***GMACS GOALS***

1. Merge the branch used for terminally molting crab with the branch used for king crab.
2. Produce scripts that automatically compare the output from two versions of GMACS to improve workflow as improvements are made going forward
3. Clean up the gmacs repo
4. a publication describing GMACS
5. more detailed documentation describing how a user would walk through implementation of GMACS for a new stock
6. Norton Sound red king crab

***Merge the branch used for terminally molting crab with the branch used for king crab.***

The github repository ‘szuwalski/gmacs\_comp’ holds the most recent assessments for BBRKC, SMBKC, and snow crab. BBRKC and SMBKC use the same .TPL; snow crab uses a different one.

‘gmacs\_orig’ has the currently used assessment .TPL and needed files for BBRKC and SMBKC; ‘src’ is the folder that holds the .TPL and the make file that compiles and copies ‘gmacs.exe’ to ‘bbrkc’ and ‘smbkc’. The folder ‘src\_mod’ has a .TPL that includes the code necessary to use the package ‘gmr’ to plot output.

‘gmacs\_term’ holds the code with the terminally molting life history incorporated. However, the .TPL in ‘gmacs\_orig’ has a few features that are not present in ‘gmacs\_term’. Ultimately, we need an assessment run for BBRKC, SMBKC, and snow crab with the current code for each assessment and a run with the fully merged code. Then, we need a document for each of those stocks that compares the output from the ‘current’ to the ‘merged’.

To do this, I might create a new folder in ‘gmacs\_term’ that has the same .TPL as ‘src\_rbar’, but is then used to incorporate the changes from the .TPL in ‘gmacs\_orig’. I would do this step by step, frequently compiling and running the code and checking if changes have occurred by running the .Rmd file that compares the output of two versions of GMACS. Note when things change.

While modifying the .TPL, the .DAT and .CTL files will also likely need to be changed.

***Produce scripts that automatically compare the output from two versions of GMACS to improve workflow as improvements are made going forward***

The basic scripts are already prepared for plotting, but matching estimated parameter values and standard errors is not yet done. It would also be nice for the comparison process to be as automated as possible.

***Clean up the GMACS repo***

Currently, there are many old and out-of-date files that do not work in the repo (sorry, Matthieu!). We need to have a clean repo for when the publication goes out, but it’s not clear to me what needs to stay and what needs to go. Nor is it clear to me where the repo should live.

**A publication describing GMACS**

A fair amount of work has already been put into this and hopefully bringing together the different pieces will be relatively straightforward. The high-level hope is to describe the population dynamics and then present one or two examples of how GMACS can be used (probably BBRKC and snow crab?).

***More detailed documentation describing how a user would walk through implementation of GMACS for a new stock***

Once the hooks are in from the publication, a new user will be interested in how exactly to implement GMACS. This ‘detailed’ documentation should walk a user through the entire process of how to prepare a .DAT file, a .CTL file, and a .PROJ file. It should also describe how to use the Rmarkdown documents and ‘gmr’ to produce an assessment document.

***Norton Sound red king crab***

It may be useful to use NSRKC as a test case for Matthieu to provide the detailed documentation of how a user would implement GMACS for a new stock.