Myxomatosis example using ADMB via R2admb

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August 1, 2011

1 Introduction

This model is found in chapter 6 of *Ecological Models and Data in R* by Bolker 2008 (hereafter EMD book) and also in Dwyer et al 1990. The mean titer is predicted to follow a Ricker function through time and to be gamma distributed.
$m = ate^{-bt}$
$T \sim$Gamma(shape $= s$, scale $= m/s$)

2 ADMB Code

The ADMB code (in a file called myxomatosis.tpl) looks like this:

```
DATA_SECTION
        init_int nobs
        init_vector titer(1,nobs)
        init_vector day(1,nobs)

PARAMETER_SECTION
        init_number a
        init_number b
        init_number s
        vector m(1,nobs)
        objective_function_value nll

PROCEDURE_SECTION
        m=Ricker(day, a, b);
        nll=dgamma(titer, s, s/m);//shape=s, rate=s/m

GLOBALS_SECTION
        #include <admodel.h>
        #include </Users/molliebrooks/admb-trunk/contrib/ecolib/
            pow_vectorized_RE.cpp>
```

```
20 #include </Users/molliebrooks/admb-trunk/contrib/ecolib/Ricker.cpp>
21 #include </Users/molliebrooks/admb-trunk/contrib/statslib/dgamma.cpp>
```

2.1 DATA_SECTION

This is where you define and initialize data objects. It is typical to first define data objects, such as `nobs`, that control the size of data objects defined further down in the code. This is so that the same .tpl file can be used on different data sets without making changes to the code.

2.2 PARAMETER_SECTION

This is where you define and initialize parameters to be fit. These will start with `init_`. Also in this section, you can define objects, such as `m` where you'll store calculated values. The last thing in this section is the `objective_function_value` which will get minimized. I like to call it `nll` for "negative log likelihood".

2.3 PROCEDURE_SECTION

This is where the negative log likeihood is calculated and stored in the `objective_function_value`. Line 14 is where we calculate the mean `m` through time as following a Ricker function with parameters `a` and `b`. You can find out how the function is parametarized by going to http://admb-project.org/documentation/api/ and searching for "ricker". Then line 15 calculates the negative log likelihood of the data as being gamma distributed. The function `dgamma` takes a shape and rate parameter, so we need to know that the rate is the shape divided by the mean.

2.4 GLOBALS_SECTION

This is where we include any libraries that we want to use in our calculations. In this example, we need the `Ricker.cpp` and `dgamma.cpp` for the two functions used in our `PROCEDURE_SECTION`. The extensions in the .tpl file are specific to my computer. You will have to find the admb-trunk and contrib directory on your own computer and change the extension. The first two libraries are necessary for using the latter two.

3 R Libraries (if you want to use R to organize the data and read the results)

```
> library(emdbook)
> library(R2admb)
> setup_admb()
```

```
[1] "/usr/local/admb"
```

The command `setup_admb()` tries to find the location of ADMB so that it can be used by R2admb.

4 Data

Data organization is the same as in the EMD book. Then we use `write_dat()` to put the values for the `DATA_SECTION` of our .tpl file into a .dat file. The order of the objects in the list must match lines 2 through 4 of the .tpl file. `write_pin()` puts the initial values for our parameters into a .pin file. The order of these objects must match lines 7 through 9 of our .tpl file. `m` and `nll` are the only objects in our `PARAMETER_SECTION` that do not need to be initialized because they are calculated in the `PROCEDURE_SECTION`. Also, note that `m` and `nll` are the only objects not beginning with `init_`

```
> data(MyxoTiter_sum)
> myxdat=subset(MyxoTiter_sum, grade==1)
> write_dat("myxomatosis", L=list(nobs=nrow(myxdat), titer=myxdat$titer, day=myxdat$day))
> write_pin("myxomatosis", L=list(a=1, b=0.2, s=50))
```

5 Running the model via R2admb

```
> compile_admb("myxomatosis")
> run_admb("myxomatosis", verbose=FALSE)
```

6 Reading the results via R2admb

```
> myxo1_admb=read_admb("myxomatosis")
> summary(myxo1_admb)

Model file: myxomatosis
Negative log-likelihood: 29.5091
Coefficients:
   Estimate Std. Error z value Pr(>|z|)
a  3.561247   0.190280  18.716  < 2e-16 ***
b  0.171329   0.009818  17.451  < 2e-16 ***
s 90.511940  24.589000   3.681 0.000232 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> logLik(myxo1_admb)

[1] -29.5091
```

7 Conclusion

We got the same parameter estimates and log likelihood as the example in the book. It might seem like this isn't worth the extra effort, but if you wanted to increase the complexity of the model and/or include any random effects, then the flexibility of ADMB would be selling point.