment for Bspr calculation.
 0.35     # Target SPR ratio for Bmsy proxy.
 1        # Gear index for SPR calculations (i.e., directed fishery).
 1        # Lambda (proportion of mature male biomass for SPR reference points.)
 0        # Use empirical molt increment data (0=FALSE, 1=TRUE)
 1        # Stock-Recruit-Relationship (0 = none, 1 = Beverton-Holt)
## ———————————————————————————————————————————————————————————————————————— #
```

Command line options

-i	Information, Contributors, and Acknowledgements
-sim seed#	Simulate data based on pin file for self-testing
-retro n	Retrospective analysis with n terminal years
- ?	List all other ADMB command line options

Main Routines

```
PROCEDURE_SECTION
    initialize_model_parameters();

// Fishing fleet dynamics ...
    calc_selectivities();
    calc_fishing_mortality();

// Population dynamics ...
    calc_growth_increments();
    calc_molting_probability();
    calc_growth_transition();
    calc_natural_mortality();
    calc_total_mortality();
    calc_recruitment_size_distribution();
    calc_initial_numbers_at_length();
    update_population_numbers_at_length();
    calc_stock_recruitment_relationship();

// observation models ...
    calc_predicted_catch();
    calc_relative_abundance();
    calc_predicted_composition();

// objective function ...
    calculate_prior_densities();
    calc_objective_function();
```

Initial setup

Fishing dynamics

Population dynamics

Predict observations

Objective function

Source files

stevenmartell1 — bash — bash — RockJock — ttys000 — 82×20 — ⌘1

bash | bash | bash

```
.
|____gmacs.tpl
|____include
| |____libgmacs.h
| |____nloglike.h
| |____selex.hpp
| |____spr.h
|____lib
| |____equilibrium.cpp
| |____Makefile
| |____moltIncrement.cpp
| |____multinomial.cpp
| |____nloglike.cpp
| |____robust_multi.cpp
| |____spr.cpp
| |____tailcompression.cpp
|____make.bat
|____make.sh
|____makefile
bash-3.2$
```

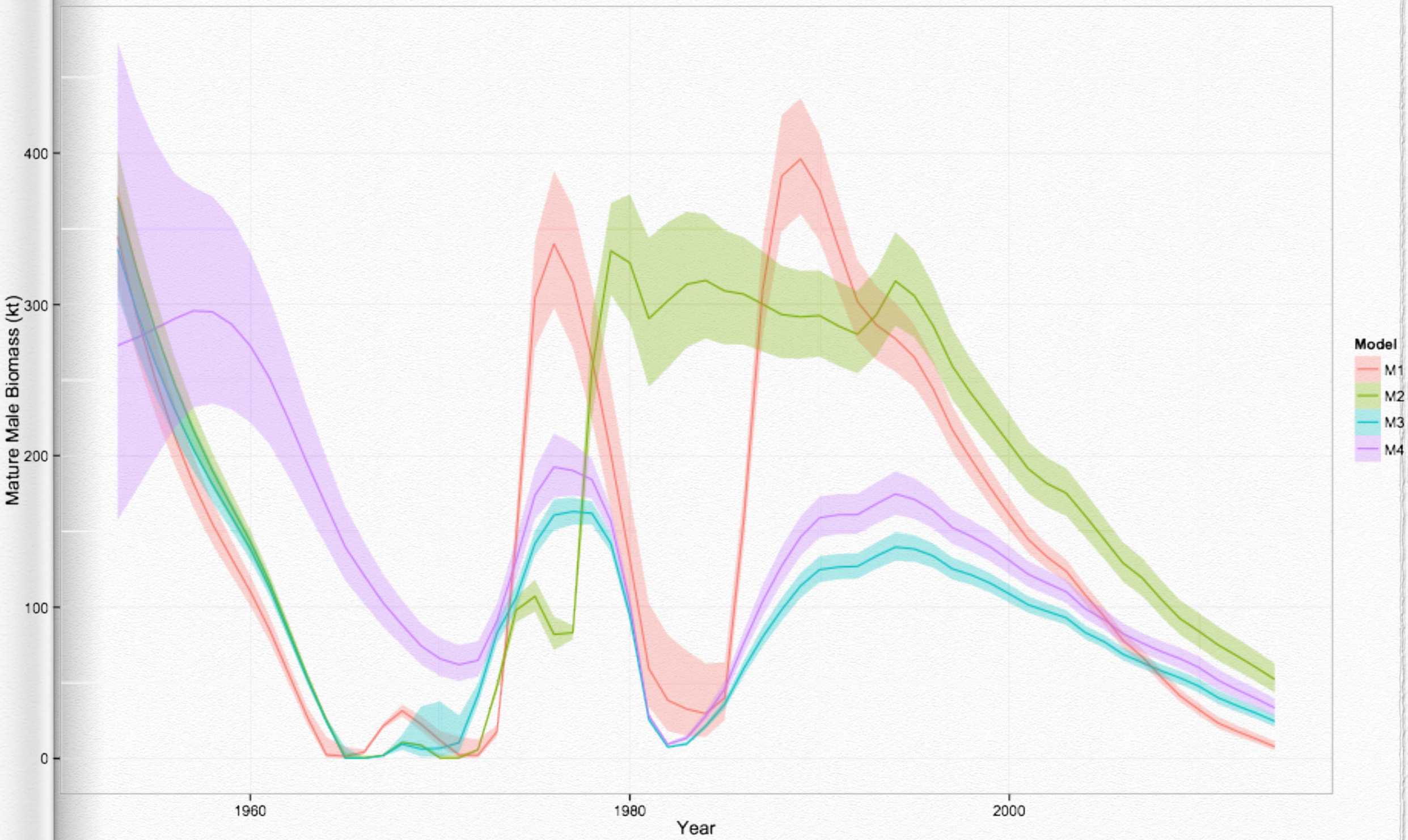
Assessment Model Summary

- GMACS can currently accommodate two sexes, new & old shell conditions, and molt increment data.
- Required features that are still missing:
  - maturity state, tagging information, fishing effort

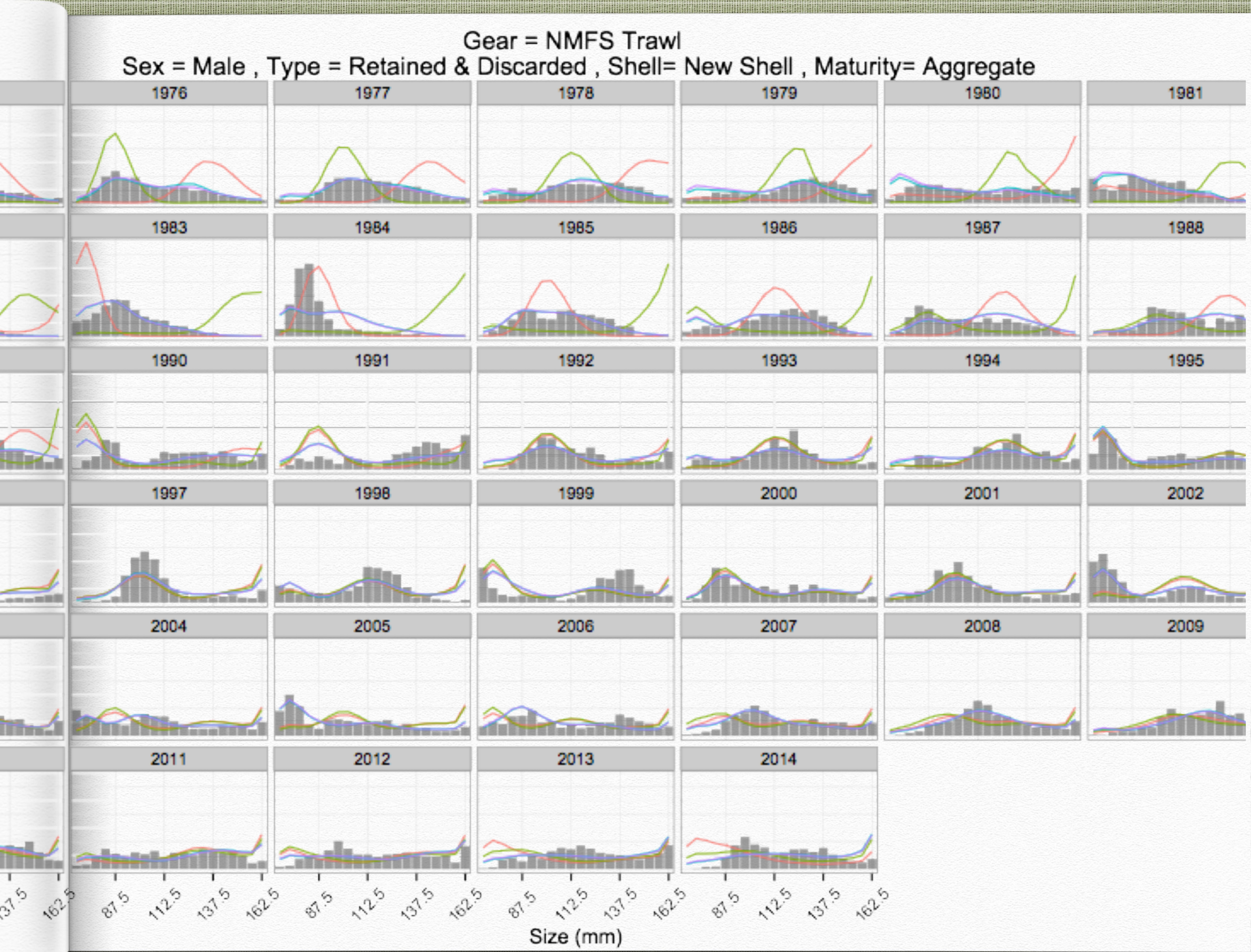
R-packages (gmr)

- gmr is an R-package that works with a GMACS object.
  - GMACS object -> (report file, model fit, posterior samples)
  - Series of plotting routines for summarizing data and model fits to the data.

```
plot.ssb( M );
```


Mature Male Biomass (kt)
400
300
200
100
0
1960
1980
2000
Year
Model
M1
M2
M3
M4

```
plot.sizeComps ( M, 4 );
```


Gear = NMFS Trawl
Sex = Male , Type = Retained & Discarded , Shell= New Shell , Maturity= Aggregate
1976
1977
1978
1979
1980
1981
1983
1984
1985
1986
1987
1988
1990
1991
1992
1993
1994
1995
1997
1998
1999
2000
2001
2002
2004
2005
2006
2007
2008
2009
2011
2012
2013
2014
87.5
112.5
137.5
162.5
Size (mm)

gmr package features

- Minimal amount of r-code required to summarize model fits and other output.
- Easily scalable: users can add additional functionality.

Status of gmr package

- Package can be installed directly from Github using devtools
- > devtools::install_github("seacode/gmacs/gmr", ref = "V1.0")

Package Index

R Help

< > Print Help Search

Plotting and analysis tools for the Gmacs stock assessment framework

Documentation for package 'gmr' version 1.00

- DESCRIPTION file.

Help Pages

gmr-package	gmr: R code for Gmacs
gmr	gmr: R code for Gmacs
gmr.version	Function to return version number
plot_catch	Plot observed and predicted catch values
plot_cpue	Plot cpue or other indices
plot_cpue_res	Plot residuals of cpue or other indices
plot_datarange	Plot data range by fleet and year
plot_gmr	Do all gmr plots
plot_growth	Plot growth from arbitrary start age
plot_growth_inc	Plot growth from arbitrary start age
plot_models_recruitment	Plot predicted recruitment across model runs
plot_multiple	Plot multiple figures on a page
plot_recruitment	Plot predicted recruitment and approximate asymptotic error-bars
plot_selectivity	Plot selectivity
plot_sizeCompRes	plot_sizeCompRes Get observed and predicted size composition values
plot_sizeComps	plot_sizeComps Get observed and predicted size composition values
plot_sizeTransition	Plot size transition
plot_ssb	Plot predicted spawning stock biomass (ssb)
plot_type	Specify the type of plot you would like to create
read_admb	Read ADMB output files
read_fit	Read ADMB .par, .std, and .cor file and return an R object of type 'list' of estimates and correlations
read_psv	Read ADMB .psv file
read_rep	Read ADMB .rep file
set_ggtheme	Set plotting theme for ggplot2 via gmr
shiny_gmacs	Plot Gmacs on shiny app

Code Repository

- https://github.com/seacode/gmacs
- github overview & workflow (developers)
- github statistics.

Github Overview

- Primary function is a code repository.
- Developers: "Don't break the code!"
  - Track issues, milestones, branching automated testing (Travis CI), discussions, …, record of historical development.
- Users:
  - Wiki & API (A Program Interface) documentation.
  - Get latest release version, or current state of the source code.
  - Check out previous versions.

Github Use

seacode / gmacs

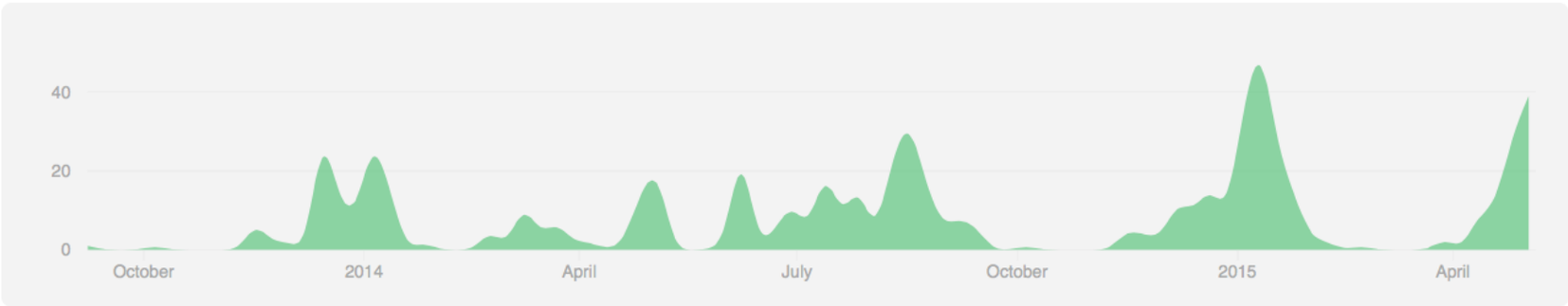
Unwatch 15 | Star 5 | Fork 9

Contributors | Traffic | Commits | Code frequency | Punch card | Network | Members

Sep 8, 2013 – May 6, 2015

Contributions to develop, excluding merge commits

Contributions: **Commits**

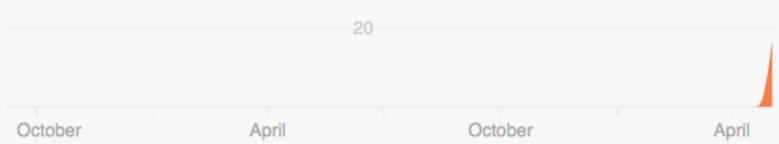


smartell #1
303 commits / 63,894 ++ / 32,346 --

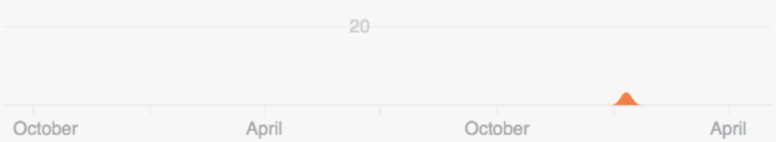
awhitten #2
187 commits / 74,361 ++ / 79,710 --

jimianelli #3
155 commits / 42,722 ++ / 69,613 --

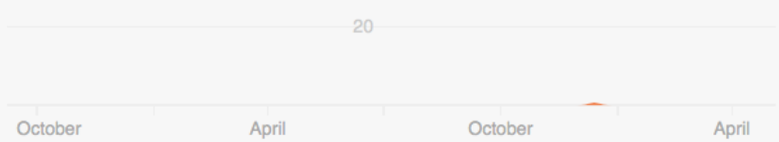
quantifish #4
17 commits / 17,874 ++ / 17,416 --



kellijohnson #5
5 commits / 40 ++ / 1 --



huihualee #6
1 commit / 2 ++ / 0 --



Documentation

- Important but work in progress…
- Recent improvements (inspired by pending CIE…)
  - Reorganized documents (reduced redundancies)
  - Updated wiki pages (**user manual**)
  - Self-documenting the code (Doxygen-API)
- Manuscript in development
  - Generalizable framework

file:///Users/stevenmartell1/Documents/CURRENT%20PROJECTS/GMACS/docs/api/html/an

Fishing mortality for old and new s... | LaTeX/Tables - Wikibooks, open b... | Issues · seacode/gmacs | Producing White Space in LaTeX | Failed to open page | GMACS: Class List

GMACS 0.1

Length structured assessment model for crustaceans

Main Page | Related Pages | Modules | Namespaces | Classes | Files | Search

Class List | Class Index | Class Hierarchy | Class Members

- GMACS
  - Modules
  - Namespaces
  - Classes
    - Class List
    - Class Index
    - Class Hierarchy
    - Class Members
  - Files

Class List

Here are the classes, structs, unions and interfaces with brief descriptions:

[detail level 1 2]

N acl	
C negativeLogLikelihood	
C multinomial	Class for multinomial negative loglikelihood
C robust_multi	
N cstar	
C Selex	An abstract class for Selectivity functions
C logisticTrait	
C logisticTrait< double >	
C logisticTrait< named_dvariable >	
C LogisticCurve	Logistic curve
C LogisticCurve95	Logistic curve parameterised with 5% and 95% selectivity
C SelectivityCoefficients	Selectivity coefficients
C ParameterPerClass	Parametric selectivity function
C spr	
C test_comm	

Generated on Tue Jan 20 2015 07:29:12 for GMACS by doxygen 1.8.4

Self documenting code

```
/**
 * @ingroup GMACS
 * @brief Calculate equilibrium vector n given A, S and r
 * @authors Steve Martell and Dave Fournier
 * @details Solving a matrix equation for the equilibrium number
 * of crabs in length interval.
 * @param[out] n vector of numbers at length
 * @param[in] A size transition matrix
 * @param[in] S diagonal matrix of length specific survival rates
 * @param[in] r vector of new recruits at length.
 */
void calc_equilibrium(dvar_vector& n,
                      const dvar_matrix& A,
                      const dvar_matrix& S,
                      const dvar_vector r)
{
      int nclass = n.indexmax();
      dmatrix Id = identity_matrix(1,nclass);
      dvar_matrix At(1,nclass,1,nclass);

      At = trans(A*S);
      n  = -solve(At-Id,r);

}
```

GMACS 0.1

Length structured assessment model for crustaceans


```
void calc_equilibrium ( dvar_vector &        n,
                        const dvar_matrix &  A,
                        const dvar_matrix &  S,
                        const dvar_vector    r
                      )
```

Calculate equilibrium vector n given A, S and r.

Authors

Steve Martell and Dave Fournier

Solving a matrix equation for the equilibrium number of crabs in length interval.

Parameters

[out] **n** vector of numbers at length

[in] **A** size transition matrix

[in] **S** diagonal matrix of length specific survival rates

[in] **r** vector of new recruits at length.

Definition at line 33 of file equilibrium.cpp.

```
void calc_equilibrium ( dvar_vector &        n,
                        dvar_vector &        o,
                        const dvar_matrix &  A,
                        const dvar_matrix &  S,
                        const dvar_matrix &  P,
                        const dvar_vector &  r
                      )
```

Manuscript in development

A generalized size-structured assessment model for Crustaceans

Athol Whitten, Andre Punt, Dave Fournier, James Ianelli,
John Levitt, and Steve Martell

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Abstract

Gmacs is a statistical size-structured stock assessment modelling framework for molting crustacean species. The framework makes use of a wide variety of data, including both fishery- and survey-based size-composition data, and fishery-dependent and -independent indices of abundance. Gmacs has initially been designed for application to the king crab stocks of Alaska. Models of these stocks serve as a testing ground for the first versions of the modeling framework. Gmacs is coded using AD Model Builder, so inherits its capability to efficiently estimate hundreds of parameters. In this paper we describe details of the underlying population dynamics and statistical framework. The description is based upon modelling for crustaceans that undergo molting and with each subsequent molt increase in size.

Introduction

Statistical catch age models have several advantages over simple production type models in that age and size composition data can be used to better inform structural features such as recruitment variability, and total mortality rates. There are a number of generic age-structured models in use today, but there are very few generic size-based, or staged-based models that are used in stock assessment. In this paper we describe a generalized statistical catch-at-size model that is well suited for animals that cannot be aged, and where only precise length measurements are available. The description is based on a crustaceans that undergo molting and with each subsequent molt increase in length.

Methods

The analytical details of the generalized model is summarized using tables of equations (e.g., Table 2). These tables serve two purposes: (1) to clearly provide the logical order in which calculations proceed, and (2) organization of a relatively large integrated model into a series

M1 vs M2

```
## GROWTH PARAM CONTROLS
## nGrwth
##
+-- 44 lines: ## Two lines for each parameter if split sex, o
##  TYPE: 0 = UNINFORMATIVE, 1 - NORMAL (log-space), 2 = time
##  LAMBDA: Arbitrary relative weights for each series, 0 = d
## ----------------------------------------------------------
## SURVEYS/INDICES ONLY
## NMFS  BSFRF
## TYPE     Mean_q    SD_q      LAMBDA
     0      0.896     0.13      0
     0      0.001     0.01      0
## ----------------------------------------------------------
## ----------------------------------------------------------
## PENALTIES FOR AVERAGE FISHING MORTALITY RATE FOR EACH GEAR
## ----------------------------------------------------------
## Trap  Trawl NMFS  BSFRF
## Mean_F  STD_PHZ1  STD_PHZ2     PHZ
+-- 24 lines: 0.30      0.07      0.50     1----------------
## ----------------------------------------------------------
## TYPE:
##      0 = constant natural mortality
##      1 = Random walk (deviates constrained by variance in
##      2 = Cubic Spline (deviates constrained by nodes & nod
##      3 = Blocked changes (deviates constrained by variance
  0
## Phase of estimation
 -3
## STDEV in m_dev for Random walk
  0.20
## Number of nodes for cubic spline or number of step-changes
  4
## Year position of the knots (vector must be equal to the nu
  1976 1980 1985 1994
```

```
## GROWTH PARAM CONTROLS
## nGrwth
##
+-- 44 lines: ## Two lines for each parameter
##  TYPE: 0 = UNINFORMATIVE, 1 - NORMAL (log-
##  LAMBDA: Arbitrary relative weights for ea
## ----------------------------------------------
## SURVEYS/INDICES ONLY
## NMFS  BSFRF
## TYPE     Mean_q    SD_q      LAMBDA
     0      0.896     0.13      1
     0      0.001     0.01      1
## ----------------------------------------------
## ----------------------------------------------
## PENALTIES FOR AVERAGE FISHING MORTALITY RA
## ----------------------------------------------
## Trap  Trawl NMFS  BSFRF
## Mean_F  STD_PHZ1  STD_PHZ2     PHZ
+-- 24 lines: 0.30      0.07      0.50     1-
## ----------------------------------------------
## TYPE:
##      0 = constant natural mortality
##      1 = Random walk (deviates constrained
##      2 = Cubic Spline (deviates constraine
##      3 = Blocked changes (deviates constra
  3
## Phase of estimation
  3
## STDEV in m_dev for Random walk
  0.20
## Number of nodes for cubic spline or number
  4
## Year position of the knots (vector must be
  1976 1980 1985 1994
```

M3 vs M4

```
+-- 11 lines: # Set up to do Stock Reduction Analysis using C
9
ival        lb        ub        phz   prior     p1      p2
0.18      0.01         1          4       2   0.18    0.02
-1.2       -10        20          2       1   -1.2     0.1
 5.0       -10        20         -2       1    3.0     5.0
 5.0       -10        20          1       1   -1.2     0.2
72.5        55       100         -4       1   72.5    7.25
0.55       0.1         5         -3       0    0.1       5
0.6931     -10      0.75         -4       0    -10    0.75
0.75      0.20      1.00          2       3    3.0    2.00
0.001     0.00      1.00         -3       3   1.01    1.01

+-- 89 lines: ##
      0 = constant natural mortality
      1 = Random walk (deviates constrained by variance in M)
      2 = Cubic Spline (deviates constrained by nodes & node-
      3 = Blocked changes (deviates constrained by variance A
3
 Phase of estimation
4
 STDEV in m_dev for Random walk
0.20
 Number of nodes for cubic spline or number of step-changes f
4
 Year position of the knots (vector must be equal to the numb
 1976 1980 1985 1994
+--  2 lines: ----------------------------------------------

 OTHER CONTROLS

3       # Estimated rec_dev phase
0       # VERBOSE FLAG (0 = off, 1 = on, 2 = objective func)
1       # INITIALIZE MODEL AT UNFISHED RECRUITS (0=FALSE, 1=T
1984    # First year for average recruitment for Bspr calcula
2014    # Last year for average recruitment for Bspr calculat
```

```
+ +-- 11 lines: # Set up to do Stock Reduction Analysis using Catch data and
9
ival        lb        ub        phz   prior     p1      p2          # param
0.18      0.01         1          4       2   0.18    0.02          # M
-1.2       -10        20          2       1   -1.2     0.1          # logR0
 5.0       -10        20          2       1    3.0     5.0          # logR1
 5.0       -10        20          1       1    3.0     5.0          # logRb
72.5        55       100         -4       1   72.5    7.25          # Recru
0.55       0.1         5         -3       0    0.1       5          # Recru
0.6931     -10      0.75         -4       0    -10    0.75          # ln(si
0.75      0.20      1.00          2       3    3.0    2.00          # steep
0.001     0.00      1.00         -3       3   1.01    1.01          # recru

+ +-- 89 lines: ##
      0 = constant natural mortality
      1 = Random walk (deviates constrained by variance in M)
      2 = Cubic Spline (deviates constrained by nodes & node-placement)
      3 = Blocked changes (deviates constrained by variance AT specific kn
3
 Phase of estimation
4
 STDEV in m_dev for Random walk
0.20
 Number of nodes for cubic spline or number of step-changes for option 3
4
 Year position of the knots (vector must be equal to the number of nodes)
 1976 1980 1985 1994
+ +--  2 lines: ----------------------------------------------------------

 OTHER CONTROLS

3       # Estimated rec_dev phase
0       # VERBOSE FLAG (0 = off, 1 = on, 2 = objective func)
0       # INITIALIZE MODEL AT UNFISHED RECRUITS (0=FALSE, 1=TRUE)
1984    # First year for average recruitment for Bspr calculation.
2014    # Last year for average recruitment for Bspr calculation
```

GMACS: A Generalized Size-Structured Model and Stock Reduction Analysis

Steve Martell, James Ianelli, and Dave Fournier

International Pacific Halibut Commission, Alaska Fisheries Science Center, and Otter Research

General Size-structured Equilibrium Model

Given a vector $\boldsymbol{n} = (n_1, n_2, \ldots, n_m)$ that represents the number of individuals in discrete size bins in a given year. Each year the numbers in each size bin are subject to growth and survival $\boldsymbol{A}$ and the addition of recruits $\boldsymbol{r}$. Assuming growth and survival is a linear function of the number of individuals in each size bin, then the following matrix equation represents the steady-state or equilibrium conditions:

$$\boldsymbol{n} = \boldsymbol{A}\boldsymbol{n} + \boldsymbol{r}$$

with the equilibrium solution for the numbers-at-size given by

$$\boldsymbol{n} = -(\boldsymbol{A} - \boldsymbol{I})^{-1}(\boldsymbol{r})$$

where $\boldsymbol{I}$ is the m x m identity matrix. In practical terms, the challenge is in developing the matrix $\boldsymbol{A}$ and the vector of new recruitment $\boldsymbol{r}$.

GMACS is based on this simple matrix equation equation for modeling the dynamics of molting probabilities, size-transition or growth, and also jointly models various life-history stages, such as, new- and old-shell crab.

Model Features

Table 1: Data inputs and dimensions implemented in GMACS, required elements in **bold**

Data Type	Dimensions	Symbol	Implemented
Catch	year, fleet, sex	C_t	✓
Discards	year, fleet, sex	D_t	✓
Effort	year, fleet	E_t	✗
CPUE	year, fleet, sex, shell	I_t	✓
Composition	year, fleet, sex, shell, type	$Q_{l,h,o}$	✓
Composition	maturity status		✗
Molt Increment	sex	g_l	✓
Tagging data	sex		✗

Generalized Model Notation (equilibrium conditions)

model parameters

$$\Theta = (M, \alpha_r, \beta_r, R_0, \kappa) \quad (1)$$

$$M > 0, \alpha_r > 0, \beta_r > 0, R_0 > 0, \kappa > 1.0, \quad \text{constraints} \quad (2)$$

$$\Phi = (\alpha, \beta, \varphi), \quad \text{Size-transition parameters} \quad (3)$$

size-transition matrix $\boldsymbol{G}$

$\vec{l}, \vec{x}$ vector of size intervals and midpoints, respectively

$$a_l = (\alpha + \beta l)/\varphi \quad (4)$$

$$p(l, l') = \boldsymbol{G} = \int_l^{l+\Delta l} \frac{l^{(a_l - 1)} \exp(l/\varphi)}{\Gamma(a_l) l^{(a_l)}} dl \quad (5)$$

recruitment size-distribution

$$\alpha = \alpha_r/\beta_r \quad (6)$$

$$p[\boldsymbol{r}] = \int_{x_l - 0.5\Delta x}^{x_l + 0.5\Delta x} \frac{x^{(\alpha-1)} \exp(-x/\beta_r)}{\Gamma(\alpha)\beta_r^{\alpha}} dx \quad (7)$$

$$\boldsymbol{r} = 0.5 p[\boldsymbol{r}] \bar{R} \quad (8)$$

growth and survival

$$\boldsymbol{A} = \boldsymbol{G}[\exp(-M)(\boldsymbol{I}_n)_{l,l'}] \quad \text{unfished} \quad (9)$$

$$\boldsymbol{B} = \boldsymbol{G}[\exp(-M - \boldsymbol{f}_l)(\boldsymbol{I}_n)_{l,l'}] \quad \text{fished} \quad (10)$$

survivorship to size-interval

$$\boldsymbol{u} = -(\boldsymbol{A} - (\boldsymbol{I}_n)_{l,l'})^{-1}(p[\boldsymbol{r}]) \quad \text{unfished} \quad (11)$$

$$\boldsymbol{v} = -(\boldsymbol{B} - (\boldsymbol{I}_n)_{l,l'})^{-1}(p[\boldsymbol{r}]) \quad \text{fished} \quad (12)$$

steady-state conditions

$$B_0 = R_0 \phi_B, \quad \text{where} \quad \phi_B = \sum_l \boldsymbol{u}_l w_l m_l \quad (13)$$

$$\tilde{B} = \tilde{R}\tilde{\phi}_B \quad \text{where} \quad \tilde{\phi}_B = \sum_l \boldsymbol{v}_l w_l m_l \quad (14)$$

stock-recruitment parameters

$$s_o = \kappa R_0 / B_0 \quad (15)$$

$$\beta = (\kappa - 1)/B_0 \quad (16)$$

$$\tilde{R} = \frac{s_o \tilde{\phi}_B - 1}{\beta \tilde{\phi}_B} \quad (17)$$

Abstract

Stock reduction analysis (SRA) is a data-poor technique that typically just uses historical catch information to estimate recruitment rates needed to explain those historical catches. The method is easily extended to accommodate sparse information on trends in abundance, composition information, and tagging data. Estimation of model parameters using maximum likelihood or Bayesian methods is possible. GMACS is a generalized framework for size-structured models suitable for data-poor to data-rich assessments. Reference points are derived from steady-state conditions by solving matrix equations that represent size-dependent mortality and growth. Our results show how the scalability of GMACS can be used as an integrated data-poor assessment method. Next steps include the evaluation of such "simple" methods testing simulated data generated from within GMACS (or from a separate R package) but configured to have greater complexity of underlying dynamics (e.g., time-varying natural mortality)

Size-based selectivity, retention, and fishing mortality

Parameters

$$\ln(f), a, \sigma_s, \lambda, \sigma_y, \xi \qquad \xi = \text{Discard mortality} \quad (18)$$

Selectivity & retention

$$s_l = (1 + \exp(-(l - a)/\sigma_s))^{-1} \qquad \text{Capture probability} \quad (19)$$

$$y_l = (1 + \exp(-(\lambda - l)/\sigma_y))^{-1} \qquad \text{Retention probability} \quad (20)$$

$$\nu_l = s_l[y_l + (1 - y_l)\xi] \qquad \text{Joint probability of dying from fishing} \quad (21)$$

Fishing mortality

$$F = \exp(\ln(f)) \qquad \text{Instantaneous fishing mortality} \quad (22)$$

$$\boldsymbol{f}_l = F\nu_l \qquad \text{Size-based fishing mortality} \quad (23)$$

Reference Points (SPR-based)

The Spawning Potential Ratio (SPR) is the ratio of spawning stock biomass in fished:unfished conditions. Or,

$$SPR = \frac{\tilde{\phi}_B}{\phi_B}$$

Fishing mortality that achieves SPR values in the range of 0.3-0.4 are often considered a proxy for rates associated with Maximum Sustainable Yield. GMACS uses an interative solution based on solving equations (13) and (14) to find the fishing mortality rate (F_{SPR}) that corresponds to a specified SPR value.

Methods

Model descriptions

- Data from the Bristol Bay red king crab fishery (BBRKC).
- Four Alternative Models (Table 2).

Table 2: Alternative model configurations where ✓ option is turned on, and ✗ is off and the number of estimated parameters.

Model	Fit to Data C_t	I_t	$\boldsymbol{Q}$	Initial States	No. Parameters
M1	✓	✗	✗	✗	184
M2	✓	✓	✗	✗	188
M3	✓	✓	✓	✗	189
M4	✓	✓	✓	✓	190

Results

- The joint probability model (21) attempts to simultaneously estimate retained and discarded catch (Fig. 1).
- Catch only method requires prior information on one of the following:
  - Average fishing mortality rates, or
  - an estimate of current depletion level, or
  - an estimate of absolute fishing mortality for one or more gears.
- Estimates of $F_{SPR=35\%}$ are consistent across models because same natural mortality and selectivity are assumed (Table 3).

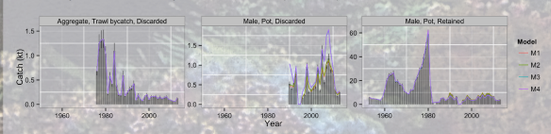

Figure 1: Observed and predicted catch.

Table 3: SPR-based reference points from each model

Model	$F_{SPR=35\%}$	$B_{SPR=35\%}$	F_{OFL}	OFL	$R_{SPR=35\%}$
M1	0.26	22.17	0.07	0.31	5.95
M2	0.25	33.46	0.25	3.33	7.36
M3	0.25	25.04	0.24	1.80	5.52
M4	0.28	28.06	0.28	2.63	7.15

Results cont.

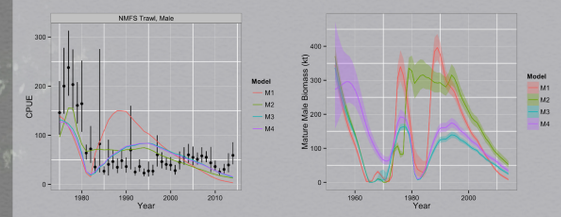

Figure 2: Fits to relative abundance data (left) and estimates of mature male biomass. Shaded regions approximate 95% confidence intervals.

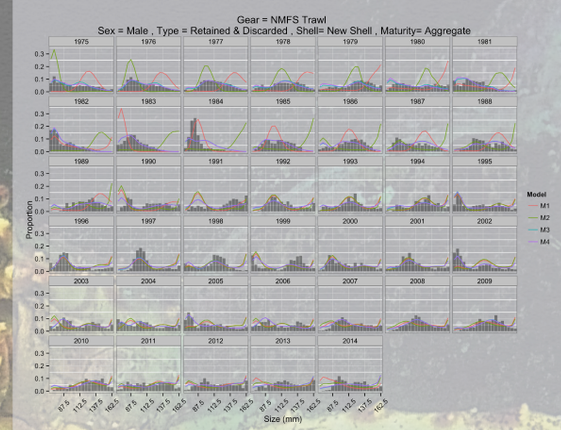

Figure 3: Observed and predicted size composition of newshell crabs in NMFS trawl survey.

Discussion

- Size- or stage-structured models contain additional confounding between estimates of recruitment, size-transition, and size-based mortality in contrast to age-structured models.
- It is possible to conduct Stock Reduction Analysis (using only catch data) and additional assumptions about natural mortality, growth, and the size-distribution of new recruits.
- The generalized size-structured equilibrium model also extends to additional classes such as sex, new and old-shell, immature and mature animals.

Acknowledgements

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No crabs were eaten during the production of this poster.

Working Examples

Working examples

- examples/bbrkc/OneSex
- examples/bbrkc/TwoSex
- examples/pirkc/
- examples/nsrkc/