

To perform statistic analysis we'll use [PLINK/SEQ](#), which accdcepts VCF files. It is similar in lexic to [PLINK](#), traditionally used for GWAS data.

As today (March, 2015) there are some features of PLINK/SEQ which do not perform perfect, such as its [R library](#), because they say they are developing a beta version to be released "soon". However, there is a [basic tutorial](#), and a [extended tutorial](#) which are sufficient to allow you to play around with your data, get basic statistics and analysis.

From:

<https://cortafuegos.fundacioace.com/wiki/> - **Detritus Wiki**

Permanent link:

https://cortafuegos.fundacioace.com/wiki/doku.php?id=genetica:stats_process

Last update: **2020/08/04 10:58**

