

# *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 analyzing high-throughput sequencing data in polyploids. It was designed for research in non-model polyploids (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)

### 1.3 OpenMP

(2)

### 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 . . .

## References

- [1] Boost C++ Library (v1.59.0) – <http://boost.org/>.
- [2] OpenMP – <http://openmp.org/>.