

Guide for xerxes v1.0.1.0

Contents

| | | |
|----------|--|----------|
| 1 | Installation | 1 |
| 2 | Fstats command | 1 |
| 2.1 | Allowed statistics | 3 |
| 2.2 | Defining statistics directly via <code>--stat</code> | 4 |
| 2.3 | Defining statistics in a simple text file | 4 |
| 2.4 | Input via a configuration file | 4 |
| 2.4.1 | Group Definitions | 5 |
| 2.4.2 | Statistic input using YAML | 5 |
| 2.4.3 | Ascertainment (experimental feature) | 5 |
| 2.5 | Output | 6 |
| 2.6 | Degenerate statistics | 6 |
| 2.7 | Ploidy and illegal cases | 6 |
| 2.8 | Whitepaper | 7 |
| 3 | RAS (in development) | 7 |

1 Installation

See the Poseidon website (<https://www.poseidon-adna.org/#/xerxes>) or the GitHub repository (<https://github.com/poseidon-framework/poseidon-analysis-hs>) for up-to-date installation instructions.

2 Fstats command

Xerxes allows you to analyse genotype data across Poseidon packages, including your own, as explained above by “hooking” in your own package via a `--baseDir` (or `-d`) parameter. This has the advantage that you can compute arbitrary F-Statistics across groups and individuals distributed in many packages, without the need to explicitly merge the data first. Xerxes also takes care of merging PLINK and EIGENSTRAT data on the fly. It also takes care of different genotype base sets, like Human-Origins vs. 1240K. It also flips alleles automatically across genotype files, and throws an error if the alleles in different packages are incongruent with each other. Xerxes is also smart enough to select only the packages relevant for the statistics that you need, and then streams through only those genotype data.

Here is an example command for computing several F-Statistics:

```
xerxes fstats -d ... -d ... \
  --stat "F4(<Chimp.REF>, <Altai_published.DG>, Yoruba, French)" \
  --stat "F3(<Chimp.REF>, <Altai_snpAD.DG>, Spanish)" \
  --statFile fstats.txt
  --statConfig fstats.yaml
  -f outputfile.txt
```

31 First, the two options `-d ...` exemplify that you need to provide at least one base directory for Poseidon
 32 packages, but can also give multiple. Second, F-Statistics can be entered in three different ways:

- 33 1. Directly via the command line using `--stat`.
- 34 2. Using a simple text file using `--statFile`
- 35 3. Using a powerful configuration file that allows more options.

36 These three input ways can be mixed and matched, and given multiple times. They are explained below.

37 Last, option `-f` can be used to write the output table into a tab-separated text file, beyond just printing a table
 38 into the standard out when the program finishes. Note that there are more options, which you can view using
 39 `xerxes fstats --help`:

```
Usage: xerxes fstats (-d|--baseDir DIR) [-j|--jackknife ARG]
      [-e|--excludeChroms ARG]
      (--stat ARG | --statConfig ARG | --statFile ARG)
      [--noTransitions] [-f|--tableOutFile ARG]
      [--blockTableFile ARG]
```

Compute f-statistics on groups and individuals within and across Poseidon packages

Available options:

| | |
|-------------------------------------|--|
| <code>-h,--help</code> | Show this help text |
| <code>-d,--baseDir DIR</code> | A base directory to search for Poseidon packages. |
| <code>-j,--jackknife ARG</code> | Jackknife setting. If given an integer number, this defines the block size in SNPs. Set to "CHR" if you want jackknife blocks defined as entire chromosomes. The default is at 5000 SNPs |
| <code>-e,--excludeChroms ARG</code> | List of chromosome names to exclude chromosomes, given as comma-separated list. Defaults to X, Y, MT, chrX, chrY, chrMT, 23,24,90 |
| <code>--stat ARG</code> | Specify a summary statistic to be computed. Can be given multiple times. Possible options are: F4(a, b, c, d), F3(a, b, c), F3star(a, b, c), F2(a, b), PWM(a, b), FST(a, b), Het(a) and some more special options described at https://poseidon-framework.github.io/#/xerxes?id=fstats-command . Valid entities used in the statistics are group names as specified in the *.fam, *.ind or *.janno files, individual names using the syntax "<Ind_name>", so |

| | |
|------------------------------------|---|
| | enclosing them in angular brackets, and entire packages like <code>"*Package1"</code> using the Poseidon package title. You can mix entity types, like in <code>"F4(<Ind1>,Group2,*Pac*,<Ind4>)"</code> . Group or individual names are separated by commas, and a comma can be followed by any number of spaces. |
| <code>--statConfig ARG</code> | Specify a yaml file for the Fstatistics and group configurations |
| <code>--statFile ARG</code> | Specify a file with F-Statistics specified similarly as specified for option <code>--stat</code> . One line per statistics, and no new-line at the end |
| <code>--maxSnps ARG</code> | Stop after a maximum nr of snps has been processed. Useful for short test runs |
| <code>--noTransitions</code> | Skip transition SNPs and use only transversions |
| <code>-f,--tableOutFile ARG</code> | a file to which results are written as tab-separated file |
| <code>--blockTableFile ARG</code> | a file to which the per-Block results are written as tab-separated file |

2.1 Allowed statistics

The following statistics are allowed in the `--stat`, `--statFile` and `--statConfig` options. In all of the following, symbols `a`, `b`, `c` or `d` stand for arbitrary entities allowed in Poseidon, so groups (such as `French`), individuals (such as `<MA1.SG>`) or packages (such as `*2012_PattersonGenetics*`).

- `F2vanilla(a, b)`: F2-Statistics - Vanilla version. Computed using $F2vanilla(a, b) = (a-b)^2$ across the genome.
- `F2(a, b)`: F2-Statistics (bias-corrected version). Computed as $F2(a, b) = F2vanilla(a, b) - hA/sA - hB/sB$, where where sA is the number of non-missing alleles in entity A, and $hA = nA * nA' / sA * (sA - 1)$ is an estimator of half the heterozygosity (see `Het(a)`), and likewise for sB and nB etc.
- `F3vanilla(a,b,c)`: F3-Statistics - Vanilla version, recommended if used as Outgroup-F3 statistics or with group `c` being pseudo-haploid: Are computed as $F3(a, b, c) = (c-a)(c-b)$ across all SNPs.
- `F3(a,b,c)`: F3-statistics (bias-corrected version). Computed as $F3(a, b, c) = F3vanilla(a, b) - hC/sC$.
- `F3star(a,b,c)`: F3-Statistics as defined in [1] - normalised and bias-corrected version, recommended for Admixture-F3 tests. Are computed by i) first subtracting per SNP from the vanilla-F3 statistic a bias-correction term hC/sC , as above for F2, and ii) then normalising the genome-wide estimate by a genome-wide estimate of the heterozygosity of entity C (`Het(c)`), in order to make results comparable between different groups C.
- `F4(a,b,c,d)`: F4 statistics. Are computed by averaging the quantity $(a-b)(c-d)$ across all SNPs. No bias correction is necessary for this statistic.
- `Het(a)`: An estimate of the heterozygosity across all SNPs, computed as $2*hA$, with hA defined as above in F2
- `FST(a, b)`: An estimate of FST across the genome, following the estimator presented in [2] and implemented in the ADMIXTOOLS package. This amounts to a ratio of genome-wide ranges, where the numerator is an unbiased estimate of F2 (see above), and the denominator is $PWM(a, b)$, see below.

- `FSTvanilla(a, b)`: Similar to `FST(a, b)` but without the bias correction in the numerator, mainly useful for teaching and learning.
- `PWM(a, b)`: The pairwise mismatch rate between entities a and b, computed from allele frequencies as $\frac{a}{(1 - b) + (1 - a) b}$.

Most of these equations can also be found in [1]. See also Appendix A of this paper for the unbiased estimators used above.

For each of the “slots” A, B, C or D, you can enter: * Individuals, using the syntax `<Individual_Name> *` Groups, using no special syntax “Group_Name” * Packages, using syntax `*Package_Name*` (This can be useful if you happen to have a homogenous set of individuals from multiple groups in one package and want to consider all of these as one group.)

2.2 Defining statistics directly via `--stat`

This is the simplest option to instruct the program to compute a specified statistic. Each statistic requires a separate input using `--stat` using this input method. Example:

```
xerxes fstats -d ... -d ... --stat "F3(French, Spanish, <Chimp.REF>) --stat "FST(French, Spanish)"
```

2.3 Defining statistics in a simple text file

You can prepare a text file, into which you write the above statistics, one statistics per line. Example:

```
F4(<Chimp.REF>, <Altai_published.DG>, Yoruba, French)
F4(<Chimp.REF>, <Altai_snpAD.DG>, Spanish, French)
F4(Mbuti,Nganasan,Saami.DG,Finnish)
```

you can then load these statistics using the option `--statFile fstats.txt`.

2.4 Input via a configuration file

This is the most powerful way to input F-Statistics. Here is an example:

```
groupDefs:
  CEU2: ["CEU.SG", "-<NA12889.SG>", "-<NA12890.SG>"]
  FIN2: ["FIN.SG", "-<HG00383.SG>", "-<HG00384.SG>"]
  GBR2: ["GBR.SG", "-<HG01791.SG>", "-<HG02215.SG>"]
  IBS2: ["IBS.SG", "-<HG02238.SG>", "-<HG02239.SG>"]
fstats:
- type: F2
  a: ["French", "Spanish"]
  b: ["Han", "CEU2"]
  # Ascertainment is optional
- type: F3 # This will create 3x2x1 = 6 Statistics
  a: ["French", "Spanish", "Mbuti"]
  b: ["Han", "CEU2"]
  c: ["<Chimp.REF>"]
ascertainment:
```

```

    outgroup: "<Chimp.REF>" # ascertaining on outgroup-polarised derived allele frequency
    reference: "CEU2"
    lower: 0.05
    upper: 0.95
- type: F4 # This will create 5x5x4x1 = 100 Statistics
  a: ["<I0156.SG>", "<I0157.SG>", "<I0159.SG>", "<I0160.SG>", "<I0161.SG>"]
  b: ["<I0156.SG>", "<I0157.SG>", "<I0159.SG>", "<I0160.SG>", "<I0161.SG>"]
  c: ["CEU2", "FIN2", "GBR2", "IBS2"]
  d: ["<Chimp.REF>"]
  ascertainment:
    # A missing outgroup means: ascertain on minor allele frequency
    reference: "CEU.SG"
    lower: 0.00
    upper: 0.10

```

85 The top level structure of this [YAML](#) file is an object with two fields: **groupDefs** (which is optional) and **fstats**
 86 (which is mandatory).

87 2.4.1 Group Definitions

88 You can specify ad-hoc group definitions using the syntax above. Every group consists of a name (used as object
 89 key) and then a JSON- or YAML-list of signed entities, following the same syntax as **trident forge**. Briefly:
 90 Individuals, Groups and Packages can be added or excluded (prefixed by a -) in order. In the example above,
 91 two individuals are removed from each group.

92 Note that currently, groups can be defined only independently, so not incremental to each other. That means,
 93 you cannot currently use an already defined new group name in the entity list of a following group name.

94 2.4.2 Statistic input using YAML

95 Each statistic defined in the **fstats** section of the YAML file, actually defines a loop over multiple populations
 96 in each statistic. In the example above, there are 6 F3-Statistics, each using a different combination of the input
 97 groups defined in each of the **a:**, **b:** and **c:** slots. There are also 100 (!) F4 statistics, following all combinations
 98 of 5x5x4x1 slots defined in **a:**, **b:**, **c:** and **d:**. This makes it very convenient to loop over statistics.

99 2.4.3 Ascertainment (experimental feature)

100 In addition, every statistic section allows for a definition of an ascertainment specification, using a special
 101 key **ascertainment:**, which is optional. If given, you can specify an optional **outgroup**, a **reference** group in
 102 which to ascertain SNPs, and **lower** and **upper** allele frequency bounds. If specified, only SNPs for which the
 103 **reference** group has an allele frequency within the given bounds are used to compute the statistic (note that
 104 normalisation is still using all non-missing SNPs for that given statistic). If an **outgroup** is defined, then the
 105 outgroup-polarised derived allele frequency is used. If no **outgroup** is defined, then the minor allele frequency is
 106 used instead. If an outgroup is defined, any sites where the outgroup is polymorphic are treated as missing.

107 You can save this into a text file, for example named **fstats_config.yaml**, and load it via **--statConfig**
 108 **fstats_config.yaml**.

2.5 Output

The final output of the `fstats` command looks like this:

```
.----- .----- .----- .----- .----- .----- .
| Statistic |      a      |      b      |      c      |      d      | NrSites |
:===== :===== :===== :===== :===== :===== :
| F3        | French      | Italian_North | Mbuti      |              | 593124 |
| F3        | French      | Han           | Mbuti      |              | 593124 |
| F3        | Sardinian   | Pima          | French     |              | 593124 |
| F4        | French      | Russian       | Han        | Mbuti        | 593124 |
| F4        | Sardinian   | French        | Pima       | Mbuti        | 593124 |
'-----' '-----' '-----' '-----' '-----' '-----' ->

----- .----- .----- .----- .----- .
Estimate_Total | Estimate_Jackknife | StdErr_Jackknife | Z_score_Jackknife |
===== :===== :===== :===== :
5.9698e-2      | 5.9698e-2          | 5.1423e-4          | 116.0908951980249 |
5.0233e-2      | 5.0233e-2          | 5.0324e-4          | 99.81843057232513 |
-1.2483e-3     | -1.2483e-3         | 9.2510e-5          | -13.493505348221081 |
-1.6778e-3     | -1.6778e-3         | 9.1419e-5          | -18.35262346091248 |
-1.4384e-3     | -1.4384e-3         | 1.1525e-4          | -12.481084899924868 |
'-----' '-----' '-----' '-----' '-----' '-----'
```

which lists each statistic, the slots a, b, c and d, the number of sites with non-missing data for that statistic, Ascertainment information (outgroup, reference, lower and upper bound, if given), the genome-wide estimate, its standard error and its Z-score. If you specify an output file using option `--tableOutFile` or `-f`, these results are also written as tab-separated file.

Additionally, an option `--blockOutFile` can be specified, to which then a table with estimates per Jackknife block is written.

2.6 Degenerate statistics

Specific cases of statistics are 0 by construction:

- `F2(A, B)`, `F2vanilla(A, B)`, `FST(A, B)` and `FSTvanilla(A, B)` where `A=B`.
- `F3(A, B, C)` and `F3vanilla(A, B, C)` where `C=A` or `C=B`
- `F4(A, B, C, D)` where `A=B` or `C=D`

Even though the bias-correction technically can result in non-zero and even negative values, we automatically detect these cases and output identical 0 for them. This can be useful for example when looping over pairs of populations for a pairwise matrix of FST, where we then want the diagonal to be zero to yield a proper distance matrix.

2.7 Ploidy and illegal cases

Genotype ploidy in input samples is important for many of the statistics, because the bias-correction terms require the number of chromosomes. Ploidy information is automatically read through the field of `Genotype_Ploidy` in the `.janno` file. A warning is printed if that information is missing, in which case we assume diploid genotypes.

130 But often with low-coverage data from ancient DNA we create pseudo-haploid genotypes, so in that case it is
131 important to provide that information correctly through the .janno file.

132 In specific cases, statistics are illegal, in case of only a single haplotype. Specifically:

- 133 • $F_2(A, B)$ and $F_{ST}(A, B)$ is undefined if either one of A or B contains only a single haplotype.
- 134 • $F_3(A, B, C)$ is undefined if C contains only a single haplotype.
- 135 • $Het(A)$ unsurprisingly is undefined if A contains only a single haplotype.

136 These cases are detected and an error is thrown. For F_2 , F_3 and F_{ST} it suggests to use the “vanilla” versions
137 of the statistics if that makes sense. This is particularly relevant for so-called “Outgroup- F_3 -Statistics”, where
138 we sometimes use a single haploid reference genome in position C . Use `F3vanilla` in that case.

139 2.8 Whitepaper

140 The repository comes with a [detailed whitepaper](#) that describes some more mathematical details of the methods
141 implemented here.

142 3 RAS (in development)

143 The RAS command computes pairwise RAS statistics between a collection of “left” entities, and a collection of
144 “right” entities. Every Entity is either a group name or an individual, with the similar syntax as in F-Statistics
145 above, so `French` is a group, and `<IND001>` is an individual.

146 The input of left-pops and right-pops uses a YAML file via `--popConfigFile`. Here is an example:

```
groupDefs:
  group1: a,b,-c,-<d>
  group2: e,f,-<g>
popLefts:
- <I13721>
- <I14000>
- <I13722>
- <Iceman.SG>
popRights:
- Mbuti
- Mixe
- Spanish
outgroup: <Chimp.REF>
```

147 In this case, two groups are defined on the fly: `group1` comprises groups `a` and `b`, but excludes group `c` and
148 individual `d`. Note that inclusions and exclusions are executed in order. `group2` comprises of group `e` and group
149 `f`, but excludes individual `<g>`.

150 As in [RAScalculator](#) [3], the allele frequency ascertainment is done across right populations only.

151 There are a couple of options, as specified in the CLI help (`xerxes ras --help`):

```
Usage: xerxes ras (-d|--baseDir DIR) [-j|--jackknife ARG]
               [-e|--excludeChroms ARG] --popConfigFile ARG
               [-k|--maxAlleleCount ARG] [-m|--maxMissingness ARG]
```

(-f|--tableOutFile ARG)

Compute RAS statistics on groups and individuals within and across Poseidon packages

Available options:

| | |
|-------------------------|--|
| -h,--help | Show this help text |
| -d,--baseDir DIR | a base directory to search for Poseidon Packages (could be a Poseidon repository) |
| -j,--jackknife ARG | Jackknife setting. If given an integer number, this defines the block size in SNPs. Set to "CHR" if you want jackknife blocks defined as entire chromosomes. The default is at 5000 SNPs |
| -e,--excludeChroms ARG | List of chromosome names to exclude chromosomes, given as comma-separated list. Defaults to X, Y, MT, chrX, chrY, chrMT, 23,24,90 |
| --popConfigFile ARG | a file containing the population configuration |
| -k,--maxAlleleCount ARG | define a maximal allele-count cutoff for the RAS statistics. (default: 10) |
| -m,--maxMissingness ARG | define a maximal missingness for the right populations in the RAS statistics. (default: 0.1) |
| -f,--tableOutFile ARG | the file to which results are written as tab-separated file |

The output gives both cumulative (up to allele-count k) and per-allele-frequency RAS (for allele count k) for every pair of left and rights. The standard out contains a pretty-printed table, and in addition, a tab-separated file is written to the file specified using option -f.

xerxes ras makes a few important assumptions:

1. It assumes that the Right Populations are “nearly” completely non-missing. Any allele that is actually missing from the rights is in fact treated as homozygous-reference! A different approach would be to compute the actual frequencies on the non-missing right alleles, but then we cannot any more nicely accumulate over different ascertainment allele counts.
2. If no outgroup is specified, the ascertainment operates on minor-allele frequency (as in fstats)
3. If an outgroup is specified and missing from a SNP, or if the SNP is polymorphic, the SNP is skipped as missing

-
- [1] N. Patterson *et al.*, “Ancient admixture in human history,” *Genetics*, vol. 192, no. 3, pp. 1065–1093, Nov. 2012, doi: [10.1534/genetics.112.145037](https://doi.org/10.1534/genetics.112.145037).
 - [2] G. Bhatia, N. Patterson, S. Sankararaman, and A. L. Price, “Estimating and interpreting FST: The impact of rare variants,” *Genome Research*, vol. 23, no. 9, pp. 1514–1521, Jul. 2013, doi: [10.1101/gr.154831.113](https://doi.org/10.1101/gr.154831.113).
 - [3] P. Flegontov *et al.*, “Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America,” *Nature*, vol. 570, no. 7760, pp. 236–240, Jun. 2019, doi: [10.1038/s41586-019-1251-y](https://doi.org/10.1038/s41586-019-1251-y).