PBSadmb 0.65: User's Guide

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ABSTRACT

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This report describes the R package `PBSadmb`, an R wrapper for the powerful software package ADMB (AD Model Builder, http://admb-project.org/) released into the public domain in 2009. The ADMB framework constitutes a remarkably efficient tool for estimating parameters and their uncertainty, based on complex nonlinear statistical models. Its effectiveness stems partly from the use of *automatic differentiation* (AD, also called *algorithmic differentiation*) to compute the gradient of an objective function to be minimized. It includes robust algorithms for modal estimation and Markov chain Monte Carlo (MCMC) sampling from Bayesian posterior distributions. It also supports other common inference methods, such as asymptotic covariances and likelihood profiles. With the package `PBSadmb`, commands to ADMB can be integrated with R commands in the same script file. We introduce standards that make it possible to preserve variable names between R scripts and ADMB template files. For example, a single R script can use ADMB to make an executable file, generate an MCMC sample, and draw a `pairs` plot of the results. More generally, `PBSadmb` allows a user to treat ADMB as just another R application, with the same interface in all supported operating systems (currently Windows, Linux, or Mac OS).

Preface

(Eventually, this section should include some colourful history of ADMB.)

User's Guide to the R Package `PBSadmb`

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1. Introduction

Perhaps only a small minority of R users know about the powerful software package ADMB (AD Model Builder, http://admb-project.org/) released into the public domain in 2009. It provides a remarkably efficient tool for estimating parameters and their uncertainty, based on complex nonlinear statistical models. Its effectiveness stems partly from the use of *automatic differentiation* (AD, also called *algorithmic differentiation*) to compute the gradient of an objective function to be minimized. It includes robust algorithms for modal estimation and Markov chain Monte Carlo (MCMC) sampling from Bayesian posterior distributions. Other common inference methods, such as asymptotic covariances and likelihood profiles, are also supported. ADMB allows you to examine your data with any statistical model that has a properly defined likelihood function or Bayesian posterior. The model can have hundreds or even thousands of unknown parameters that require estimation.

Originally, ADMB was developed commercially by its principal author David Fournier and the company Otter Research Ltd. (http://www.otter-rsch.com/). It quickly gained wide use in fishery data analyses, although it has potential value in many scientific fields. Thanks to a generous grant from the Gordon and Betty Moore Foundation (http://www.moore.org/), the ADMB Project (http://admb-project.org/) acquired rights to the software and began releasing it to the public domain in 2008. Several releases have now been completed, and many people have worked hard to make this possible. We thank all of them for their efforts and mention a few names in the Acknowledgements below. An authoritative history of ADMB remains to be written, but it would make a very colourful story for an ambitious historian of computer science who has a lively sense of humour. It involves a cast of remarkable personalities who know how to develop serious scientific tools while having a great deal of fun. Not by accident, some of the spin-off packages bear the names of New Zealand wines, such as Coleraine (http://fish.washington.edu/research/coleraine/) and Awatea (http://code.google.com/p/pbs-awatea/). Currently, `PBSadmb` supports ADMB version 10 or higher (we hope!).

The R software environment easily accommodates external programs. R packages routinely include C/C++ code, and the packaging system automatically compiles the code for all supported operating systems. More generally, R can connect to a wide range of software written independently. For example, the open source program `ggobi` (http://www.ggobi.org/, "*Good pictures force the unexpected upon us*") allows users to visualize high dimensional data in a number of creative ways. This software runs independently from R, but the package `rggobi` allows R users to think of it as just another R application. Commands in R allow you to do anything that you could otherwise do with `ggobi`. To make things work, a user may need to install `ggobi` in the operating system of choice before installing the R package `rggobi`.

ADMB necessarily involves a C++ environment that cannot be entirely masked by R. The automatic differentiation algorithms, implemented with C++ classes, require a user to express the posterior or likelihood in C++. The author (Dave Fournier) had the ingenious idea of making this process as easy as possible with a *template* that handles most of the annoying bookkeeping, so that a user need only write code (very similar to R code) that expresses the model analytically. Program development involves three distinct steps: (1) converting the template to true C++ code, (2) compiling the C++ code, and (3) linking the resulting object module to ADMB libraries. The complete cycle makes an executable file that recognizes a variety of command line arguments. `PBSadmb` implements these steps with the R commands `convAD` (convert to C++), `compAD` (compile C++), and `linkAD` (link to libraries). A composite command `makeAD` performs all three steps sequentially. Another command `runAD` runs the executable file with specified arguments.

The native interface to ADMB differs slightly among operating systems. For example, a Windows platform uses DOS batch files, whereas a Linux system uses bash scripts. Although this doesn't create any serious problems, it does require a bit of adjustment when moving from one system to another. The R platform, available on Windows, Linux, and MacOS X, offers a common interface that appears the same, regardless of the operating system. We have designed `PBSadmb` to take advantage of this fact. Consequently, a user who interacts with ADMB via R sees exactly the same interface on every platform.

`PBSadmb` allows a user to enter all ADMB commands in an R terminal, rather than a DOS or bash terminal. Furthermore, because R is now the language of choice, commands to ADMB can be integrated with R commands in the same script file. We introduce standards that make it possible to preserve variable names between R scripts and ADMB template files. A single R script can use ADMB to make an executable file, generate an MCMC sample, and produce a `pairs` plot of the results.

Although `PBSadmb` has the primary goal of accessing ADMB via R scripts, we also provide a Graphical User Interface (GUI) that greatly facilitates ADMB model development. New users may find it particularly helpful for editing code, testing it rapidly, and inspecting results (such as MCMC simulations). The GUI gives links to help files and examples that illustrate key aspects of ADMB model development. Use of the GUI is, however, entirely optional, and experienced users of ADMB and R may confine their applications of `PBSadmb` entirely to R script files. They might also find the GUI useful for configuring the software to run properly.

The initials 'PBS' refer to the Pacific Biological Station, a major fisheries laboratory operated by Fisheries and Oceans Canada on the Pacific coast in Nanaimo, British Columbia, Canada (http://www.pac.dfo-mpo.gc.ca/science/facilities-installations/pbs-sbp/index-eng.htm). We have developed a number of packages for R, each starting with the acronym PBS. Three of these (`PBSmapping`, `PBSmodelling`, and `PBSddesolve`) existed prior to `PBSadmb` on the Comprehensive R Archive Network (CRAN, http://cran.r-project.org/). We use Google Code web sites to maintain a source code archive for each of our packages. See http://code.google.com/p/pbs-software/ for links to all of them. In particular, http://code.google.com/p/pbs-admb/ has the source code and other information about `PBSadmb`.

Arguably, this package should have been called `pbsADMB` to put the proper emphasis on the role of ADMB. We have chosen, however, to preserve the naming style of our other packages because they tend to be closely linked. For example, `PBSadmb` uses numerous functions from `PBSmodelling` and extends many of the programming goals of that earlier package. We encourage users to try all of our packages, or at least read their descriptions.

If you are an R user who wants the freedom to build arbitrarily complex statistical models, we believe you'll find this package an invaluable tool. Although ADMB was motivated by problems in fisheries science, professionals in many other fields (such as economics, finance, medicine, genetics, physics, and chemistry) will likely be surprised, if not astonished, at its power. We've written this package to help make ADMB transparent, useful, and available to a much wider audience than its traditional core in fishery science.

2. Using `PBSadmb`

To use `PBSadmb`, you first need to install it properly by the detailed procedure in Appendix A. As suggested in the introduction, this involves the two R packages `PBSadmb` and `PBSmodelling`, as well as ADMB itself. A C/C++ compiler is also required, which needs special installation on a Windows platform, but may come automatically as part of Linux or MacOS X. The GUI also requires a suitable choice of text editor.

Because this package applies to R, we assume that our readers have at least some familiarity with R itself and the standard methods of installing packages from the CRAN repository. If you are new to ADMB, you need to know that a typical project has a file prefix (`*`) and three associated files to hold the code (`*.tpl`), input data (`*.dat`), and initial parameter values (`*.pin`).

We illustrate the use of ADMB by considering a very simple estimation problem for the familiar von Bertalanffy growth curve:

(1) $y_i = L_\infty[1 - e^{-K(a_i - t_0)}] + \sigma\varepsilon_i$, where $i = 1,\ldots,n$.

This formula calculates observed lengths y_i from observed ages a_i and a vector $(L_\infty, K, t_0, \sigma)$ of four unknown parameters. The residuals ε_i in (1) are assumed to be independent normal random variables with mean 0 and standard deviation 1. From the density function for a normal distribution, the negative log likelihood ℓ for this model is:

(2) $\ell(L_\infty, K, t_0, \sigma \mid a_1,\ldots,a_n, y_1,\ldots,y_n) = n\log\sigma + \frac{1}{2\sigma^2}\sum_{i=1}^{n}(y_i - z_i)^2$,

where the predicted length z_i at age a_i is

(3) $z_i(a_i; L_\infty, K, t_0, \sigma) = L_\infty[1 - e^{-K(a_i - t_0)}]$.

We drop an additive constant in (2) that does not affect the analysis. The notation emphasizes that we regard ℓ as a function of the parameters for fixed values of the data.

If the ADMB prefix for this project is `vonb`, then the three text files `vonb.tpl`, `vonb.dat`, `vonb.pin` would contain, respectively:

- the code for ℓ in (2),
- the data (a_i, y_i) for $i = 1, \ldots, n$, and
- initial values of the parameters $(L_\infty, K, t_0, \sigma)$.

This operational framework motivates the scripting language developed in `PBSadmb`, which includes the following commands (some mentioned previously):

`convAD`	convert `*.tpl` to `*.cpp`,
`compAD`	compile `*.cpp` to a binary object,
`linkAD`	link the binary object with ADMB libraries and create an executable file,
`makeAD`	convert, compile, and link to make an executable file,
`runAD`	run an ADMB executable with specified command line arguments,
`showArgs`	show all possible command line arguments for an ADMB executable,
`runMC`	run an ADMB executable in MCMC mode,
`plotMC`	plot the results of an MCMC simulation,
`editAD`	edit text files for the current project in the text editor,
`readRep`	read one of the standard reports generated by an ADMB executable,
`startLog`	start a log file (`*.log`) of ADMB activity,
`appendLog`	append to a log file of ADMB activity,
`cleanAD`	remove files created by ADMB that tend to proliferate in the working directory,
`convOS`	convert text files to the format for the operating system (Windows or Unix).

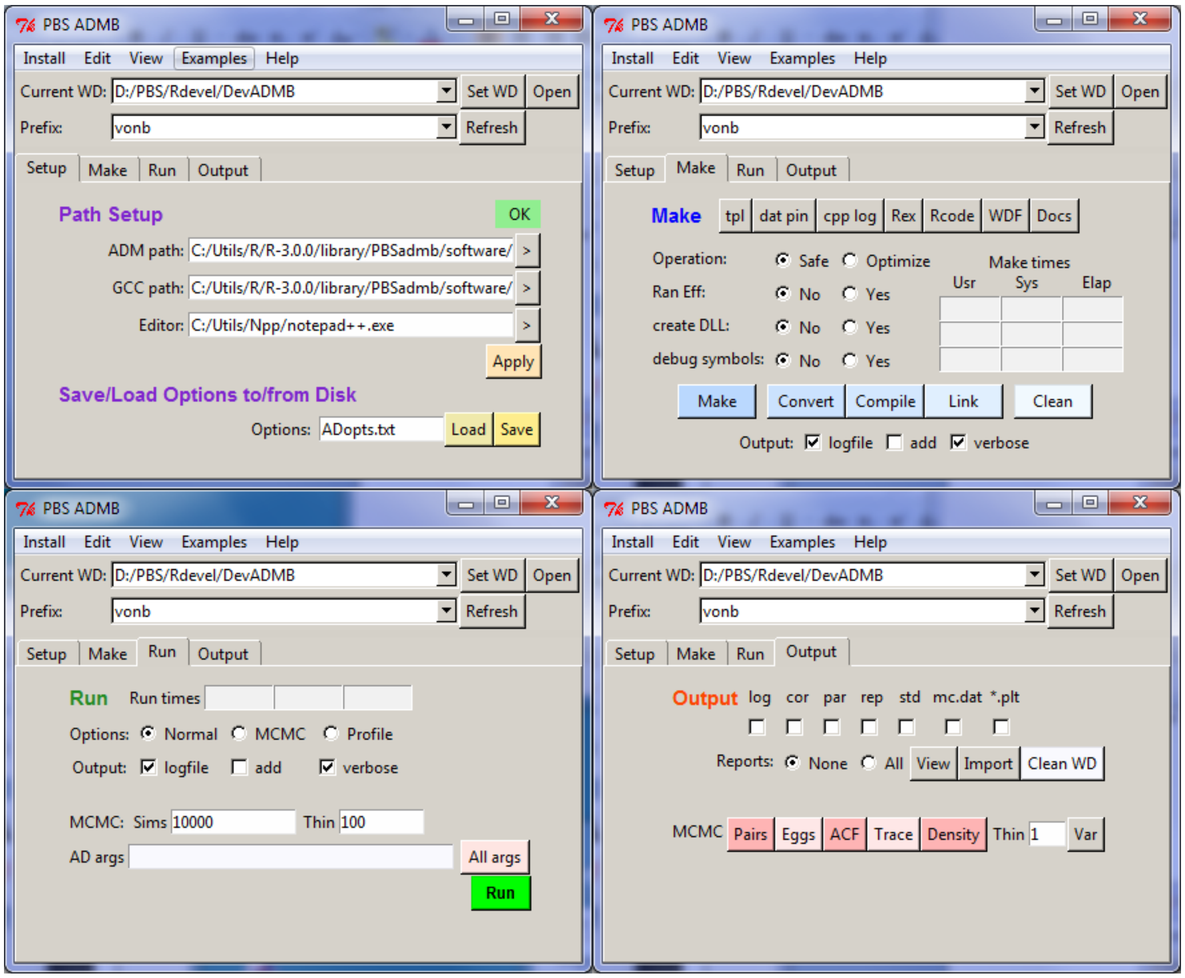
These commands illustrate the functions available in `PBSadmb`. For a complete list, see Appendix C.

3. The `PBSadmb` GUI

As we have emphasized, `PBSadmb` principally defines a scripting language for interacting with ADMB. However, the package ADMB itself is quite complex, and new users sometimes find it rather intimidating. Even experienced users like us sometimes forget key details needed to accomplish certain tasks. For this reason we offer a GUI that greatly facilitates ADMB model development. In our own workshops, we have found it an invaluable tool for educational purposes.

The GUI (Figure 1) allows a user to explore all aspects of ADMB model development. The interface emphasizes four distinct phases:

- **Initialize** the package with appropriate paths , check that they make sense, and save them in a file normally called `Adopts.txt`.
- **Make** the executable file for a chosen prefix, with options between “Safe” and “Optimized” compilation and a choice to have random effects or not.
- **Run** the executable code with suitable command line arguments, where the “All args” button shows all available arguments. The interface gives particular support for generating MCMC samples and likelihood profiles. Turn off “Verbose” while producing MCMC samples.
- Inspect the **Output** by “View”ing various reports or “Import”ing them into the R working environment. As mentioned earlier, we give special support to MCMC samples with plots that allow a user to inspect the sampled chain. The widgets “Thin and “Var” (for “Variables”) enable a user to thin the current chain and select variables for plotting.



Current WD: D:/PBS/Rdevel/DevADMB
Prefix: vonb

ADM path: C:/Utils/R/R-3.0.0/library/PBSadmb/software/
GCC path: C:/Utils/R/R-3.0.0/library/PBSadmb/software/
Editor: C:/Utils/Npp/notepad++.exe
Options: ADopts.txt

Operation: [✓ Safe] Optimize
Ran Eff: [✓ No] Yes
create DLL: [✓ No] Yes
debug symbols: [✓ No] Yes
Output: [✓ logfile] add [✓ verbose]

Options: [✓ Normal] MCMC Profile
Output: [✓ logfile] add [✓ verbose]
MCMC: Sims 10000 Thin 100
AD args

Reports: [✓ None] All
MCMC Thin 1

Figure 1. The graphical user interface (GUI) in `PBSadmb`, generated by the R command `admb()` on a Windows platform. The window makes use of `notebook` tabs: from left to right – `Setup`, `Make`, `Run`, and `Output`.

Buttons labelled “>” in the “Initialize” and “Make” sections allow a user to browse for available choices. Text boxes in the “Make” section show the times required for converting (row 1) compiling (row 2), and linking (row 3). The R function `proc.time` reports the ‘user time’ and ‘system time’, as well as the elapsed time, and these correspond to the three columns in the interface. Similarly, text boxes in the “Run” section show the run times.

Experienced ADMB users know that ADMB leaves many “footprints” as files in the current working directory. The interface gives you “Clean” buttons to help clean them up. To make things easy, each “Clean” button activates a second GUI that displays potential files associated with the project prefix, as well as other debris files spawned by ADMB. The user can fine-tune the selection using the “Select” and “Deselect” buttons. When the “Clean” button is pressed, a final prompting GUI pops up to confirm deletion of the selected files. Once the files have been deleted, the Clean window remains and the user can choose another prefix (by typing manually or pressing the selection button “>”) AND hitting the “Refresh” button. This causes the GUI to rebuild itself with files having the newly selected prefix. If no additional files are apparent, the Clean window disappears. Files with suffixes `.tpl`, `.dat`, `.pin`, `.r`, and `.pdf` are never picked for potential deletion. Be careful when cleaning; for example don’t delete an output file until you’re sure you’re ready to do so.

After you’ve successfully installed `PBSadmb`, we encourage you to experiment with the GUI. You can quickly see the functionality available in the main menu items. <Edit> allows you to edit the main project files, and <View> displays the output files. <Examples> copies various examples (discussed below) into your working directory. <Package> shows the R code for this package and the Window description file used to create the GUI in Figure 1. <Help> points to manuals in the package, online resources, and this User’s Guide.

4. ADMB in action

If you’re like us, whenever you install a software package, you immediately want to see it do something. `PBSadmb` includes a number of examples that teach new users (and remind experienced users) how to write, test, and implement an ADMB template. To see them click <Examples> on the GUI menu. If you click one of them (the file prefix), the program will load all related files into your current working directory. Typically, these have the suffixes

- `.tpl` – the ADMB template file;
- `.dat` – the data used for this template;
- `.pin` – initial values for the parameter estimates;
- `.r` – R code that can be sourced to obtain an extended analysis using both ADMB and R;
- `.pdf` – documentation for this example.

When the GUI copies text files to the working directory, they automatically get converted (via the function `convOS`) to the correct format for the operating system, with line endings <CR><LF> in Windows and <LF> in Unix. Sometimes ADMB fails when the input files have a format inappropriate for the OS. (We encountered this problem with the ADMB command `tpl2rem`, called by our function `convAD`.) If you move files across platforms, remember that conversion might be necessary. Linux users probably have the native OS commands `todos` and `fromdos` for this purpose. Windows users can get similar utilities from the Internet.

`PBSadmb` includes the examples listed below. We encourage new users to focus particularly on `vonb`.

`simple`, adapted from an example in the ADMB manual, codes the likelihood for regressing a vector `y` on a vector `x`. Take special note of how code is written for the four SECTIONs (DATA, PARAMETER, PROCEDURE, REPORT). Values initialized in the DATA_SECTION come from `simple.dat`, and values initialized in the PARAMETER_SECTION come from `simple.pin`.

`simple_mc`, a variant of `simple`, can give a Bayesian posterior sample of the parameters. The GUI allows you to perform a run with "MCMC" options (the number of simulations and the thinning frequency). You can then view results visually with plots generated from the "Output" section of the GUI.

`simple_pbs`, a variant of `simple_mc`, has a REPORT_SECTION written explicitly for `PBSadmb` to ensure that variable names in R code match those from ADMB. In this case, the file `simple_pbs.r` performs four tasks:

- making the executable file `simple_pbs.exe` (in Windows) or `simple_pbs` (in Linux) from `simple_pbs.tpl`,
- running the executable file,
- loading the data from `simple_pbs.rep` into R, while preserving variable names, and
- producing a standard regression plot for the data exported imported from `simple_pbs.rep`.

`vonb`, similar to `simple_pbs`, implements the estimation problem posed by equations (1)–(3) in Section 2. It can also generate a likelihood profile for the parameter `Linf`, renamed for this purpose as `VonBLinf`. In this case, ADMB generates a file named `VonBLinf.plt`, with the parameter name prefix, *not* the prefix `vonb`.

`catage`, taken from ADMB web sites, implements a more complex model designed for estimating biological parameters from fishery data on catch and age structure. In the case, the code allows a user to compute a likelihood profile for the predicted biomass `pred_B`.

`pheno`, also taken from ADMB web sites, implements a model with the "random effects" feature. The lines declaring a `random_effects_vector` play a role similar to `init_vector` in earlier examples, except that the estimation method for random effects variables works differently (and much more slowly). The file `pheno.pin` includes initial values for the two random effects vectors declared in `pheno.tpl`.

5. R scripts to run ADMB

The examples `simple_pbs` and `vonb` both contain R files (`*.r`) that illustrate the use of R scripts to code ADMB analyses in R. We focus here on the `vonb` example. Table 1 shows the

Report Section in the model template. It writes variable names (preceded by $) and variable values. Running the executable file produces the report file vonb.rep listed in Table 2. This file has "PBS format", defined in the package PBSmodelling. Think of it as an R list object with named components.

Once you understand the relationship between the Report Section in Table 1 and the report file in Table 2, examine the R code in Table 3. It produces the plot in Figure 2, based entirely on data exported from the ADMB model. The functions readList and unpackList from PBSmodelling produce R variables with the same names as corresponding variables in the template file, given the structure of the Report Section in Table 1. This technique represents a standard in PBSadmb for writing ADMB template code to ensure variables with identical names and values in the R environment. *Just write the Report Section to export both names and values*, as illustrated in Table 1.

Table 1. The Report Section in vonb.tpl. It generates a report file vonb.rep that contains both variable names and values for easy import into the R environment. This technique ensures variables with common names and values in both ADMB and R.

```
REPORT_SECTION
  report << "$Linf"    << endl;
  report << Linf       << endl;
  report << "$K"       << endl;
  report << K          << endl;
  report << "$t0"      << endl;
  report << t0         << endl;
  report << "$sigma"   << endl;
  report << sigma      << endl;
  report << "$fval"    << endl;
  report << fval       << endl;
  report << "$age"     << endl;
  report << age        << endl;
  report << "$y"       << endl;
  report << y          << endl;
  report << "$ypred"   << endl;
  report << ypred      << endl;
  report << "$mcnames" << endl;
  report << "Linf K t0 sigma LK fval" << endl;
  report << "$mcest"   << endl;
  report << Linf << " " << K << " " << t0 << " " << sigma << " "
    << LK << " " << fval << endl;
```

Table 2. The report file `vonb.rep` produced by running `vonb.exe`. To fit in the space available on this page, the vectors `y` and `ypred` have been truncated. The file represents an R list with named components.

```
$Linf
57.2689
$K
0.164044
$t0
0.152865
$sigma
0.492146
$fval
-3.34367
$age
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
$y
 7.36 14.3 21.8 27.6 31.5 35.3 39 41.1 43.8 45.1 ...
$ypred
 7.43029 14.9707 21.3702 26.8015 31.4111 35.3233 ...
$mcnames
Linf K t0 sigma LK fval
$mcest
57.2689 0.164044 0.152865 0.492146 9.39464 -3.34367
```

Table 3. The R source file `vonb.r`. In the R console, the command `source("vonb.r")` initializes `PBSadmb` from a file `Adopts.txt` (presumably available and correct), makes `vonb.exe` from `vonb.tpl`, generates the plot in Figure 2, and compares results computed independently by ADMB and R.

```
# Initialize
require(PBSmodelling); require(PBSadmb); readADopts("Adopts.txt")

# Make and run "vonb.exe"
makeAD("vonb"); runAD("vonb");

# Read and unpack the report;
# i.e., create R variables with the same names used in "vonb.tpl"
vonb <- readList("vonb.rep"); unpackList(vonb);

# Plot the data
plot(age,y); lines(age,ypred,col="red",lwd=2);

# Check the calculations in R
ypredR <- Linf*(1-exp(-K*(age-t0)));
nobs   <- length(age);
fvalR  <- nobs*log(sigma) + sum((ypredR-y)^2)/(2.0*sigma^2)

cat("Functions values (ADMB & R):\n");
cat(fval,"   ",fvalR,"\n")

cat("Predictions (ADMB & R):\n");
cat(ypred,"\n");
cat(ypredR,"\n");
```

The code in Table 3 can be supplemented by two simple commands:

```
> runMC("vonb",100000,100)
> plotMC("vonb")
```

to give the Bayesian posterior scatter plot shown in Figure 3. The first line runs 100,000 simulations, thinning to keep only 1 of every 100 results. The second line plots the 1,000 points that result from this calculation. The following lines from the Report Section (Table 1) play a key role in producing Figure 3:

```
report << "$mcnames" << endl;
report << "Linf K t0 sigma LK fval" << endl;
report << "$mcest" << endl;
report << Linf << " " << K << " " << t0 << " " << sigma << " "
  << LK << " " << fval << endl;
```

by communicating the names of the variables preserved in the MCMC simulation (`$mcnames`) and their values at the posterior mode (`$mcest`). These provide the graph with variable names along the diagonal and coordinates of the mode, shown as a red point corresponding to the minimum ℓ (`fval`).

The results in Figure 3 can also be obtained directly from the GUI. Furthermore, `plotMC` can also draw a variety of plots, as indicated by the five coloured buttons along the bottom line of the GUI. Try them!

Acknowlegements

Our intrepid programmer, Alex Couture-Beil, greatly assisted the development of `PBSadmb` by improving its integration with `PBSmodelling`. In some cases, this meant changing `PBSmodelling` to enhance support for external packages. We thank all members of the ADMB community for their efforts on the open source project, particularly Dave Fournier, John Sibert, Mark Maunder, and Johnoel Ancheta. Ian Taylor helped us experiment with early conversions of `PBSadmb` from Windows to Linux. Saang-Yuan Hyun conducted tests and made a number of helpful suggestions. Andy Edwards generously contributed funding to support programming expenses.

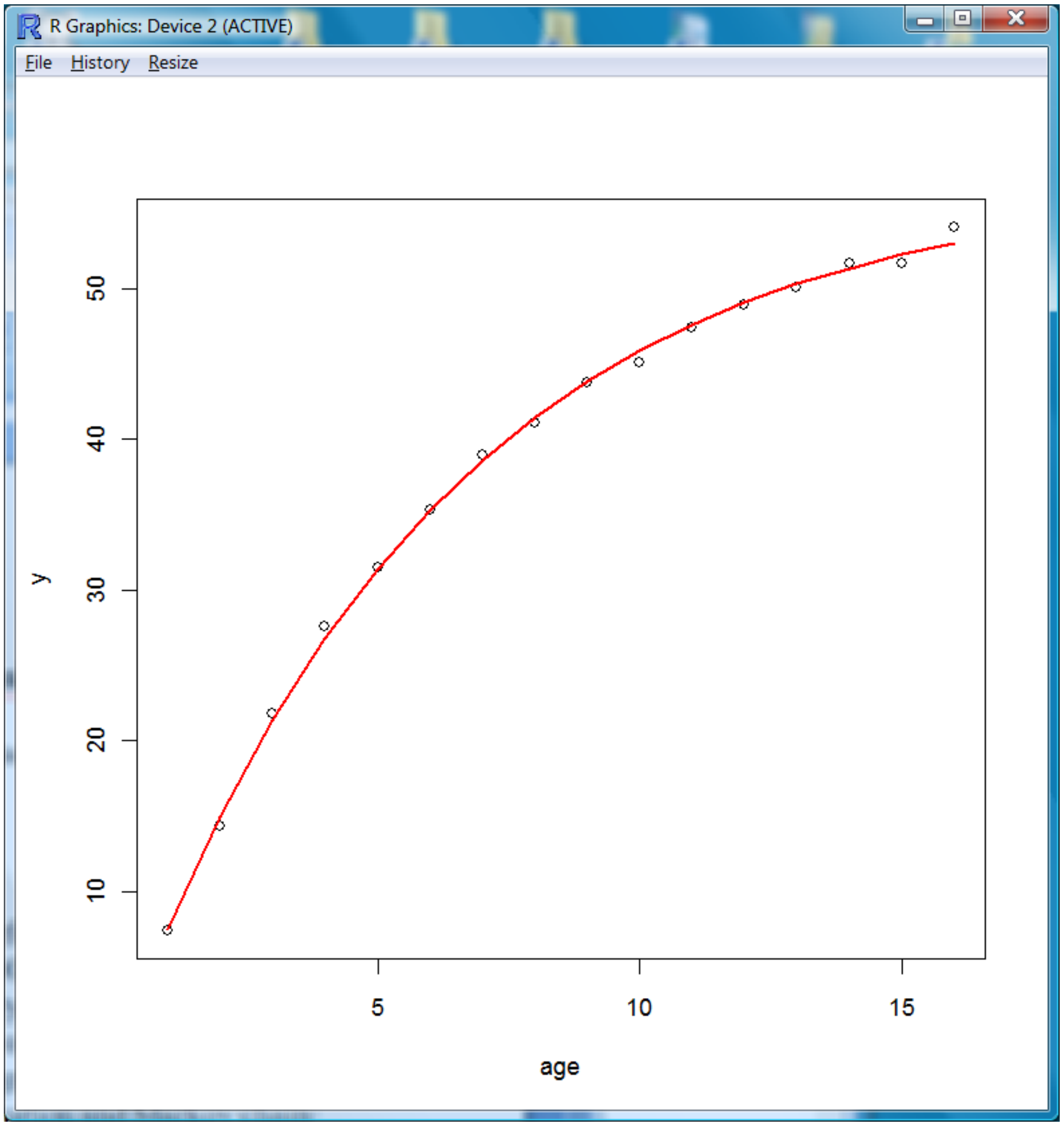


Figure 2. Plot of data points and a fitted von Bertalanffy growth curve, obtained by sourcing the R code in Table 3. The data portrayed here come entirely from the ADMB model. The source code compares these numbers with independent calculations in R.

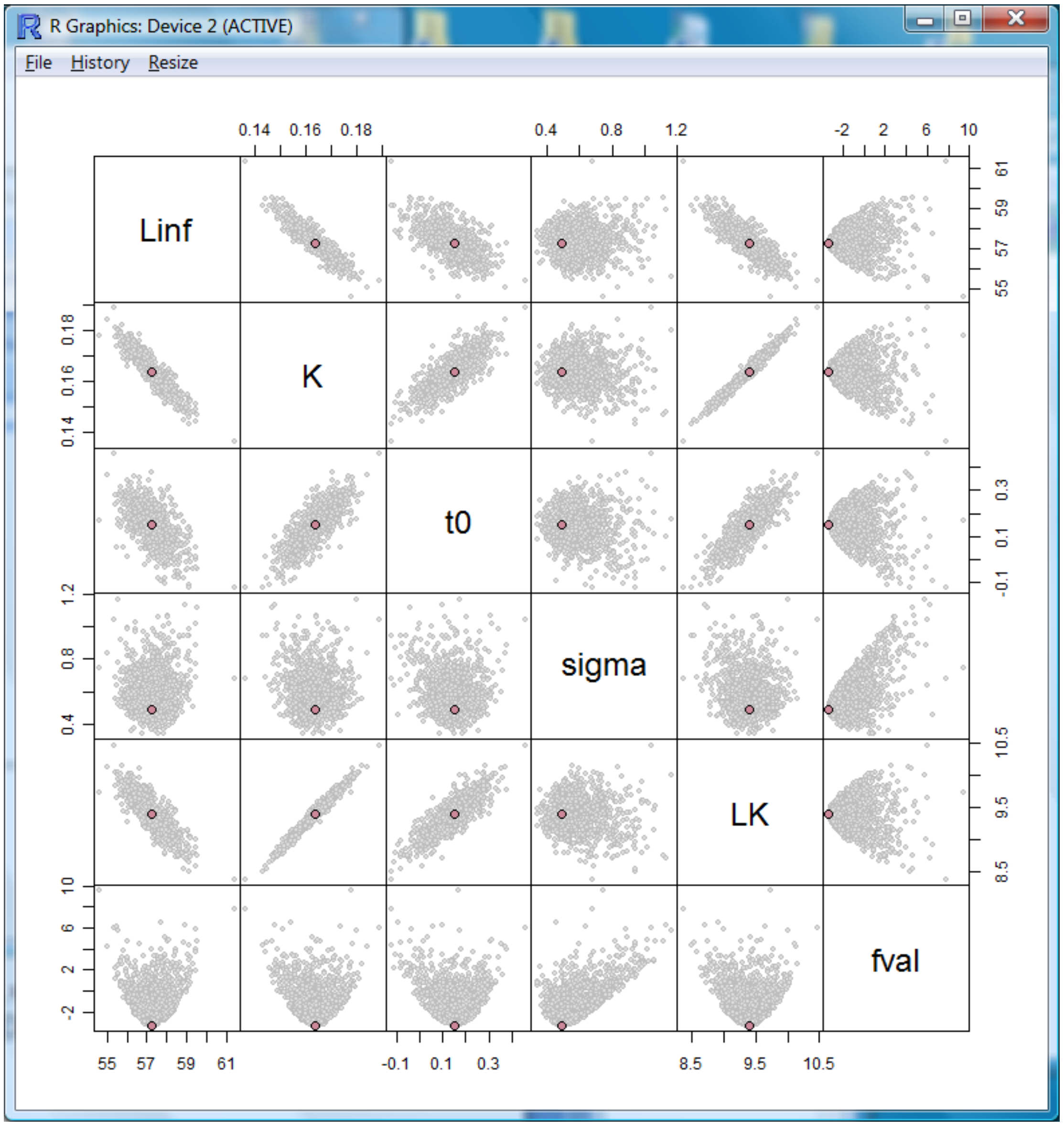


Figure 3. Scatter plot of 1,000 points from the `vonb` posterior distribution, generated by the code in `vonb.r` and the two additional commands: `runMC("vonb",100000,100); plotMC("vonb")`. The red point indicates the posterior mode, where `fval` is minimized. The variables labelled `Linf, K, t0, sigma, LK, and fval` represent L_∞, K, t_0, σ, the product $L_\infty K$, and ℓ, respectively.

Appendix A. Installing `PBSadmb`

As for most R packages, installation of `PBSadmb` is fairly easy. Unfortunately, this one requires other software as well, so please be patient while going through all the required steps. Essentially, you need to install R, `PBSmodelling`, `PBSadmb`, a C/C++ compiler (which normally comes installed on a Unix platform), and a text editor suitable for writing templates and viewing reports. Then you need to run R, load PBSadmb, and give it some configuration information. At this point, you should have a working version of the interface in Figure 1. Here are the details.

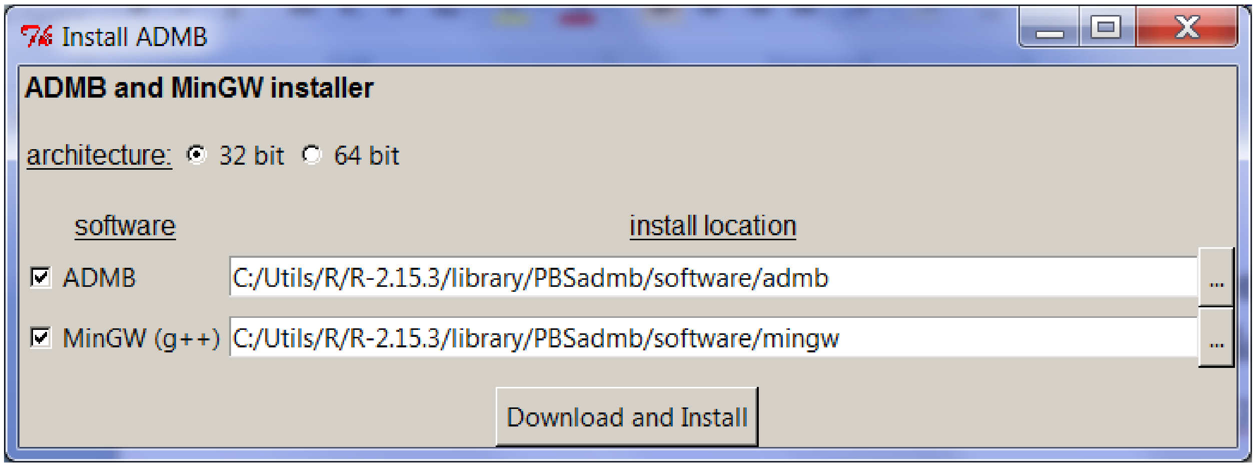
Step 1. Install the current version of R for your operating system from a package manager or the CRAN web site http://cran.r-project.org/. For fast downloads, choose a mirror near you. We assume that you have enough familiarity with R to do this without difficulty. If you have a version of R already installed, update it to the current version (R 2.15.3 at the time of revising this report) if necessary.

Step 2. Run R and install current versions of the packages PBSmodelling and PBSadmb. Ideally, both of these should be available on CRAN, but we also plan to keep current versions of Windows binary (*.zip) and package source (*.tar.gz) files on our web sites:

http://code.google.com/p/pbs-modelling/ for PBSmodelling,
http://code.google.com/p/pbs-admb/ for PBSadmb.

In Windows, you can install packages from the R GUI, but on all systems you can use the command install.packages().

Step 3 (Windows). Next you need to install a suitable C++ compiler for Windows, along with a corresponding version of the ADMB package. In the current implementation of PBSadmb, we make this step easy by using the GUI (Figure 1, Setup tab). Select the menu item Install and then the (only available) choice ADMB and MinGW for Windows. This gives the interactive window shown below, where the default paths for these two packages lie in the software directory of the R library for PBSadmb. You can choose other directories with the "..." buttons.



software	install location
✓ ADMB	C:/Utils/R/R-2.15.3/library/PBSadmb/software/admb
✓ MinGW (g++)	C:/Utils/R/R-2.15.3/library/PBSadmb/software/mingw

The files used for this installation are archived on our Google code site at http://code.google.com/p/pbs-admb/downloads/list, as referenced in the file versions.txt.

Please note that we do not support other compilers such as those by Borland or Microsoft. Users interested in such a compiler need to ensure that it is properly installed, along with corresponding version of ADMB. Correct paths must also be specified in the configuration file (by default ADopts.txt).

Step 3 (Linux or MacOS X). If you have a Unix system, hopefully you already have compiler support for C/C++. To check this, open a bash terminal window and type

```
g++ --version
```

Hopefully, you'll see a result like

```
g++ (Ubuntu 4.3.3-5ubuntu4) 4.3.3
```

You also need to know where the executable `g++` is located. On our Ubuntu system, it's in the directory `/usr/bin/`, but you may to go to the root directory (`cd /`) and run a command (`whereis g++`) to find the path.

You also need to obtain ADMB for your system. Start at the "Downloads" page: http://www.admb-project.org/downloads and look for support for your operating system. The most reliable method will probably come from downloading the full source distribution and following the instructions to build and install the package from source. That way, you guarantee that the binary version of ADMB matches the compiler on your system. You also need to find the path to the installed version of ADMB.

Step 4. Obtain a good text editor that you can use for code development. On Windows, the Notepad will work, but much better options are available. Currently, we recommend Notepad++, available free at http://notepad-plus-plus.org/. Other colleagues have used the Crimson Editor (http://www.crimsoneditor.com/) or Tinn-R (http://www.sciviews.org/Tinn-R/). Ideally, use an editor that supports syntax highlighting and displays multiple files in a single window, with tabs to select among them.

On Linux systems, `gedit` seems to work reasonably well. In Mac OS X, you might consider using `TextWrangler` available free at http://www.barebones.com/products/textwrangler/download.html.

Step 6. Run R in an empty working directory. Then type these two commands into the R console:

```
> require(PBSadmb)
> admb()
```

The GUI should appear at the `Setup` tab, probably with a red field **`Fix`** and a warning message about missing files. You can use the GUI to set the three required paths, always using the Unix syntax in which the forward slash `/` (rather than the Windows backslash `\`) separates subdirectories.

- The "ADM path" should refer to the directory with the installed ADMB binary version. Typically it includes a few files (such as `LICENSE` and `README`.txt) and several subdirectories, including `bin`, `include`, and `lib`.
- The "GCC Path" should be the path discussed in Step 3. It should include a `bin` subdirectory with the file `g++.exe`.
- The "Editor" should be the complete path to executable file for the editor chosen in Step 4, such as `C:/Utils/Npp/notepad++.exe`.

You can use the buttons labelled “>” to navigate to the appropriate directories or files.

Step 7. Click the **`Apply`** button. If everything is OK, the red **`Fix`** should be replaced by a green **`OK`**. If **`Fix`** persists, then something essential can’t be found on the paths you’ve specified. Either you haven’t installed something correctly, or one of the paths is wrong.

When everything is **`OK`**, click **`Save`** to save your options in a text file in your current working directory, with the default name `ADopts.txt`. You can inspect it with the text editor. Potentially, you can have multiple options files that point to different text editors or different compilers (e.g., 32 bit or 64 bit).

In the future, when you issue the R command `admb()` with this working directory, the file `Adopts.txt` will automatically determine the paths in the GUI. Furthermore, you can copy this file to any other directory from which you want to use `PBSadmb`. Conceivably, you might use different option files for projects in different directories.

Appendix B. ADMB scripts

As we have discussed, ADMB involves the three basic operations `convAD`, `compAD`, and `linkAD` to convert, compile, and link a template file. These are implemented in ADMB with scripts written as `batch` files for Windows or `bash` files for Unix. The scripts generally have the file prefix as an argument, along with other arguments that determine compilation options like safe or optimized code. The `Make` tab of the `PBSadmb` GUI has radio buttons that support four binary alternatives – safe or optimized code, normal or random effects model, create `.exe` or `.dll`, and include debugging symbols or not.

Appendix C. Detailed `PBSadmb` documentation

C.1. Functions in ADMB

The list of functions in this section comes from the `PBSmodelling` command

```
> viewCode("PBSadmb",output=2)
```

Function	**Description**
admb	Start the PBS ADMB GUI
appendLog	Append Data to Log File
checkADopts	Check ADMB Options for Link Integrity
cleanAD	Clean ADMB-Generated Files from the Working Directory
compAD	Compile C Code
convAD	Convert TPL Code to CPP Code
convOS	Convert Text Files to Default OS Format
copyFiles	Copy System Files
editAD	Edit ADMB Files

editADfile	Edit a File
installADMB	Install windows admb binary (for gcc)
linkAD	Link Object Files to Make an Executable
makeAD	Make an Executable Binary File from a C File
makeADopts	Creates the ADMB Options List
plotMC	Plot Results of MCMC Simulation
readADopts	Reads an ADMB Options List into Memory From a File
readRep	Read an ADMB Report into R Memory
runAD	Run an Executable Binary File
runMC	Run an Executable Binary File in MCMC Mode
setADMBPath	Creates the ADMB Options List
showADargs	Show All Arguments for an ADMB Executable
startLog	Start a Log File
writeADopts	Writes the ADMB Options List from Memory to a File

C.2. `PBSadmb` manual

The following pages show the standard R manual for `PBSadmb`, including help pages for all objects, a table of contents, and an index. This manual also appears on the CRAN web site: http://cran.r-project.org/web/packages/PBSadmb/index.html. (Or from CRAN's root, locate "Packages" and find "PBSmodelling".)

For a description of the method used to generate the pages that follow, see Appendix D.2 of the *PBSmodelling User's Guide* included with `PBSmodelling`.

Package ‘PBSadmb’

May 13, 2013

Version 0.65

Date 2013-05-06

Title ADMB for R Using Scripts or GUI

Author Jon T. Schnute, Rowan Haigh, Alex Couture-Beil

Maintainer Jon T. Schnute <`schnutej-dfo@shaw.ca`>

Depends R (>= 2.15.0), methods, tcltk, PBSmodelling (>= 2.65)

Description R Support for ADMB (Automatic Differentiation Model Builder)

License GPL (>=2)

URL `http://code.google.com/p/pbs-admb/`

R topics documented:

`admb` *Start the PBS ADMB GUI*

Description

Start up the PBS GUI for running ADMB.

Usage

```
admb(prefix="", wdf="admbWin.txt", optfile="ADopts.txt")
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).
`wdf`	string name of the *window description file* that creates the GUI.
`optfile`	string name of options file (usually in user's working directory).

Author(s)

Rowan Haigh, Pacific Biological Station, Nanaimo BC, Canada

See Also

`makeADopts`

`appendLog` *Append Data to Log File*

Description

Append summary information or output to a previously created log file.

Usage

```
appendLog(prefix, lines)
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).
`lines`	data to append to `'prefix'.log`).

Value

No explicit value reurned. Appends data into a log file `'prefix'.log`.

Note

A wrapper function that can be called from a GUI exists as `.win.appendLog`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`startLog`, `editADfile`

`atget` *Get/Print Objects From or Put Objects Into Temporary Work Environment*

Description

These functions are wrappers to the PBSmodelling accessor functions that get/print objects from or put objects into a temporary work environment, in this case `.PBSadmbEnv`. Working objects include `PBSadmb`, which acts as a storage object for some of the functions, and `.PBSadmb`, which controls the options for the user's project.

Usage

```
atget(...)
atcall(...)
atprint(...)
atput(...)
alisp(...)
```

Arguments

`...`	For `atget` through to `atput`, the only free argument is: `x` – name (with or without quotes) of an object to retrieve or store in the temporary environment; cannot be represented by a variable. Fixed arguments: `penv = parent.frame(), tenv = .PBSadmbEnv` See `tget` for additional information. For `alisp`, there is only one fixed argument: `pos = .PBSadmbEnv` All other arguments are available – see `lisp`

Details

These accessor functions were developed as a response to the CRAN repository policy statement: "Packages should not modify the global environment (user's workspace)."

Value

Objects are retrieved from or sent to the temporary working environment to/from the place where the function(s) are called. Additionally, `atcall` invisibly returns the object without transferring, which is useful when the object is a function that the user may wish to call, for example, `atcall(myfunc)()`, or as arguments in other functions.

Note

Additional wrapper functions to access functions in `.PBSadmbEnv` are named with the prefix `.win` (none at the moment).

Author(s)

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

References

CRAN Repository Policy: `http://cran.r-project.org/web/packages/policies.html`

See Also

`tget` and `lisp` in **PBSmodelling**

`checkADopts` *Check ADMB Options for Link Integrity*

Description

Check that `.ADopts` has all required components and that links point to actual files on the hard drive.

Usage

```
checkADopts(opts=getOptions(atcall(.PBSadmb)),
   check=c("admbpath","gccpath","editor"), warn=TRUE, popup=FALSE)
```

Arguments

`opts`	ADMB options values.
`check`	components of `.ADopts` to check.
`warn`	logical: if `TRUE`, print the results of the check to the R console.
`popup`	logical: if `TRUE`, display program location problems in a popup GUI.

Value

Boolean value where `TRUE` indicates all programs were located in the specified directories and `FALSE` if at least one program cannot be found. The returned Boolean scalar has two attributes:
`warn` - named list of test results, and
`message` - named vector of test results.

Note

A wrapper function that can be called from a GUI exists as `.win.checkADopts`.

Author(s)

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

See Also

`makeADopts`,`readADopts`

`cleanAD` *Clean ADMB-Generated Files from the Working Directory*

Description

Detects files in the working directory with the specified `prefix` and removes them all save those with the suffix `.tpl`, `.dat`, and `.pin`.

Usage

```
cleanAD(prefix)
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).

Details

Aside from potential garbage files with the specified `prefix`, other files associated with ADMB are detected. Also files `*.tmp` and `*.bak` are displayed. Calling `cleanAD` invokes the hidden function `.cleanUp`, which creates a GUI menu of the potential garbage files. The user can select whichever files s/he wishes for disposal.

Value

Returns nothing. Invokes a GUI menu of potential garbage files.

Note

A wrapper function that can be called from a GUI exists as `.win.cleanAD`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`makeAD`, `runAD`, `readRep`

`compAD` *Compile C Code*

Description

Compile C++ code in `'prefix'`.cpp to create a binary object file `'prefix'`.o.

Usage

```
compAD(prefix, raneff=FALSE, safe=TRUE, dll=FALSE, debug=FALSE, logfile=TRUE, add=TRUE, verbose=TRUE)
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).
`raneff`	logical: use the random effects model, otherwise use the normal model (currently does not influence the compile stage, but the argument is preserved here for future development).
`safe`	logical: if `TRUE`, use safe mode with bounds checking on all array objects, otherwise use optimized mode for fastest execution.
`dll`	create dll (rather than executable)
`debug`	compile with debug symbols
`logfile`	logical: if `TRUE`, create a log file of the messages from the shell call.
`add`	logical: if `TRUE`, append shell call messages to an exsiting log file.
`verbose`	logical: if `TRUE`, report the shell call an its messages to the R console.

Details

This function uses the C++ comiler declared in `.ADopts`. If `logfile=TRUE`, any errors will appear in `'prefix'.log`. If `verbose=TRUE`, they will appear in the R console.

Value

Invisibly returns the shell call and its messages.

Note

A wrapper function that can be called from a GUI exists as `.win.compAD`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`convAD`, `linkAD`, `makeAD`

`convAD` *Convert TPL Code to CPP Code*

Description

Convert code in `'prefix'.tpl` to C++ code in `'prefix'.cpp`.

Usage

```
convAD(prefix, raneff=FALSE, safe=TRUE, dll=FALSE, debug=FALSE, logfile=TRUE, add=TRUE, verbose=TRUE)
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).
`raneff`	logical: if `TRUE`, use the random effects model executable `tpl2rem.exe`, otherwise use the normal model executable `tpl2cpp.exe`.
`safe`	logical: if `TRUE`, use safe mode with bounds checking on all array objects, otherwise use optimized mode for fastest execution.
`dll`	create dll (rather than executable)
`debug`	compile with debug symbols
`logfile`	logical: if `TRUE`, create a log file of the messages from the shell call.
`add`	logical: if `TRUE`, append shell call messages to an exsiting log file.
`verbose`	logical: if `TRUE`, report the shell call an its messages to the R console.

Details

This function invokes the ADMB command `tpl2cpp.exe` or `tpl2rem.exe`, if `raneff` is `FALSE` or `TRUE` respectively. If `logfile=TRUE`, any errors will appear in `'prefix'.log`. If `verbose=TRUE`, they will appear in R console.

Value

Invisibly returns the shell call and its messages.

Note

A wrapper function that can be called from a GUI exists as `.win.convAD`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`compAD`, `linkAD`, `makeAD`

`convOS` *Convert Text Files to Default OS Format*

Description

Convert text files to the default format of the operating system.

Usage

```
convOS(inam, onam = inam, path = getwd() )
```

Arguments

`inam`	string vector of names specifying files to be converted to the format of the operating system.
`onam`	string vector of name specifying the output files (the default overwrites the input file).
`path`	string specifying the path where the input files are located (defaults to current working directory).

Value

Text file(s) formatted in accordance with standards of the operating system.

Note

This function essentially executes a `readLines` command followed by a call to `writeLines`.

Author(s)

Rowan Haigh, Pacific Biological Station, Nanaimo BC

See Also

`copyFiles`, `.addQuotes`

`copyFiles` *Copy System Files*

Description

Copy files with specified prefixes and suffixes from one location to another.

Usage

```
copyFiles(prefix, suffix=NULL, srcdir=getwd(), dstdir=getwd(), ask=TRUE)
```

Arguments

`prefix`	string scalar/vector of potential file prefixes.
`suffix`	string scalar/vector of potential file suffixes.
`srcdir`	source directory from which to copy files.
`dstdir`	destination directory to copy files to.
`ask`	logical: if `TRUE`, popup boxes will prompt the user for every instance that a file will be overwritten.

Details

This function uses R's `list.files` and `file.copy` functions. The pattern recognition tends not to work when given the wildcard character `*`; however, the user may use this character, and the code will interpret it.

Value

Invisibly returns a Boolean vector with names of files that have been copied or not.

Author(s)

Rowan Haigh, Pacific Biological Station, Nanaimo, BC

See Also

`editAD`

editAD *Edit ADMB Files*

Description

Edit files associated with specified prefix and suffixes.

Usage

```
editAD(prefix, suffix=c(".tpl",".cpp",".log"))
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).
`suffix`	string scalar/vector specifying one or more suffixes.

Value

Invisibly returns Boolean vector with elements `TRUE` if files exist, `FALSE` if they do not.

Note

A wrapper function that can be called from a GUI exists as `.win.editAD`.

This function explicitly uses the editor chosen for PBSadmb. PBSmodelling has another function `openFile` that uses Windows file associations or an application specified with `setPBSext`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`editADfile`, `makeADopts`

editADfile *Edit a File*

Description

Edit a file using the text editor specified in `.ADopts`.

Usage

```
editADfile(fname)
```

Arguments

`fname`	string name of file in current working directory (or elsewhere if path delimited by `/` or `\`).

Value

Returns Boolean: `TRUE` if file exists, `FALSE` if it does not.

Note

This function explicitly uses the editor chosen for PBSadmb. PBSmodelling has another function `openFile` that uses Windows file associations or an application specified with `setPBSext`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`editAD`, `makeADopts`

`installADMB` *Install windows ADMB and MinGW binaries*

Description

Only applicable for Windows: Downloads and installs the windows ADMB and MinGW binaries.

A user interface is displayed which allows to select to install either ADMB and/or MinGW for either 32bit or 64bit versions of Windows. Default installation directories are suggested for installation; however, a user may choose to install the binaries elsewhere.

A file "pathconfig.txt" is saved in the PBSadmb library (under R), which keeps track of the most recently installed locations.

Usage

```
installADMB()
```

`linkAD` *Link Object Files to Make an Executable*

Description

Links the binary object file `'prefix'.o` to the ADMB libraries and produces the executable file `'prefix'.exe`.

Usage

```
linkAD(prefix, raneff=FALSE, safe=TRUE, dll=FALSE, debug=FALSE, logfile=TRUE, add=TRUE, verbose=TRUE)
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).
`raneff`	logical: use the random effects model, otherwise use the normal model.
`safe`	logical: if `TRUE`, use safe mode with bounds checking on all array objects, otherwise use optimized mode for fastest execution.
`dll`	create dll (rather than executable)
`debug`	compile with debug symbols
`logfile`	logical: if `TRUE`, create a log file of the messages from the shell call.
`add`	logical: if `TRUE`, append shell call messages to an exsiting log file.
`verbose`	logical: if `TRUE`, report the shell call an its messages to the R console.

Details

This function uses the C++ comiler declared in `.ADopts`. If `logfile=TRUE`, any errors will appear in `'prefix'.log`. If `verbose=TRUE`, they will appear in the R console.

Value

Invisibly returns the shell call and its messages.

Note

A wrapper function that can be called from a GUI exists as `.win.linkAD`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`convAD`, `compAD`, `makeAD`

`makeAD` *Make an Executable Binary File from a C File*

Description

Essentially a wrapper function that calls in sequence: `convAD`, `compAD`, and `linkAD`.

Usage

```
makeAD(prefix, raneff=FALSE, safe=TRUE, dll=FALSE, debug=FALSE, logfile=TRUE, add=TRUE, verbose=TRUE)
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).
`raneff`	logical: use the random effects model, otherwise use the normal model.
`safe`	logical: if `TRUE`, use safe mode with bounds checking on all array objects, otherwise use optimized mode for fastest execution.
`dll`	create dll (rather than executable)
`debug`	compile with debug symbols
`logfile`	logical: if `TRUE`, create a log file of the messages from the shell call.
`add`	logical: if `TRUE`, append shell call messages to an exsiting log file.
`verbose`	logical: if `TRUE`, report the shell call an its messages to the R console.

Details

This function uses the C++ comiler declared in `.ADopts`. If `logfile=TRUE`, any errors will appear in `'prefix'.log`. If `verbose=TRUE`, they will appear in the R console.

Value

Returns nothing. The three functions called by `makeAD` each return the shell call and its messages.

Note

A wrapper function that can be called from a GUI exists as `.win.makeAD`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`convAD`, `compAD`, `linkAD`, `cleanAD`

`makeADopts` *Creates the ADMB Options List*

Description

Creates a global list object detailing the pathways to the ADMB directory, the GCC bin, and the user's preferred text editor.

Usage

```
makeADopts(admbpath, gccpath, editor)
```

Arguments

`admbpath`	explicit path to the user's ADMB directory.
`gccpath`	explicit path to the user's GCC bin (C-compiler) directory.
`editor`	explicit path and program to use for editing text.

Value

Creates a global, hidden list object called `.ADopts`.

Note

A wrapper function that can be called from a GUI exists as `.win.makeADopts`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`makeADopts`, `writeADopts`

plotMC *Plot Results of MCMC Simulation*

Description

Plot results of an ADMB MCMC simulation using various plot methods.

Usage

```
plotMC(prefix, act="pairs", pthin=1, useCols=NULL)
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).
`act`	string scalar: action describing plot type (current choices: `"pairs"`, `"eggs"`, `"acf"`, `"trace"`, and `"dens"`).
`pthin`	numeric scalar indicating interval at which to collect records from the `.mc.dat` file for plotting.
`useCols`	logical vector indicating which columns of `.mc.dat` to plot.

Note

A wrapper function that can be called from a GUI exists as `.win.plotMC`. Use the PBSadmb GUI to explore these plots easily.

Author(s)

Rowan Haigh, Pacific Biological Station, Nanaimo BC, Canada

See Also

`runMC`, `showADargs`

readADopts *Reads an ADMB Options List into Memory From a File*

Description

Reads ADMB options into a global, hidden list object called `.ADopts` from an ASCII text file using `PBSmodelling::readList`).

Usage

```
readADopts(optfile="ADopts.txt")
```

Arguments

`optfile`	string name of an ASCII text file containing ADMB options information.

Value

No values returned. Reads the ADMB options into the list object `.ADopts`.

Note

A wrapper function that can be called from a GUI exists as `.win.readADopts`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`makeADopts`,`writeADopts`

`readRep` *Read an ADMB Report into R Memory*

Description

Import ADMB-generated report files into R's memory using the names of the report files to name the R-objects.

Usage

```
readRep(prefix, suffix=c(".cor",".rep",".std",".mc.dat"), global=FALSE)
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).
`suffix`	string scalar/vector specifying one or more suffixes.
`global`	logical: if `TRUE`, save the imported reports as objects to global environment using the same names as the report files.

Details

If the report object is one of `c(".cor", ".std", ".mc.dat")`, the report object is a data frame, otherwise it is a string vector. Multiple report objects are returned as a list of objects. A single report object is returned as the object itself.

This function attempts to detect the file format from a number of possibilities. For example, if the file has the special format recognized by PBSmodelling, then the function returns a list with named components. The example `vonb` included with this package shows how to write the template to get consistent variable names between ADMB and R. See the User's Guide for complete details.

Value

Invisibly returns the list of report objects. If only one report is imported, a single report object is returned.

Note

A wrapper function that can be called from a GUI exists as `.win.readRep`.

Author(s)

Rowan Haigh, Pacific Biological Station, Nanaimo BC, Canada

See Also

`editADfile`, `.win.viewRep`

`runAD` *Run an Executable Binary File*

Description

Run the executable binary file `'prefix'.exe` that was created by `makeAD`.

Usage

```
runAD(prefix, argvec="", logfile=TRUE, add=TRUE, verbose=TRUE)
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).
`argvec`	string scalar/vector of arguments appropriate for the executable `'prefix'.exe`.
`logfile`	logical: if `TRUE`, create a log file of the messages from the shell call.
`add`	logical: if `TRUE`, append shell call messages to an exsiting log file.
`verbose`	logical: if `TRUE`, report the shell call an its messages to the R console.

Details

This function typically reads the two files `'prefix'.dat` and `'prefix'.pin`, although in same cases one or both of these files may not be necessary.

If `logfile=TRUE`, output (including error messages, if any) will appear in `'prefix'.log`. If `verbose=TRUE`, it will appear in the R console.

Value

Invisibly returns the results of the shell call.

Note

A wrapper function that can be called from a GUI exists as `.win.runAD`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`runMC`, `makeAD`, `cleanAD`

runMC — *Run an Executable Binary File in MCMC Mode*

Description

Run the executable binary file `'prefix'.exe`, created by `makeAD`, to generate MCMC simulations.

Usage

```
runMC(prefix, nsims=2000, nthin=20, outsuff=".mc.dat",
      logfile=FALSE, add=TRUE, verbose=TRUE)
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).
`nsims`	numeric scalar indicating number of MCMC simulations to perform.
`nthin`	numeric scalar indicating the sampling rate or thinning of the `nsims` MCMC simulations to report.
`outsuff`	string name suffix of the MCMC output data file.
`logfile`	logical: if `TRUE`, create a log file of the messages from the shell call.
`add`	logical: if `TRUE`, append shell call messages to an exsiting log file.
`verbose`	logical: if `TRUE`, report the shell call an its messages to the R console.

Details

This function runs `'prefix'.exe` twice, first with the arguments `-mcmc 'nsims' -mcsave 'nthin'` and second with the argument `-mceval`. By default, output goes to the file `'prefix'.mc.dat`, although a user can specify a different output suffix.

To see this function in action, use the PBSadmb GUI with the example `vonb` or `simpleMC`.

Value

Invisibly returns the results of the shell call.

Note

A wrapper function that can be called from a GUI exists as `.win.runMC`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`runAD`, `makeAD`, `cleanAD`

`setADMBPath` *Creates the ADMB Options List*

Description

Creates a global list object detailing the pathways to the ADMB directory, the GCC bin, and the user's preferred text editor.

Usage

```
setADMBPath(admbpath, gccpath, editor)
```

Arguments

`admbpath`	explicit path to the user's ADMB directory.
`gccpath`	explicit path to the user's GCC bin (C-compiler) directory.
`editor`	explicit path and program to use for editing text.

Value

Creates a global, hidden list object called `.ADopts`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`makeADopts`, `writeADopts`

`showADargs` *Show All Arguments for an ADMB Executable*

Description

Show all arguments available for an ADMB executable in the default text editor.

Usage

```
showADargs(prefix, ed=TRUE)
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).
`ed`	logical: if `TRUE`, write the ADMB arguments to a file and view them with the text editor, else display the arguments on the R console.

Value

Invisibly returns the argument list.

Note

A wrapper function that can be called from a GUI exists as `.win.showADargs`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`editADfile`, `runAD`

`startLog` *Start a Log File*

Description

Start a log file by removing any previous version and appending header information.

Usage

```
startLog(prefix)
```

Arguments

`prefix`	string name prefix of the ADMB project (e.g., `"vonb"`).

Value

No explicit value reurned. Writes header lines into a log file `'prefix'.log`.

Note

A wrapper function that can be called from a GUI exists as `.win.startLog`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`appendLog`, `editADfile`

`writeADopts` *Writes the ADMB Options List from Memory to a File*

Description

Writes the global ADMB options list to a file in 'PBS' format (see `PBSmodelling::writeList`).

Usage

```
writeADopts(optfile="ADopts.txt")
```

Arguments

`optfile`	string name of the intended output file.

Value

Returns `opts` invisibly. Writes the options list object to an ASCII file.

Note

A wrapper function that can be called from a GUI exists as `.win.writeADopts`.

Author(s)

Jon T. Schnute, Pacific Biological Station, Nanaimo BC, Canada

See Also

`makeADopts`, `readADopts`

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