

PPGtk: the polyploid pop-gen toolkit

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Source code: <https://github.com/pblischak/ppgtk>

Online docs: <http://pblischak.github.io/ppgtk>

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PPGtk is a set of tools written in C++ for population genetic/genomic analyses with polyploids using high-throughput sequencing data. It was designed for research in non-model taxa (i.e., no reference genome), and provides a number of functions for conducting population genomics analyses in these taxa.

1 Installation

Installing PPGtk follows the typical workflow for Unix-based operating systems using a Makefile and the commands ‘make && sudo make install’.

1.1 Obtaining PPGtk

A “bleeding edge” version of the source code for PPGtk can be cloned from GitHub using:

```
$ git clone https://github.com/pblischak/ppgtk.git
```

from the command line. You can also download the latest stable release from GitHub by following the **releases** link in the PPGtk repository.

```
$ cd ppgtk-v1.0.0
```

```
[R]> dat <- read.table("tot-reads.txt")
```

1.2 Boost C++ Libraries

1.3 OpenMP

can be used for parallelization.

1.4 Compiling the executable

To enable parallelization with OpenMP, you will need to change the OPENMP variable in the Makefile to yes, like so:

```
OPENMP ?= yes
```

If you installed Boost in /usr/local/bin, then the paths to the header files and libraries should already be correctly specified in the Makefile. If you installed it somewhere else, then you will need to change the BOOST_LIB and BOOST_INC variables to point to where it was installed.

If you are on a Mac, type:

```
$ make darwin
```

If you are on a Linux computer, type:

```
$ make linux
```

2 Getting Started

```
$ ppgtk -n 100 -l 2000 -p 4 -t total.txt -r reference.txt -q
```

total.txt:

24 39 12 0 63 0 33 45 . . .
20 33 21 0 0 78 27 11 . . .
.
.
.
7 4 80 22 26 22 18 4 . . .