ADMB
Automatic Differentiation Model Builder

Dave Fournier receives AFS Ricker award

Dave Fournier received the American Fisheries Society's Ricker award. This is a prestigious award and provides Dave recognition not only for the great contribution AD Model Builder has made to fisheries stock assessment, but also Dave's contribution to fisheries stock assessment methodology, such as being the pioneer of integrated analysis (see Fournier and Archibald 1982).

The ADMB Foundation initiated and coordinated the nomination of Dave for this award. Prof. Ray Hilborn, a previous recipient of the award, volunteered to be the nominator. Several of you provided letters of support and we thank you for your efforts.

Dave was first nominated in 2008 and was the runner up for the award. This meant that his nomination would be carried over to 2009. Since the 2008 nomination, the Moore Foundation grant was awarded, and provided additional support for Dave's nomination.

Below are some statements taken from selected supporting letters. Several supporting letters are available on the ADMB website. Prof. Ray Hilborn's supporting letter is reproduced on page 2.

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"If Ricker is considered the grandfather of modern fisheries stock assessment, then Fournier should be considered the father. "

Prof. Ray Hilborn, University of Washington

"His theoretical, practical, and technical contributions have helped reshape modern stock assessment science, not just in North America, but throughout the world"

Michael H. Prager, U.S. National Marine Fisheries Service

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"Dr. Fournier's work has allowed population assessment methodology in fisheries to advance further than population assessment methodology in other related fields."

Mark Maunder, Inter-American Tropical Tuna Commission

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"Dr. Fournier's publications on assessment theory and methods, and the software tools developed by Dr. Fournier (especially ADMB) have been essential in the widespread application of statistically rigorous integrated stock assessments for marine fisheries throughout the world."

Prof. James Bence, Michigan State University

"It is difficult to exaggerate the importance of this intellectual and computational breakthrough."

John Sibert, University of Hawaii

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"It is no exaggeration to state that Dr. Fournier's development of ADMB has empowered an entire generation of fishery stock assessment scientists. "

Richard Methot, NOAA Fisheries

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"[ADMB] is of crucial importance in allowing the European Community to develop recovery and long-term management plans that meet commitments under the World Summit on Sustainable Development"

Laurence Kell, Center for Environment, Fisheries, Aquaculture Science, UK.

Dave Fournier receiving the AFS Ricker award from Bill Franzin at the AFS annual meeting in Nashville

ADMB presented at the workshop on automatic differentiation

The eighth European workshop on Automatic Differentiation (AD) was held Friday 17th July 2009 in Oxford, UK. The workshop was hosted by NAG (Numerical Algorithms Group) which currently is working on incorporating AD functionality in their Fortran compiler. The theme was "AD Software Development", and about 20 people attended the workshop. The programme can be found at http://www.autodiff.org/?module=Workshops&submenu=EuroAD%2F8%2Fmain

The talk focused on both ADMB (the software package) and the ADMB open source project. ADMB was unique among the software packages presented at the workshop, in that it seamlessly automatic differentiation with statistical functionality. The talk will soon be available from the workshop webpage.

Continued from page 1: Nomination letter for the AFS Ricker award

Below is the letter sent to the American Fisheries Society nominating Dave Fournier for the Ricker award.

20 April, 2008

Dr. Jennifer Nielsen

AFS Ricker Award Committee

Dear Jennifer,

I would like to nominate Dr. David Fournier for the William E. Ricker Resource Conservation Award. If Ricker is considered the grandfather of modern fisheries stock assessment, then Fournier should be considered the father. Ricker laid the foundation for quantitative analysis of fisheries data. Fournier extended Ricker's work, made it more statistically rigorous, and developed the tool (AD Model Builder) that has become central to the implementation of these stock assessment methods around the world.

The landmark paper "Fournier, D. and Archibald, C.P. (1982) A general theory for analyzing catch at age data. Canadian Journal of Fisheries and Aquatic Science 39, 1195-1207" is the basis for all modern stock assessment methods. Fournier and Archibald describe how multiple sources of data can be integrated into a single analysis, using a maximum-likelihood context. This integrated approach is now standard in fisheries stock assessment. The integrated approach has also become standard for research in wildlife and other fields. The Fournier and Archibald article has been cited 147 times in ISI web of science, which is impressive for an article published in a fisheries journal. Dr Fournier has furthered the methodology in a number of subsequent papers.

Of even more practical importance, to implement the integrated modeling approach, Dr Fournier developed the software package AD Model Builder (ADMB), which has become the standard for developing fisheries stock assessment models and has earned acceptance by researchers working on all aspects of resource management. Population models based on the ADMB software are used to monitor more than 150 different species around the world. The populations modeled using ADMB include such diverse species as whales, dolphins, sea lions, penguins, albatross, abalone, lobsters, tunas, billfishes, sharks, rays, anchovies, and pollock.

ADMB applications extend beyond stock assessment. ADMB-based software is used for applications critical to the development of place-based management policies. ADMB is an essential building block of the methods used to reconstruct movements of many species of animals tracked with electronic tags. Spatially-resolved population models treat movement as an integral component of population dynamics, and depend on ADMB for estimating movement parameters from data.

ADMB applications are critical to the missions of fishery management agencies in North America and elsewhere. Stock assessments of commercially-important fish stocks and ecologically-sensitive protected species around the world depend on ADMB. For example, ADMB underlies the Stock Synthesis II software that is immensely popular in North America. In the United States, every NOAA Fisheries Science Center uses ADMB in some fashion, and many commercially-important and sustainably-managed fisheries depend on ADMB-based stock assessments. These fisheries include, for example, the Gulf of Alaska pollock fishery, which is widely hailed as sustainably managed. The value of the fisheries dependent on ADMB-based assessments is enormous. The combined landed value of tropical Pacific tunas and Gulf of Alaska and Bering Sea ground fish exceeds US$10 billion.

ADMB is also used at universities and other academic and research institutions. Due to ADMB's wide use in fisheries assessment and management, it is now taught in courses at several universities. The research organizations, government departments, and companies using ADMB, the types of applications being used, and a list of ADMB-based publications can be found on-line at http://admb-project.org.

I hope that you find the nomination of Dr. Fournier favorable, so that he gets the recognition that he deserves for advancing fisheries stock assessment to where it is today.

Sincerely,

Ray Hilborn

Richard C. and Lois M. Worthington Professor of Fisheries Management

ADMB course at Michigan State University

The Quantitative Fisheries Center (QFC) at Michigan State University (MSU) taught two short courses on the use of AD Model Builder on the MSU campus on August 18-21, 2009. Eleven participants signed up for both courses. Participants included personnel from the Ontario Ministry of Natural Resources, Ohio Department of Natural Resources, Michigan Department of Natural Resources, National Marine Fisheries Service, and Michigan State University. Most participants indicated that their reason for taking the course was to use or potentially use ADMB as part of their work or research. Most also indicated that their prior knowledge of ADMB was poor or very poor. Overall, the courses received an excellent/good rating. This was the 3rd time that the QFC has taught ADMB short courses on the MSU campus. Future courses are being planned.

Creating Custom Libraries for use in ADMB

By Steve Martell

Often I find that I'm repeatedly writing the same code in my ADMB template files for various projects; for example, the negative log-likelihood for the normal distribution. Wouldn't it be nice to just call a function such as `dnorm(x,mu,sd)` and have it return the negative log density. Many such functions have already been implemented in the ADMB library (e.g., `posfun`). The purpose of this article is to show you how to develop your own personal libraries that contain your own custom functions. Building custom libraries is a great way to organize your code, make the code more readable, and reduce the probability of making a coding error in future projects. Custom functions from these libraries can be included in your ADMB project using `#include <library_name>` statement in the `GLOBALS_SECTION` of your ADMB template. When you compile the ADMB project the functions written in the library are included in the project. There are two options for creating your own custom libraries for use in ADMB: 1) is to create a static-library application which involves the creation of a header and cpp files and compiling these into a binary library, or 2) create a new cpp file with various functions to include into your ADMB project. The second option is by far the simplest option as it does not require any header files and compiling static-libraries. The remainder of this article will focus on the much simpler second option.

To create your own custom library all you need to do is create a new file (e.g., "mylib.cpp" and be sure that this file is saved in the project root folder or the ADMB/lib folder), and at the top of that file be sure to include the admodel header file (`#inlcude <admodel.h>`). Following the include statements, write your own custom functions that return or modify variables. For example, I have a `stats.cxx` file saved in my ADMB Lib directory where I have compiled over the years many statistical functions (many of which are adopted from R) to carry out routine negative log-likelihood calculations for various statistical distributions. An example of the `stats.cxx` file containing two functions for computing the negative logdensity for a normal distribution is shown in the following code. Notice that you may overload functions, by declaring more than one function using the same name in the same scope. The declarations of the functions must differ from each other either the number of arguments and/or the type of arguments. When you call an overloaded function, the correct function is selected by comparing the argument list with the variable list.

```cpp
#include <admodel.h>
dvariable dnorm(const double& x, const dvariable& mu, const dvariable& std)
{
       double pi=3.14159265358979323844;
       return(0.5*log(2.*pi)+log(std)+0.5*square(x-mu)/(std*std));
}
dvariable dnorm(const dvector& x, const dvar_vector& mu, const dvar_vector& std)
{
       double pi=3.14159265358979323844;
       int n=size_count(x);
       dvar_vector var=square(std);
       dvar_vector SS=square(x-mu);
       return(0.5*n*log(2.*pi)+sum(log(std))+0.5*sum(elem_div(SS,var)));
}
```

If you're not familiar with C++ code, you might find the above code a bit challenging at first. The above two functions return a single differentiable variables (`dvariable dnorm(...)`), require three arguments (`x,mu,std`) where the first argument is defined as a data-type variable/vector and the second and third arguments are differentiable variables (`dvariable` or `dvar_vector`). All three of these arguments are given "read-only" access to the variables via pointers (e.g., `const double& x`) which is faster than creating copy of the object (e.g., `double x`) for the argument list. The second function also declares two differentiable vectors on the fly (e.g., `dvar_vector`); the scope of these two vectors is only within the `dnorm` function. You can also write your own function within the ADMB template file, and copy the corresponding C++ code from the cpp file that is produced by `tpl2cpp.exe` and remove the class member name (`model_parameters::`) from the function.

Creating Custom Libraries for use in ADMB continued from page 3

Note also you may need to add the RETURN_ARRAYS_INCREMENT() and RETURN_ARRAYS_DECREMENT() statements if your function returns a variable object (see 3-7 in the Autodiff manual for more information). To use this function within my ADMB project I first must include the file in the GLOBALS_SECTION then call the dnorm function in the PROCEDURE_SECTION, e.g.,

```
GLOBALS_SECTION
  #include <stats.cxx> //include functions from my custom library
PROCEDURE_SECTION
  dvar_vector plen = linf*(1.-exp(-k*(age-to)));
  dvar_vector stdev = cv*plen;
  f = dnorm(len,plen,stdev); //neg loglike for normal density.
```

where x is a data vector, mu and std are differentiable vectors.
The following is a simple example of fitting a von Bertalanffy growth model to some length-age data that uses the custom library stats.cxx and calls the dnorm function.

```
DATA_SECTION
  init_int nobs;
  init_vector age(1,nobs);
  init_vector len(1,nobs);
PARAMETER_SECTION
  init_number linf;
  init_number k;
  init_number to;
  init_number cv;
  !! linf = 100.;
  !! k = 0.2;
  !! to = -0.5;
  !! cv= 0.1;
  objective_function_value f;
PROCEDURE_SECTION
  dvar_vector plen = linf*(1.-exp(-k*(age-to)));
  dvar_vector stdev = cv*plen;
  f = dnorm(len,plen,stdev); //neg loglike for normal density.
GLOBALS_SECTION
  #include <stats.cxx> //custom library that contains the dnorm function
––––––––––––––– Example data –––––––––––––––––––
# nobs
20
# age
1 2 2 3 3 3 3 3 4 6 5 5 7 4 4 6 7 7 7 9
# length
27 41 43 49 51 53 55 57 57 59 65 67 69 71 71 73 75 83 85 101
```

ADMB Foundation newsletter

Newsletter Editor:
Mark Maunder
Inter-American Tropical Tuna Commission

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The objectives of the ADMB Foundation are to (a) advance the ADMB project for improving data analysis and non-linear statistical modeling; (b) act as an official voice for the ADMB project, providing means of communication with the press, commercial and noncommercial organizations interested in the ADMB software; (c) coordinate development and promote use of ADMB.

The ADMB Foundation is a non-profit organization working in the public interest for charitable, educational and scientific purposes under section 501(c)(3) of the United States Internal Revenue Code.

President: John Sibert

Treasurer: Mark Maunder

Secretary: Anders Nielsen

Recent ADMB based publications

Aires-da-Silva, A.M., Maunder, M.N. Gallucci, V.F., Kohler, N.E. and Hoey, J.J. (2009) A spatially-structured tagging model to estimate movement and fishing mortality rates for the blue shark (*Prionace glauca*) in the North Atlantic Ocean. Marine and Freshwater Research 60: 1029-1043.

Cubillos, L.A., Aguayo, M., Neira, M., Sanhueza, E., and Castillo-Jordán, C. (2009) Age verification and growth of the Chilean cardinalfish Epigonus crassicaudus (de Buen, 1959) admitting ageing error. Revista de Biología Marina y Oceanografía 44: 417-427

Frédoua, T., Ferreira, B.P., Letourneur, Y. (2009) Assessing the stocks of the primary snappers caught in Northeastern Brazilian Reef Systems. 2-A multi-fleet age-structured approach. Fisheries Research, 99: 97-105.

Hart, D.R. and Chute, A.S. (2009) Verification of Atlantic sea scallop (*Placopecten magellanicus*) shell growth rings by tracking cohorts in fishery closed areas Can. J. Fish. Aquat. Sci. 66: 751–758.

Kim, S.W., Hudson, I.L. and Keatley. M.R (2009). Modelling the flowering of four eucalypts species via MTDg with interactions. In Anderssen, R.S., R.D. Braddock and L.T.H. Newham (eds) 18th World IMACS Congress and MODSIM09 International Congress on Modelling and Simulation. Modelling and Simulation Society of Australia and New Zealand and International Association for Mathematics and Computers in Simulation, July 2009, pp. 2625-2631. ISBN: 978-0-9758400-7-8. http://www.mssanz.org.au/modsim09/F12/kragt.pdf

McGarvey, R. and Linnane, A. (2009) Estimating historical commercial rock lobster (*Jasus edwardsii*) catch inside Australian State territorial waters for marine protected area assessment: the binomial likelihood method. Biodivers Conserv 18: 1403–1412.

Montenegro, C., Maunder, M.N., and Zilleruelo, M. (2009) Improving management advice through spatially explicit models and sharing information. Fisheries Research 100: 191–199.

Olea, P.P. and Mateo-Tomás, P. (2009) The role of traditional farming practices in ecosystem conservation: The case of transhumance and vultures. Biological Conservation, 142: 1844-1853.

Roel, B.A., De Oliveira, J.A.A, and Beggs, S. (2009) A two-stage biomass model for Irish Sea herring allowing for additional variance in the recruitment index caused by mixing of stocks. ICES Journal of Marine Science, 66: 1808-1813.

Sadykova, D., Skurdal, J., Sadykov, A., Taugbol, T., and Hessen, D.O. (2009). Modelling crayfish population dynamics using catch data: A size-structured model. Ecological Modelling, 220: 2727-2733.

Wilberg, M.J. (2009) Estimation of recreational bag limit noncompliance using contact creel survey data. Fisheries Research. 99: 239-243.

Wilderbuer, T.K. and Turnock, B.J. (2009) Sex-Specific Natural Mortality of Arrowtooth Flounder in Alaska: Implications of a Skewed Sex Ratio on Exploitation and Management. North American Journal of Fisheries Management, 29: 306-322.