

Introduction to PBSadmb

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

November 9, 2023

What is PBSadmb?

The R package **PBSadmb** gives complete R support to the external program AD Model Builder (**ADMB**) released into the public domain in 2009. ADMB offers users a remarkably efficient tool for estimating parameters and their uncertainty, based on complex nonlinear statistical models.

Installation instructions for ADMB can be found at:

Windows – <http://www.admb-project.org/downloads/admb-12.0/QuickStartWindows.html>

MacOS – <http://www.admb-project.org/downloads/admb-12.0/QuickStartMacOS.html>

Linux – <http://www.admb-project.org/downloads/admb-12.0/QuickStartUnix.html>

Detailed guidance on building ADMB from source in Windows is supplied in the **PBSadmb** package: `./library/PBSadmb/doc/ADMB-IG.pdf`. However, these instructions have not been tested for a number of years and may no longer work.

In a standard ADMB installation, users would interact with the program via a DOS command shell (in Windows) or a bash shell (in Linux or MacOS X). The package **PBSadmb** makes it possible to interact entirely from an R console, as a common interface for all operating systems. A single R script can encapsulate commands to ADMB, as well as all analyses that follow. The package includes protocols for writing code to make the integration between R and ADMB almost seamless.

PBSadmb also provides a Graphical User Interface (GUI) that facilitates the steps required for a complete ADMB analysis. Both new and experienced users can use the GUI for tutorial and educational purposes.

You can obtain **PBSadmb** from the Comprehensive R Archive Network (**CRAN**). Always use the current version of **PBSadmb** with the most recent version of **PBSmodelling**, another package available from CRAN. The **GitHub** web site features the most recent revisions to **PBSadmb**, including tagged versions of the package.

PBSadmb represents just one of a series of R packages developed at the Pacific Biological Station (PBS). For further information about the series, see **PBS Software** on GitHub.

What is PBS?

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.

Where is the User's Guide?

The R directory `./library/PBSadmb/doc` includes a complete User's Guide `PBSadmb-UG.pdf`. To use this package effectively, please consult the Guide. Note: once **PBSadmb** has been loaded, you can access the UG from the R console using a **PBSmodelling** function: `openUG("PBSadmb")`.

Reference

Fournier, D.A., Skaug, H.J., Ancheta, J., Ianelli, J., Magnusson, A., Maunder, M.N., Nielsen, A., and Sibert, J. (2012). AD Model Builder: using automatic differentiation for statistical inference of highly parameterized complex nonlinear models. *Optim. Methods Softw.* **27**:233-249.

Schnute, J.T., Couture-Beil, A., Haigh, R., and Kronlund, A.R. (2013) `PBSmodelling 2.65`: user's guide revised from *Canadian Technical Report of Fisheries and Aquatic Sciences* **2674**: viii + 194 p. Last updated Mar 28, 2013.