Report of Crab Modeling Workshop

North Pacific Fishery Management Council
January 13-15, 2015
Alaska Fisheries Science Center

Introduction/background

This 3-day meeting was planned to provide a forum for development of the Gmacs modeling framework In particular, the goal was to evaluate an application to the Bristol Bay red king crab (BBRKC) stock, make comparisons with the established assessment model, and develop an understanding of the differences between the two approaches. **Gmacs** is a generalized modeling framework for developing size-structured stock assessment models. Gmacs is an open source program developed using AD Model Builder (ADMB). ADMB is free, open source, and available for Windows, Linux, MacOS, and Sun/SPARC. Gmacs source files will build on any computer that can run ADMB.

The draft agenda below covers the intended discussion topics for the workshop. Presentations in plenary were combined with individual and/or team assignments to best focus on specific issues/topics. Longer-term plans for Gmacs include application to additional BSAI stocks (e.g., NSRKC, PIRKC, Tanner crab) to advance model development and expand the feature set. Thus, an additional workshop objective was to plan for this broader application.

Gmacs resources:
- the main Gmacs wiki: https://github.com/seacode/gmacs/wiki
- For tracking issues and developments see https://github.com/seacode/gmacs/issues (note that specific issues and discussion will be linked as applicable in this report)

Participants

Participants were provided access to model development software and documentation. Jim Ianelli and Steve Martell facilitated the workshop. The following people participated in all or part of the meeting: Jack Turnock, Buck Stockhausen, Shareef Siddeek, Jie Zheng, Anne Hollowed, Scott Goodman, Cole Monnahan, Gary Stauffer, Carey McGilliard, Teresa A'Mar, Bill Bechtol, Toshide Hamazaki, Paul Starr, Martin Dorn, Bob Foy, Bill Gaemann, Wes Jones, Ruth Christiansen, John Hilsiger, Ed Poulson, Kelly Johnson, Kaitlynn Allen, Farron Wallace, and Diana Stram.

Topics and Discussion

A major focus of the 3-day workshop was collaborative model code editing and model runs to address issues raised during the meeting.. Participants identified issues related to treatment of model data, growth transition matrices, shell condition, mortality, maturity, selectivity. Github (https://github.com/seacode/gmacs/issues) was used to track issues raised during the workshop, as well as progress in their resolution. Additional issues and resolutions (Todo list) are identified on the github site, and not repeated entirely in this report.

Participants also suggested simulation testing as way to evaluate the performance of Gmacs applications.

Specific discussions of side-by-side comparisons for BBRKC are summarized below. Routines for creating these plots and comparisons were developed and output from the current BBRKC model was brought to the repository for evaluation.

Side by side list for comparing current RKC model w/ a Gmacs implementation

The following components for comparisons were listed:
1. Initial recruitment size distribution
2. Mean weight-at-length
3. Numbers at length in 1975
4. Natural mortality
5. Recruitment
6. Fit to survey abundance indices
7. Molting probability
8. Transition matrices
9. Estimated retained catch and discards compared to observed

As a demo, a KnitR markdown file was created with each R-code snippet embedded and now part of the repository (https://github.com/seacode/gmacs/tree/develop/examples/bbrkc/doc). A draft pdf of this document is available here.

Sex specific aspects for BBRKC assessment

The workshop participants discussed sex-specific differences in the biology and population dynamics for BBRKC. The current BBRKC model splits the survey data into sex-specific indices and Gmacs can accommodate this treatment. . However, Figure 1 shows that the biomass trends by sex are pretty similar when the trends are put on the same scale.

During the workshop a male-only dataset for BBRKC was constructed in order to test a simpler formulation of the model. This was also considered a good test since the current BBRKC model estimates selectivity, recruitment, and natural mortality independently by sex.

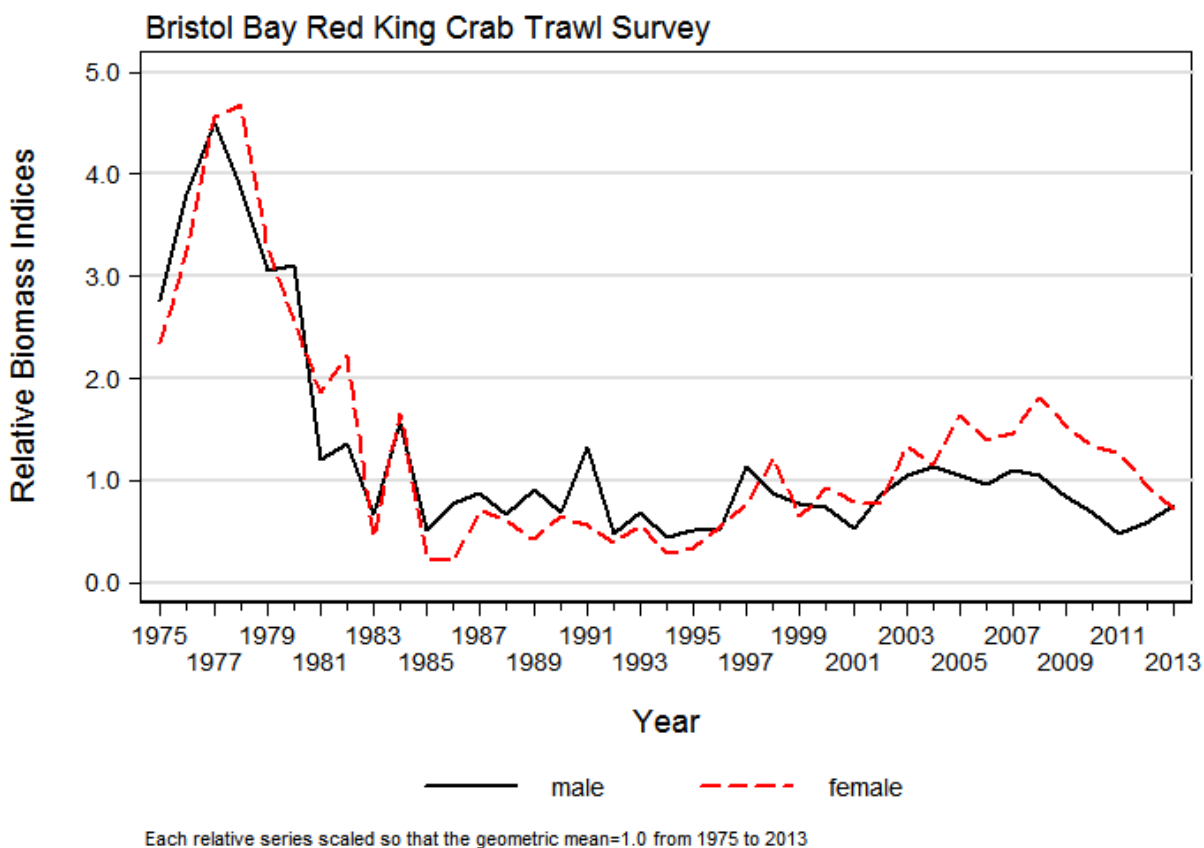Each relative series scaled so that the geometric mean=1.0 from 1975 to 2013

Figure 1:   Plot of the relative biomass indices for Bristol Bay Red King Crab by sex. Each series has been normalized to a geometric mean to put each series on the same relative scale.

On the last afternoon of the workshop, the group focussed on how Gmacs parameter settings affected the growth matrices. The ADF&G biologists identified issues with the model coding and also scale parameters for the growth transition matrices. Once corrected, these provided growth transitions closer to expected (and similar to the current BBRKC model). An example size transition matrix (and component growth transition) from this exercise is shown below (Figure 2).

Figure 2. Example growth transition matrix (top) and size-transition (accounting for molting probabilities; bottom) as specified for male BBRKC in the Gmacs model. The colored cells signify...

Comparative features of Gmacs and BSAI stock assessment models

Workshop participants compiled a table comparing and contrasting features of different assessment models and Gmacs formulation. The draft table is attached ***Need link here***). This table will continue to be available on google docs for live updating.

Recommendations for moving forward

Gmacs specific issues

Note that the repository has an active list of issues [here](#).
Progress has been made to add shell-condition and sex-specific aspects to the model.
Continue to refine the table for all stock assessment models in conjunction with Gmacs formulation and what is being done for other crab stocks.
Continue to refine model documentation.
Include an option to estimate sex ratios and shell condition separately from composition data.
Simulate a simple dataset in R to be fit by Gmacs.
Flexibility to estimate growth increments as a function of pre-molt width

Bristol Bay red king crab

Complete the specifications comparing model results.
Compare model runs w/indices split by sex vs.combined.
Plot observed mean length by year relative to predicted.
Clarify what handling mortality is applied and when (before data entry or as values are applied).

Norton Sound RKC

Reformatting data files from Hamachan.

Tanner crab

Formatting datafiles that could be used in Gmacs.
Identify Gmacs parameterizations needed for specific cases (e.g., Tanner crab terminal molt).
Change selectivity input files

Pribilof Island red king crab

Cody has begun creating datafiles and plans to attend the May CPT, perhaps the June CIE.
Funding from AFSC ends Aug 2015.

Timeline and Planning

Move the CIE to late June.
Milestones for model developments and applications are tracked [here](#).

The modeling group will continue bi-weekly teleconferences to track updates

February SSC meeting

NSRKC model and assessment report.

Report from this workshop, SSC feedback on timeline and plans

May Crab Plan Team:

Updated BBRKC model application in Gmacs. CPT discussion of potential implementation for fall assessment.

Start preliminary runs with NSRKC and PIRKC to help debug BBRKC issues with Gmacs; priority will be to assist ADF&G in developing Gmacs for BBRKC.

Buck will develop an R simulation model to help evaluate and test Gmacs for BBRKC with results available by mid February. Progress will be tracked by bi-weekly conference calls.

Draft Gmacs documentation is available for CPT review and comment (here provide link***). A list of required revisions and documentation is solicited to prepare a late June for CIE review.

June

SSC review of CIE TOR, update of Gmacs etc.
CIE review

September CPT

Review CIE report.
BBRKC Gmacs assessment model; BBRKC assessment

January model workshop (2016)

Review Tanner crab application in Gmacs

Things to track for conference calls and progress update

BBRKC side-by-sides and debugging progress

Simulation model from Buck
NSRKC datafile

Appendix Report on conference calls for gmacs progress

Time: 12:30pm AST (1:30pm PST)

Teleconference number: 1-877-953-5415

Participant Passcode: 1709502

DATE???

Prior to workshop tasks:

1. Merge Steve's shell condition branch to develop
    a. Test on examples/bbrkc files
2. Growth increment read-in by sex
    a. Resolved to do this as "data" so that Jie's approach can be mimicked and that for alternative models, this will add flexibility
    b. Code changes needed include:
        i. read in number of "growth" observations, then subsequent pre-molt size, and corresponding increment widths
        ii. code for specifying parametric form for predictions (linear, spline, non-parametric as options; linear already exists)
        iii. code for computing predictions (given CW) and then likelihoods to these "data"
3. Comparisons of side-by-side
    a. Recruitment, SSB
    b. Summary likelihood tables
    c. Selectivities/retention curves
    d. Natural mortality estimates by period
    e. SPR values
4. Other checks
    a. Growth increment
    b. Weight-at-length by sex
    c. Check conversion of numbers of crab caught to metric tons (i.e., Table 1 in the SAFE report

Other tasks/notes

- Jie to forward CIE information (and all to review)

- Molting probability for males changing over time, two periods 75-79, 80 to present, evaluate the extent this is critical
- Legal discard rate changed in IFQ fishery; 2005 (higher than 20%).stands out higher than the usual 1-3%

Jan 5th call

Participants: Bob, Jim, Buck, Jack, Siddeek, Anne, Cody, Diana, Hamachan, Steve, Jie

Agenda

1. Old-shell new shell model specification
2. Molt increment vs. pre-molt size
3. Gmr modifications for overlaying alternative models
4. Compare model fits between Jie's and Gmacs
5. Include molting probabilities for better growth representations
6. Adopt the normal approximation to the multinomial
7. Review workshop agenda

Update on activities

Old-shell new

Steve Martell developed analytical methods for solving the initial abundance of old and new shell crabs. This equilibrium solution is also necessary for SPR-based reference points. The code has been partially implemented in the shellcond branch on the Git repository. There is still some work required to implement the changes to the observation model for size composition data. This is a significant achievement; the model can now be initialized with both new shell and old shell numbers at length. Whereas previous models initialized the numbers-at-length based on newshell only.

Given the additional generalization of the model, there are now a number of new questions regarding what type of data are available for other crab fisheries. For example the relative abundance data in surveys and commercial samples, are these CPUE for new shell, old shell, or both? The composition data can be specific to shell/maturity condition, but I'm not clear if the CPUE data are specific to shell condition.

> *Response: survey indices are all types of crab combined.*

The model dimensions dictates the model structure. For example, sex and the number of shell conditions is variable across all the crab assessments. Eg.. St Matt's Blue king crab, single sex and single shell condition, snow crabs two sexes, 2+ shell conditions, and mature and immature. I think we now have a flexible platform to accommodate all of theses different model dimension problems.

Question on landings of old-shell vs new shell.

> *For RKC, old-shell retained but that may differ for other species. Retention curve could be used to account for patterns in landings. Same selectivity for new and old shell crab may be problematic by targeting issues. I.e., moving off of higher proportions of old shell crab.*

> *If landings by new and old shell, then aging error-like matrix might be needed to transform between observations and model predictions.*

Jie asked about molting probability on diagonal,

> *Code can molt and stay within the same size interval based on update and application of the a two part approach, the element-wise multiple reflects molting and growth…?*

Catch equation question, changing to a pulse-or not, and if as specified in Maunder's specification.

> *For the time being and for the workshop, the continuous form will be retained.*

Issue on the effect of timing for SSB in reference point calculations,

> *A number of alternative approaches for doing this to time of spawning etc (using Baranovs equation)*

Molt increment / size

Jim examined Jie's model and compared increment width given pre-molt size to compare with output/estimates from gmacs. The figure below shows the current comparison and raises the question on the extent that gmacs is presently estimating sex specific growth increments. Other question is the necessity to have time-varying female growth since the differences appear minor and aren't being used in SSB calculations.

Need to have input specifications for molt increment data.

Also need mean-weight by size, add option for empirical weights.
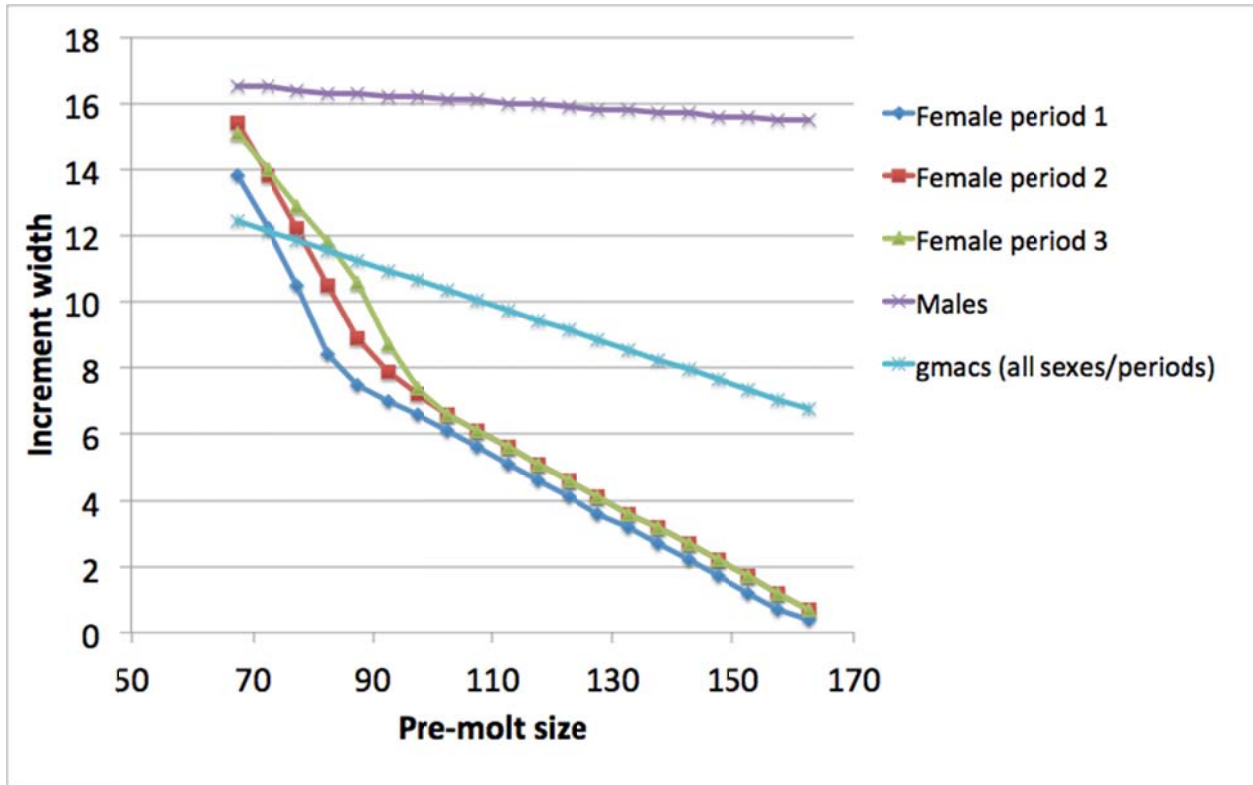
Other notes

Gmr modifications for overlaying alternative models

Some progress was made before the holidays. Namely that the MMB and recruit estimates from Jie's model can be read in and overplotted:
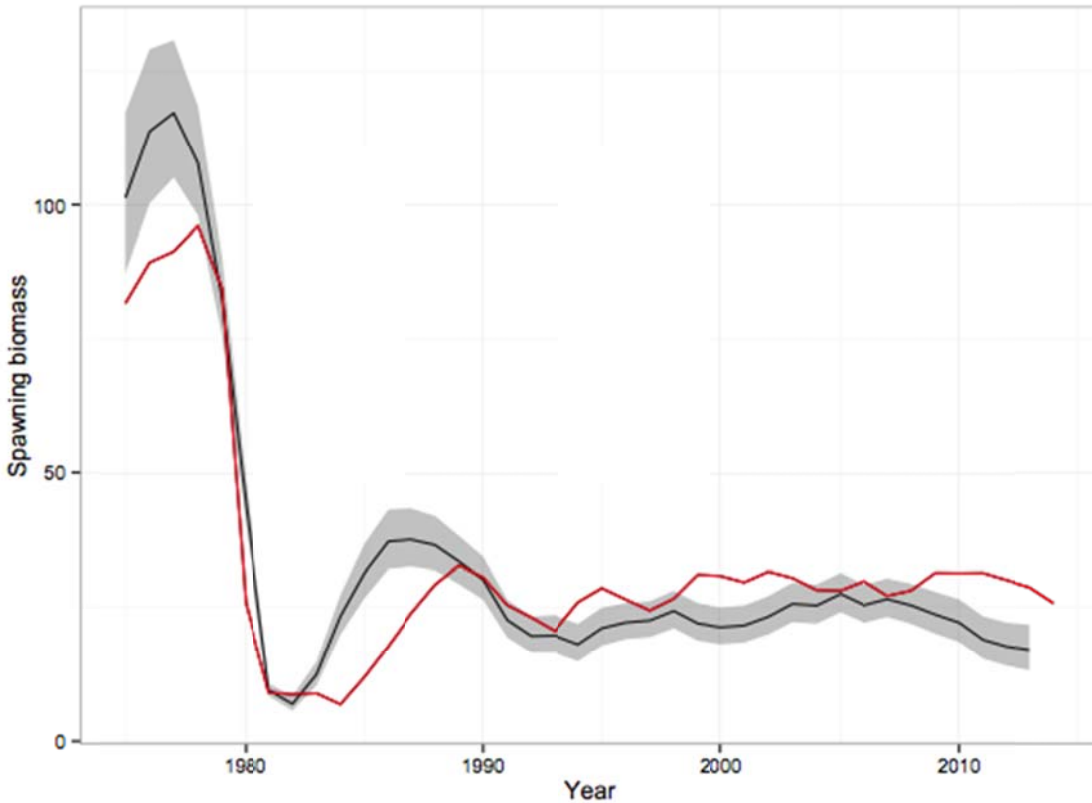
Compare model fits between Jie's and gmacs
Adopt the normal approximation to the multinomial
Include molting probabilities for better growth representations

SSC presentation

The question arose as to the extensiveness of the presentation of this work to the SSC is needed/desired. The group noted that having Jie at the SSC meeting to help present the workshop report would be desirable.

December 22nd call

Attendees: Jim, Bob, Diana, Hamachan, Buck, Jack, Siddeek, Jie, Steve, Huihua
Unavailable: Andre, Cody

Reminder: Wiki for software can be found here

Items

- Discuss details of workshop
    - agenda here

- ○ structure (daily format for work session)
- ○ report writing sections: Diana to coordinate but will need assistance on technical aspects, need to assign folks for sections to assist
- Move the gmr package within gmacs
- Test UI and compiling aspects
- Resolve the question of non-zero diagonals for new-shell crabs
- BBRKC comparisons added to github directory.

Continue with:

- construct template data and control files for new models.(no progress)
- iron out kinks in Makefiles for windows and *nix systems (done).
- Integrate growth increment data and likelihood for estimating growth. (ongoing)
- Assemble of list of observation types for which observation models need to be developed for gmacs (e.g., shell condition, maturity status, tagging).

Notes on activities

BBRKC update

Things to look at for comparisons: recruits, MMB, likelihood components (assuming same sample size), SPR calcs (OFL), survey abundance fit, selectivity functions.

Cody and Hamachan to compare notes on applying gmacs to their data.

Buck, Jack, and Steve provided feedback on new-shell and old shell issues in a number of emails, the outcome of which is??? Steve noted that the original size transition matrix resolved some speed issues. Jack pointed out that given bin-width, an old shell could molt to a new shell and stay in the same size bin. Idea now is to resolve this numerically, maturity is included as a vector.

Old shell and new shell have same molting probability? new shell and old shell have same probability. Only one growth matrix, for crabs that molting.

Question on what data are available to estimate molting probability. Steve noted that there are data on new and old shell, and some combined.

Molt increment data needs to be added to input file. question is it average, increment data from tagging for BBRKC data (outside of the model).

Jim: Fixed the GMR package and windows make file.
NOTE: http://www.admb-project.org/downloads/admb-11.2 contains the latest ADMB Tested the GMR package and updated some of the documentation on how to load package etc.

Huihua: Provided feedback on compiling and wiki page, adapted a routine for displaying data content used in gmacs. A draft using the BBRKC example is shown below.

Data by type and year
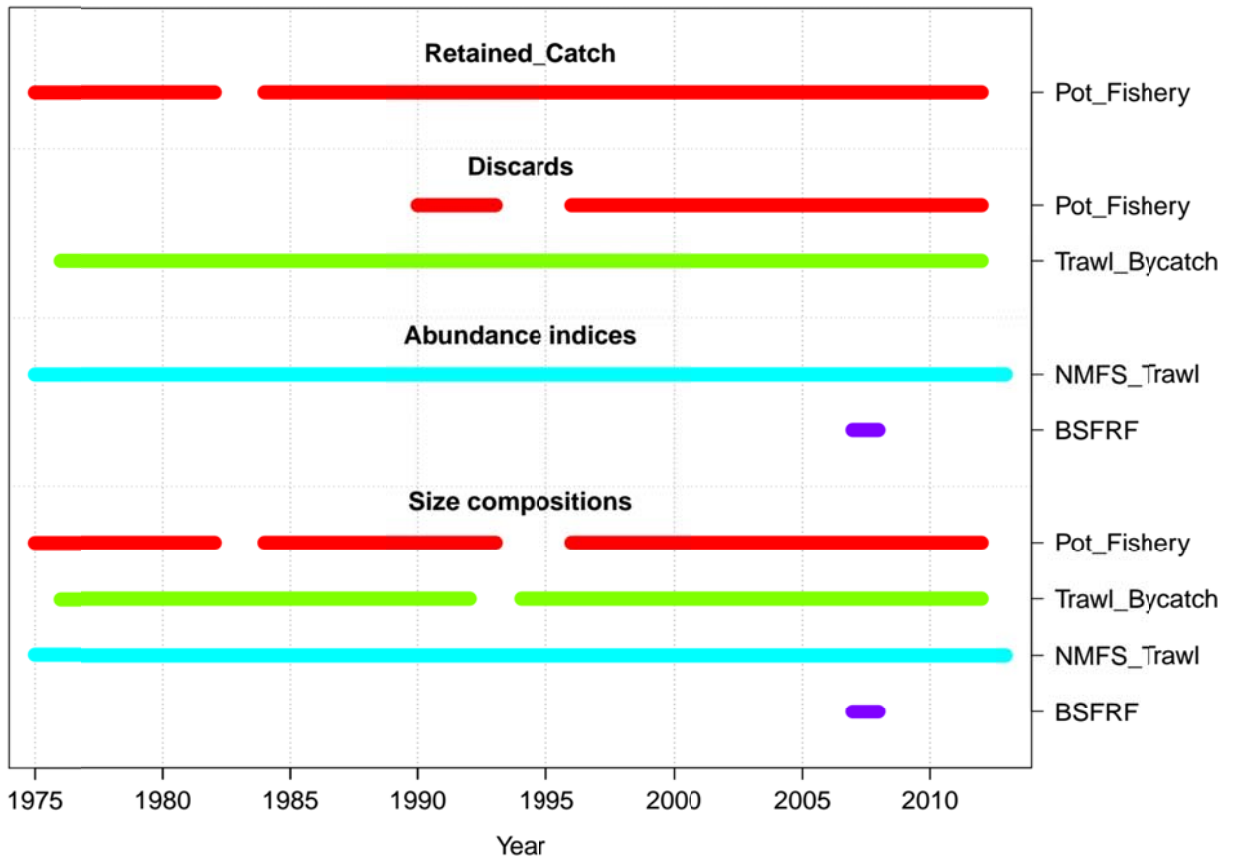
Example growth output added to gmacs
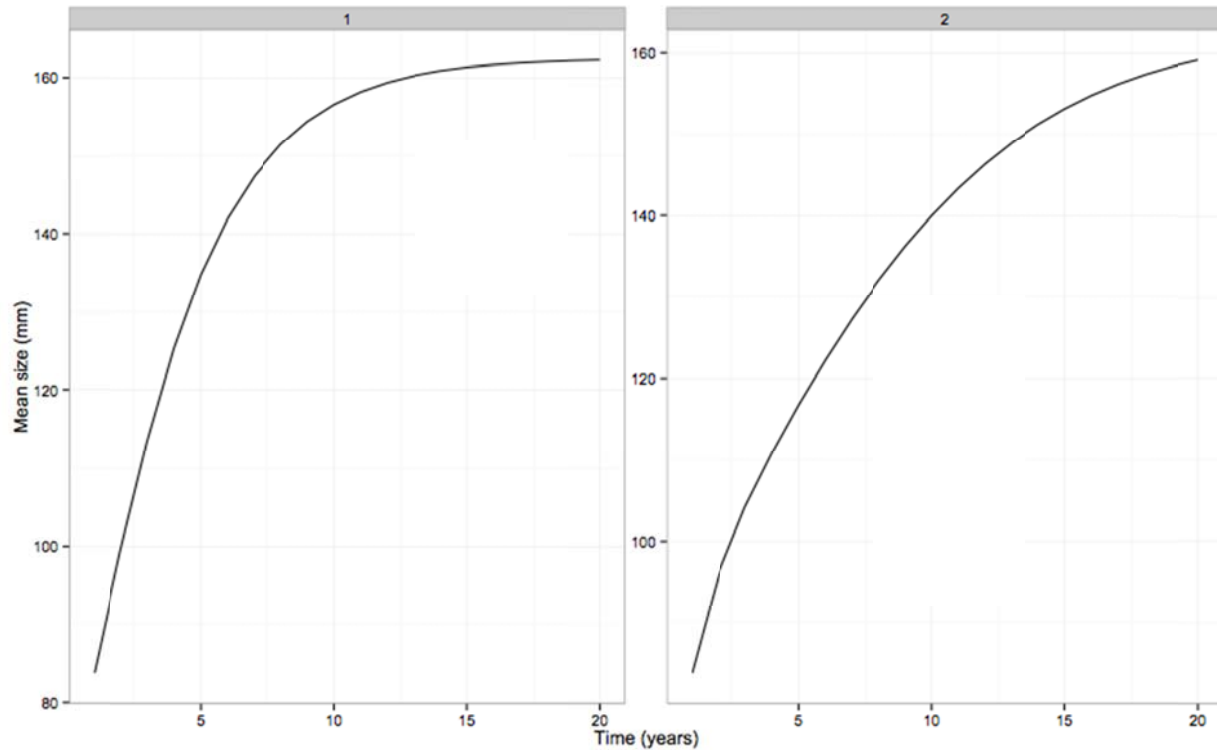
This only uses size-transition matrix ignoring molting probability. Consider plotting variability about these curves.

I think an appropriate figure would be to plot the molt increment vs carapace width. You can also overlay data on this plot. This can be compared between models easily. The data below (e.g.)

Female Snow Crab Growth
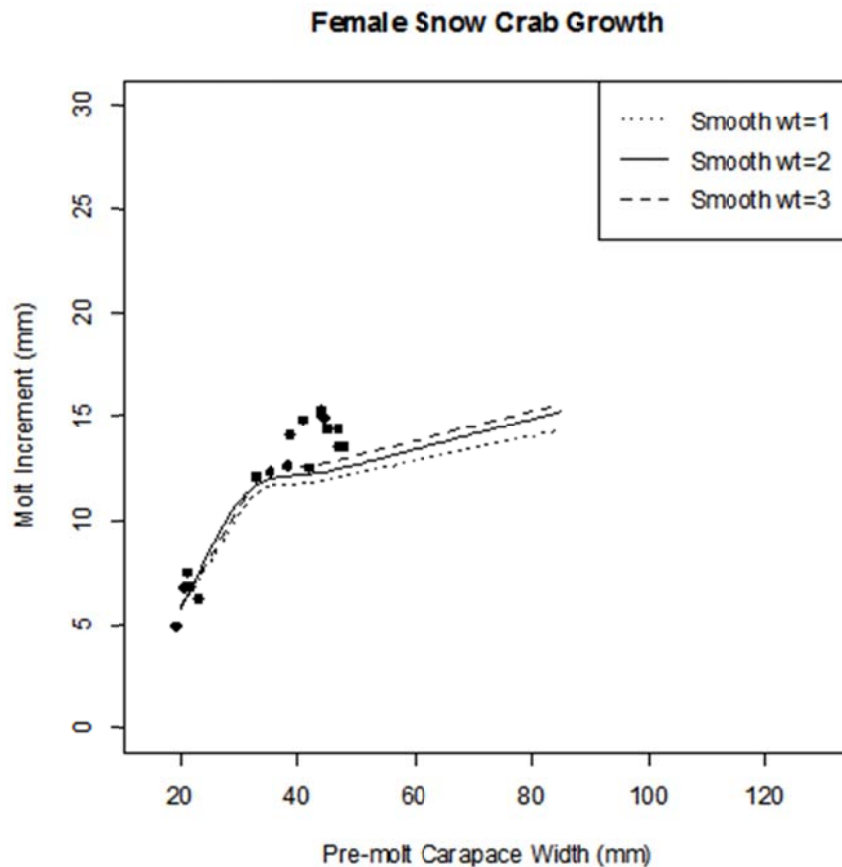
December 15 call

Participants: Jim Ianelli, Steve Martell, Huihua Lee
(note that most crab biologists were travelling to the interagency meeting on crab being held in Kodiak)

BBRKC Data and model update:
Steve worked up the equilibrium example for old and new shell situation (for the solver aspect) and got that working. Subsequently he added the code needed to the main model code.

A couple of issues arose which were similar to the problems I think Siddeek addressed at the CPT meeting. Namely the need to separate molting probability from the growth transition matrix. In this regard, checking Hamachan's code the diagonal in the growth matrix was zero yet in Jie's, the diagonal was non-zero, even though molting probability was also in the model. This

raises the question as to whether new-shell crabs can simply not grow, even if they molted (which I understand the diagonal of the transition matrix to represent).

Jack's response:

> *"If you have a separate growth matrix for new shell crab and old shell crab,,, then If new shell crab don't molt then they should go to old shell crab, not remain new shell. So, new shell crab could stay in the same length bin and molt (then they stay new shell) or they could stay in the same length bin and not molt (then they should become old shell). If the growth matrices are applied only after you separate crab that molt and don't molt, then new shell crab that molt could stay in the same length bin and stay new shell. "*

Jim reported that he began figuring out ways to move gmr into the gmacs repo and will complete that and provide some working examples.

Jim also reported that BSFRF has okayed the contract work so that can proceed.

Huihua reported that she will begin working today. We noted that her task is to document issues and UI problems and provide feedback on usability at this stage.

To do from Dec 8th call:

- construct template data and control files for new models.
- iron out kinks in Makefiles for windows and *nix systems.
- Integrate growth increment data and likelihood for estimating growth.
- Assemble of list of observation types for which observation models need to be developed for gmacs (e.g., shell condition, maturity status, tagging).

December 8 call

Attendees: Jim, Bob, Hamachan, Buck, Jack, Siddeek, Jie, Cody, Steve
Unavailable: Diana, Andre

Action items prior to December 8th call:

1. Upload another example/demo   Cody
   Cody just back, no progress, but Hamachan has begun looking into it.
2. Continue download and test ability to run/compile model (BBRKC example)   All
   Hama had difficulties, will meet this week.
3. Improve instructions for gmr installation and test plotting   Jim/Others
4. Meet in Anchorage week of 7th   Jim/Hamachan
5. Load/compile Norton Sound data   Jie/Hamachan
6. Define objectives for contractor   Jim/Steve

7. Next Meeting Monday December 8 1:30 PST, 12:30 AK

Notes

Cody/Hama to have something other than BBRKC
github question on access. Workflow would be that users would make their own branch
Protocol needed, post some tutorials for group work.
Demo folder has BBRKC as a template
Excel file w/ some formatted data and control file work
Jie, growth goes backward...gamma, size breaks, mid points or difference, source code,
Jim added this as an issue, asked users to "watch" gmacs github site for activity
Outline for 3 days TBD; no additional topics will be discussed at January workshop
Steve has written documentation that is on the repository (and on your computer if cloned)

TODO:

-   construct template data and control files for new models.
-   iron out kinks in Makefiles for windows and *nix systems.
-   Integrate growth increment data and likelihood for estimating growth.
-   Assemble of list of observation types for which observation models need to be developed for gmacs (e.g., shell condition, maturity status, tagging).

December 1st Call (2pm delayed start)

Attendees: Jim, Bob, Hamachan, Buck, Jack, Siddeek, Jie
Unavailable: Diana, Cody, Andre, Steve Martell

News

gmr install instructuctions working poorly
review of input data file set up is needed

Updates on action items:

1. Get Cody to upload his example, perhaps to assist in Hamachan's development
    Hama reports that it's unclear how to input data into the correct format etc.
2. Everyone download and test ability to run/compile model:
    https://github.com/seacode/gmacs
    Not back from China yet
3. For the R code see: https://github.com/seacode/gmr
    Jie reports that error messages causing problems.
4. Jack, Siddeek, and Buck identify unique issues with their models that will need to be addressed for GMACS to run.
    Terminal molt issue
    Shell condition
    Tanner--multiple areas for OFL partitioning, separate selectivity from those regions

5. Compiler issues and admb versions should be updated
   Jie
6. Next meeting to decide for additional topics for Jan meeting (AI GKC model, TC model, Survey time series).
   Will gmacs sufficiently complete the agenda? Will finalize at Dec 8 meeting.
7. Schedule for future meetings: Monday 1:30 PST, 12:30 AKT
8. Contract for external intern in place so work can begin in December.

Action items for December:
1. Get Cody to upload his example, perhaps to assist in Hamachan's development.
2. Everyone download continue and test ability to run/compile model.
3. Jim to provide instructions for gmr installation and test plotting.
4. Hama to try BBRKC demo.
5. Jim and Hamachan to meet in Anchorage week of 7th.
6. Jie to help Hamachan to load/compile Norton Sound.
8. Define objectives for new intern.
9. Next Meeting Monday December 8 1:30 PST, 12:30 AKT

November 24th, 2014
Attendees: No phone meeting

November 19th, 2014 call
Attendees: Jim, Bob, Jie, Diana, Sideek, Hamachan, Buck, Jack
Unavailable: Cody, Andre, Steve Martell

Topics
1. Current overall status/update   Jim
2. Github questions/issues   All
3. BBRKC data and model issues   Jie
   a. Contractor work to help with data and pulling in comparisons with Jie's model
   b. Would be good to have the comparisons done prior to January meeting,
   c. Draft terms of reference for comparisons
4. Update authors with the GMACS process
   a. Cody to apply to his stock (has begun)
   b. Hamachan requests some training, perhaps comparisons with Norton Sound stock
   c. Develop examples on github site for these stocks
5. Prepare for the January workshop. The plan was to have Bristol Bay RKC, Norton Sound RKC, and Pribilof Islands RKC models ready to compare side by side at the January workshop. Tanner crab was going to be done between January and May in collaboration with the new analyst (Darcy).

6. We will have a <u>30 minute meeting next Wednesday at 12pm (Seattle Time; 11am Alaska time)</u> to discuss expectations for the next 2 months and to set regular meeting times. Please reply with your availability for this meeting. Ill send out a conference call in number next week.

Issues

Jie:
- Stability issue in transition matrix, not fitting length data well as identified
- Group of years for natural mortality

Jack:
- Couldn't run RKC model back in Sept, due to mfexp, numerical underflow, could that still be the same

Action items

1. Get Cody to upload his example, perhaps to assist in Hamachan's development
2. Everyone download and test ability to run/compile model:
   https://github.com/seacode/gmacs
3. For the R code see: https://github.com/seacode/gmr
4. Jack, Siddeek, and Buck identify unique issues with their models that will need to be addressed for GMACS to run.
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6. Next meeting to decide for additional topics for Jan meeting (AI GKC model, TC model, Survey time series).
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