PBSplankton: User's Guide

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What is PBSplankton?

PBSplankton provides an R interface for algorithms used in biological (and fisheries) oceanography. The scope of this package is by no means comprehensive. Many of the functions provide a quick way to visualize data, and in some cases perform preliminary analyses. Though oriented to users at the Pacific Biological Station (PBS), these functions may prove to be useful to users at other locales. The User's Guide is organised into sections that loosely classify the functions by theme – (1) Utility, (2) Temporal, and (3) Satellite. Within each section, the functions are described alphabetically.

Additional functions geared toward fisheries can be found in the package **PBStools**, upon which **PBSplankton** depends. In turn, **PBStools** depends heavily on two other R packages: **PBSmapping** (Schnute *et al.*, 2004; Boers *et al.*, 2004) and **PBSmodelling** (Schnute *et al.*, 2006). **PBSplankton** has a dedicated temporary working environment called `.PBSptonEnv`. Accessor functions called `ptget`, `ptcall`, and `ptprint` enable the user to get, call, and print objects from the `.PBSptonEnv` environment, while `ptput` puts (writes) objects to `.PBSptonEnv`.

What is PBS?

The Pacific Biological Station is the oldest fisheries research centre on Canada's Pacific coast and forms part of a network of nine major scientific facilities operated by Fisheries and Oceans Canada. Located in Nanaimo, British Columbia, the Station is home to scientists, technicians, support staff and ships' crews whose common interests are the coastal waters of British Columbia, the Northeast Pacific Ocean, the Western Arctic and navigable waters east to the Manitoba, Saskatchewan border.

PBS was established in 1908 and is the principal centre for fisheries research on Canada's west coast. There are some 22 structures on the site including a four-story office/wet lab building, specialty storage structures for hazardous chemicals and salt water pumping facilities. PBS maintains a number of workshops for research support. There is a wharf used for loading, unloading, and berthage of research vessels, as well as a small boat dock for inshore research boats. PBS also maintains a library and meeting facilities. Aquatic facilities, primarily used by Aquaculture Science, include ambient temperature and heated salt water and fresh water.

Research at PBS responds to stock assessment, aquaculture, marine environment, habitat, ocean science, and fish productivity priorities. Some fisheries management activities are also conducted here.

Figure 1. Pacific Biological Station (PBS), Nanaimo BC

Datasets

phytospp

A data frame of phytoplankton species described primarily by six-letter codes (Table 1). Heterotrophic micro- and nanoplankton species also appear in the code table. Codes are those created originally by (Haigh, 1988) and only represent a small fraction of the numerous microplankton species. Information on taxonomy comes from the online databases – phytoplankton: AlgaeBase.

Table 1. Taxonomic codes for micro- and nanoplankton from coastal temperate marine waters, primarily along the coast of British Columbia.

Field	Class	Description
`code`	character	Six-letter code where typically the first three letters refer to the genus and the last three letters refer to the species. If the species is not known, then the six letters refer to the genus.
`species`	character	Species name in latin (used because no common names exist). Note that codes may refer to previously recognised taxonomic names; however, the field `species` will report the currently acceptable name.
`class`	character	Taxonomic class of the species.
`type`	character	Simplified description of class (usually without the suffix 'phyceae').
`toxin`	character	Acronym describing a potential suite of toxins (e.g., PSP).
`group`	character	General category of microplankton for summary purposes.
`gras`	logical	If `TRUE`, species is 'Generally Recognised As Safe'; potentially fallible at present.
`authority`	character	Taxonomic source description for currently accepted name.
`holotype`	logical	If `TRUE`, species is the holotype for the genus.
`basionym`	character	A previously published legitimate name-bringing or epithet-bringing synonym from which a new name is formed for a taxon of different rank or position.
`homotype`	character	Homotypic synonyms – names that have same (holo)type and same taxonomic rank.
`heterotype`	character	Heterotypic synonyms – names that have different (holo)types.
`water`	character	Habitat code (B=brackish, F=fresh, M=marine)
`sog`	logical	If `TRUE`, the species is found in the Strait of Georgia.
`bc`	logical	If `TRUE`, the species is found in British Columbia.

1 Utility functions

The utility functions described in this section (non thus far) cover a broad range of activities. The number of functions has grown over time and inevitably, some of the functions may replicate the behaviour of functions in other packages. Additionally, the utility of these functions can either decline or cease based on changes in dependent packages.

1.1 ptget, ptcall, ptprint, ptput, plisp

These functions are wrappers to the **PBSmodelling** accessor functions (`tget`, `tcall`, `tprint`, `tput`, and `lisp`) that get/print/list objects from or put objects into a temporary work environment, in this case `.PBSptonEnv`. These accessor functions were developed as a response to the CRAN repository policy statement: "Packages should not modify the global environment (user's workspace)."

2 Temporal Functions

Temporal functions help scientists see how populations change over time. Here we present a few that visualize changes in species composition and diversity for phytoplankton samples. The functions could be applied equally to any taxonomic collection. We often think of such collections as marine species portfolios. Monitoring the diversity of species portfolios can alert us to changes in an ecosystem's resilience. Haigh and Schnute (2003) explored diversity patterns for fish species composition of commercial catch tows in the longspine thornyhead (*Sebastolobus altivelis*) fishery.

2.1 boxSeason

Summarize time-dependent data using boxplots to group by a specified period pattern (Figure 2). The data file imported from a Microsoft Access table or query called `fqtName` must contain a field called either `YMD` or `Date` that depicts the date values as strings with format `YYYY-MM-DD`.

Example (boxSeason):

```
pbsfun=function(os=.Platform$OS.type, arch=.Platform$r_arch) {
  if (os=="windows" && arch=="i386")
    boxSeason(fld="S",brks="M",path=system.file("examples",package="PBSplankton"))
  else
    showMessage("Only functional for Microsoft Access on 32-bit Windows OS")
  invisible() }
pbsfun()
```

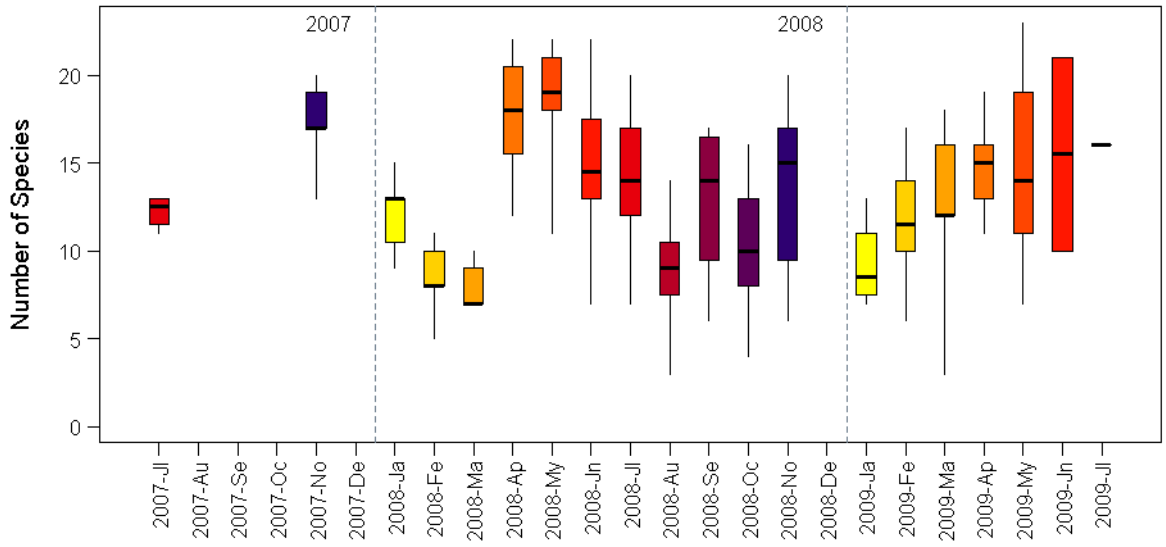

Figure 2. (*PBSplankton-boxSeason*) Number of phytoplankton species observed in samples grouped by month.

2.2 plotDiversity

Plot sample diversity (e.g., Shanon-Wiener diversity index H) as a barplot with an overlay of points using some other index (e.g., species richness S). The arguments `bars` and `pnts` can each be one of `H` = Shannon-Diversity index, `S` = species richness, or `E` = species evenness. The user can also choose to add lowess-fitted lines through the bars and the points (Figure 3).

Example (plotDiversity):

```
pbsfun=function(os=.Platform$OS.type,arch=.Platform$r_arch) {
  if (os=="windows" && arch=="i386")
    plotDiversity(bars="H",pnts="S",xnames="Batch",
      path=system.file("examples",package="PBSplankton"))
  else
    showMessage("Only functional for Microsoft Access on 32-bit Windows OS")
  invisible() }
pbsfun()
```

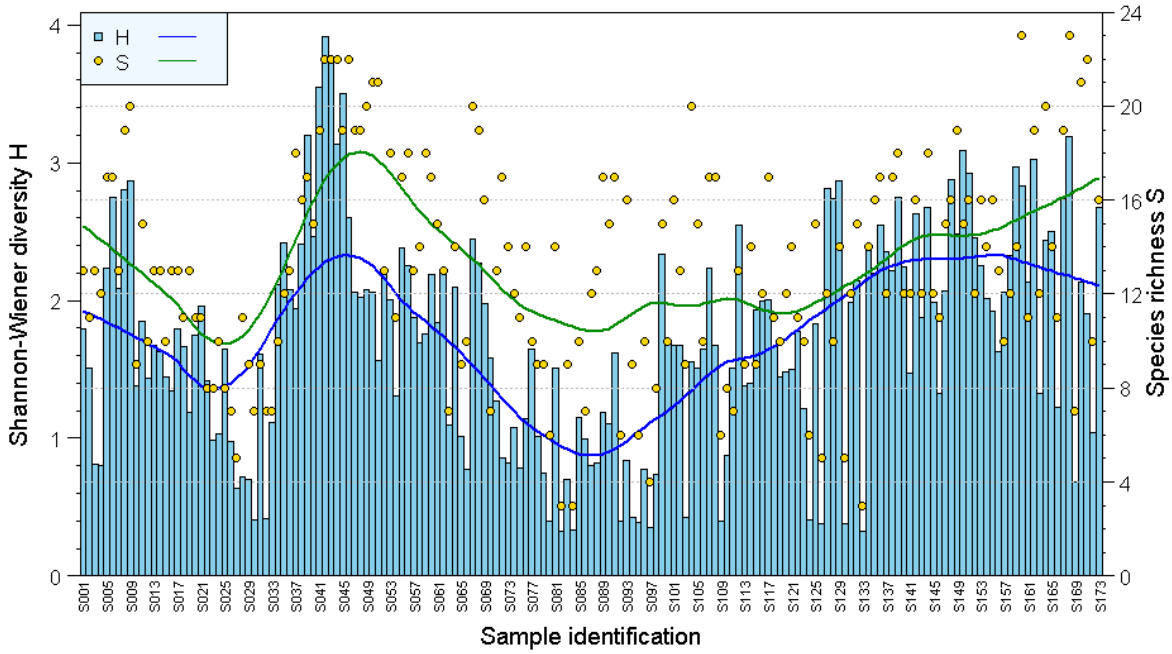

Figure 3. (*PBSplankton-plotDiversity*) Shannon-Wiener diversity index H (bars) for phytoplankton samples. Species richness S (numbers of species observed) appear as points. Smooth trend lines through H and S are calculated using the **stats** function `lowess`, which uses a locally-weighted polynomial regression.

2.3 trackComp

Track the mean composition of phytoplankton groups over time using a specified binning interval. The function creates a stacked line plot of relative composition frequencies for each group (Figure 4).

Example (trackComp):

```
pbsfun=function(os=.Platform$OS.type,arch=.Platform$r_arch) {
  if (os=="windows" && arch=="i386")
    trackComp(ndays=15,path=system.file("examples",package="PBSplankton"))
  else
    showMessage("Only functional for Microsoft Access on 32-bit Windows OS")
  invisible() }
pbsfun()
```

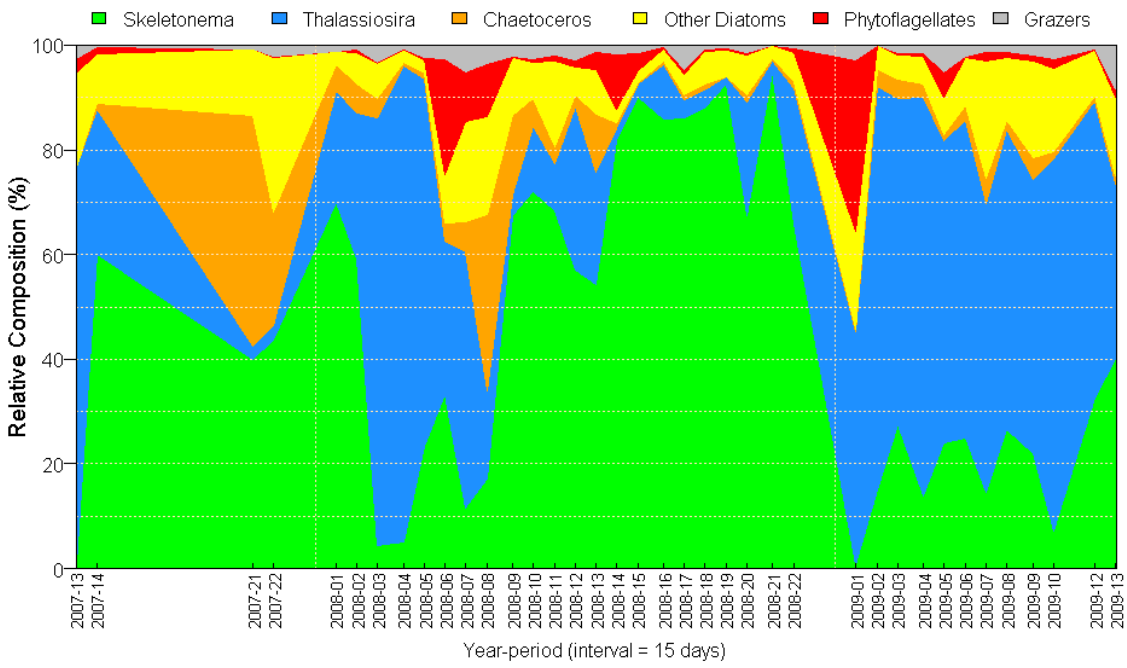

Figure 4. (*PBSplankton-trackComp*) Relative composition frequency of major phytoplankton groups in samples over time. The binning interval spans 15 days.

3 Satellite Data Functions

3.1 PBSsatellite

PBSsatellite is a collaborative effort between the Pacific Biological Station (PBS) and MacEwan University to design software that simplifies the extraction and statistical analysis of gridded satellite data. This software uses **PBSmapping**, an existing R software package, to produce plots. Additionally, users are able to produce their own functionality and data interpretation algorithms and incorporate these functions into the package's analysis methods. This provides users with a platform that simplifies the complex problem of satellite data analysis and visualization while providing the ability for personal research and method integration.

3.2 calcChloro

Contact Information

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