

Guide for trident v1.6.2.1

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32

1 Installation

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

35

2 Overview

36 Trident is a command line software tool structured in multiple subcommands. If you installed it properly you
 37 can call it on the command line by typing `trident`. This will show an overview of the general options and all
 38 subcommands, which are explained in detail below.

```
Usage: trident [--version] [--logMode MODE | --debug] [--errLength INT]
           [--inPlinkPopName MODE] (COMMAND | COMMAND)
```

trident is a management and analysis tool for Poseidon packages. Report issues
 here: <https://github.com/poseidon-framework/poseidon-hs/issues>

Available options:

<code>-h, --help</code>	Show this help text
<code>--version</code>	Show version number
<code>--logMode MODE</code>	How information should be reported: NoLog, SimpleLog, DefaultLog, ServerLog or VerboseLog. (default: DefaultLog)
<code>--debug</code>	Short for --logMode VerboseLog.
<code>--errLength INT</code>	After how many characters should a potential genotype data parsing error message be truncated. "Inf" for no truncation. (default: CharCount 1500)
<code>--inPlinkPopName MODE</code>	Where to read the population/group name from the FAM file in Plink-format. Three options are possible: asFamily (default) asPhenotype asBoth.

Package creation and manipulation commands:

<code>init</code>	Create a new Poseidon package from genotype data
<code>fetch</code>	Download data from a remote Poseidon repository
<code>forge</code>	Select packages, groups or individuals and create a new Poseidon package from them
<code>genoconvert</code>	Convert the genotype data in a Poseidon package to a different file format
<code>jannocoalesce</code>	Coalesce information from one or multiple janno files to another one
<code>rectify</code>	Adjust POSEIDON.yml files automatically to package changes

Inspection commands:

list	List packages, groups or individuals from local or remote Poseidon repositories
summarise	Get an overview over the content of one or multiple Poseidon packages
survey	Survey the degree of context information completeness for Poseidon packages
validate	Check Poseidon packages or package components for structural correctness

39 **trident** allows to work directly with genotype data (see **-p** below), but it is optimized for the interaction
40 with Poseidon packages, which wrap and contextualize the data. Most **trident** subcommands therefore have a
41 central parameter, called **--baseDir** or simply **-d** to specify one or more base directories to look for packages.
42 For example, if all Poseidon packages live inside a repository at **/path/to/poseidon/packages** you would
43 simply say **trident <subcommand> -d /path/to/poseidon/dirs/** and **trident** would automatically search
44 all subdirectories inside of the repository for valid Poseidon packages (as identified by valid **POSEIDON.yml**
45 files).

46 You can arrange a Poseidon repository in a hierarchical way. For example:

```
/path/to/poseidon/packages
  /modern
    /2019_poseidon_package1
    /2019_poseidon_package2
  /ancient
    /...
    /...
  /Reference_Genomes
    /...
    /...
```

47 This structure then allows to select only the level of packages you are interested in, even individual ones. **-d**
48 can be given multiple times, which is particularly useful as you may have your own data to co-analyse with
49 external reference data. In this case you simply need to provide your own genotype data as yet another Poseidon
50 package to be added to your **trident** command. For example, you may have genotype data in **EIGENSTRAT**
51 format (**trident** supports **EIGENSTRAT**, **PLINK** and **VCF** as formats):

```
~/my_project/my_project.geno
~/my_project/my_project.snp
~/my_project/my_project.ind
```

52 Then you can transform that into a skeleton Poseidon package with the **init** command. You can also do it
53 manually by simply adding a **POSEIDON.yml** file, with, for example, the following content:

```
poseidonVersion: 2.7.1
title: My_awesome_project
description: Unpublished genetic data from my awesome project
contributor:
  - name: Stephan Schiffels
    email: schiffels@institute.org
```

```

packageVersion: 0.1.0
lastModified: 2020-10-07
genotypeData:
  format: EIGENSTRAT
  genoFile: my_project.geno
  snpFile: my_project.snp
  indFile: my_project.ind
jannoFile: my_project.janno
bibFile: sources.bib

```

Two remarks: 1) All file paths in this POSEIDON.yml file are considered *relative* to the directory in which POSEIDON.yml resides. For this example we assume that this file is added into the same directory as the three genotype files. 2) Besides the genotype data files there are two (technically optional) files referenced in this example: `sources.bib` and `my_project.janno`. Of course you can add them manually - `init` automatically creates empty dummy versions.

Once you have set up your own Poseidon package (which is really only a skeleton so far), you can add it to your `trident` analysis, by simply adding your project directory to the command using `-d`, for example:

```

trident list -d /path/to/poseidon/packages/modern \
  -d /path/to/poseidon/packages/ReferenceGenomes \
  -d ~/my_project \
  --packages

```

2.1 Logging and command line output

For all subcommands the general argument `--logMode` defines how `trident` reports messages (to stderr) on the command line:

- *NoLog*: Hides all messages.
- *SimpleLog*: Plain and simple output.
- *DefaultLog*: Adds the severity indicators (log levels) **Info**, **Warning** and **Error** before each message. This is the default setting.
- *ServerLog*: Additionally adds timestamps before each message.
- *VerboseLog*: Shows not just messages on the log levels **Info**, **Warning** and **Error** like the other modes, but also on the more verbose level **Debug**. Use this mostly relevant for debugging.

`--debug` is short for `--logMode VerboseLog` to activate this important log level more easily.

2.2 Package duplicates and versions

- For `trident` multiple packages in a set of base directories can share the same **title**, if they have different **packageVersion** numbers. If the version numbers are also identical or missing, then `trident` stops with an exception.
- The `trident` subcommands `genoconvert`, `list`, `rectify`, `survey` and `validate` by default consider all versions of each Poseidon package in the given base directories. The `--onlyLatest` flag causes them to instead only consider the latest versions.
- `fetch` and `forge` generally consider all package versions. Their selection language (see below) allows for detailed version handling.

- `summarize` and `jannocoalesce` consider always only the latest package versions.

2.3 Individual/Sample duplicates

- `Poseidon_IDs` (so individual/sample names) within one package have to be unique, or `trident` will stop.
- We also discourage sample duplicates across packages in package repositories, but `trident` will generally continue with them. `validate` will fail though, if the `--ignoreDuplicates` flag is not set.
- `forge` offers a special mechanism to resolve sample duplicates within its selection language.

2.4 Group names in .fam files

The `.fam` file of PLINK-formatted genotype data is used inconsistently across different popular aDNA software tools to store group/population name information. The (global) `trident` option `--inPlinkPopName` with the arguments `asFamily` (default), `asPhenotype` and `asBoth` allows to control the reading of the population name from PLINK `.fam` files. The subcommands that write genotype data (`forge`, `genoconvert`) have a corresponding option `--outPlinkPopName` to specify this for the output.

2.5 Whitespaces in the .janno file

While reading the `.janno` file `trident` trims all leading and trailing whitespaces around individual cells. Also all instances of the `No-Break Space` unicode character will be removed. This means these whitespaces will not be preserved when a package is forged.

3 Init command

`init` creates a new Poseidon package from genotype data files. It adds a `POSEIDON.yml` file, a dummy `.janno` file for context information and an empty `.bib` file for literature references.

Command line details

```
Usage: trident init ((-p|--genoOne FILE) | --genoFile FILE --snpFile FILE
                  --indFile FILE |
                  --bedFile FILE --bimFile FILE --famFile FILE |
                  --vcfFile FILE) [--snpSet SET] (-o|--outPackagePath DIR)
                  [-n|--outPackageName STRING] [--minimal]
```

Create a new Poseidon package from genotype data

Available options:

<code>-h,--help</code>	Show this help text
<code>-p,--genoOne FILE</code>	One of the input genotype data files. Expects <code>.bed</code> , <code>.bed.gz</code> , <code>.bim</code> , <code>.bim.gz</code> or <code>.fam</code> for PLINK, <code>.geno</code> , <code>.geno.gz</code> , <code>.snp</code> , <code>.snp.gz</code> or <code>.ind</code> for EIGENSTRAT, or <code>.vcf</code> or <code>.vcf.gz</code> for VCF. In case of EIGENSTRAT and PLINK, the two other files must be in the same directory and must have the same base name. If a gzipped file is given, it is assumed that the file pairs <code>(.geno.gz, .snp.gz)</code> or <code>(.bim.gz, .bed.gz)</code> are

```

both zipped, but not the .fam or .ind file. If a .ind
or .fam file is given, it is assumed that none of the
file triples is zipped.
--genoFile FILE      Eigenstrat genotype matrix, optionally gzipped.
                      Accepted file endings are .geno, .geno.gz
--snpFile FILE       Eigenstrat snp positions file, optionally gzipped.
                      Accepted file endings are .snp, .snp.gz
--indFile FILE       Eigenstrat individual file. Accepted file endings are
                      .ind
--bedFile FILE       Plink genotype matrix, optionally gzipped. Accepted
                      file endings are .bed, .bed.gz
--bimFile FILE       Plink snp positions file, optionally gzipped.
                      Accepted file endings are .bim, .bim.gz
--famFile FILE       Plink individual file. Accepted file endings are .fam
--vcfFile FILE       VCF (Variant Call Format) file, optionall gzipped.
                      Accepted file endings are .vcf, .vcf.gz
--snpSet SET         The snpSet of the package: 1240K, HumanOrigins or
                      Other. Only relevant for data input with -p|--genoOne
                      or --genoFile + --snpFile + --indFile, because the
                      packages in a -d|--baseDir already have this
                      information in their respective POSEIDON.yml files.
                      (default: Other)
-o,--outPackagePath DIR Path to the output package directory.
-n,--outPackageName STRING
                      The output package name. This is optional: If no name
                      is provided, then the package name defaults to the
                      basename of the (mandatory) --outPackagePath
                      argument. (default: Nothing)
--minimal            Should the output Poseidon package be reduced to a
                      necessary minimum?

```

101 The command

```

trident init \
  --genoFile path/to/genoFile.geno \
  --snpFile path/to/snpFile.snp \
  --indFile path/to/indFile.ind \
  --snpSet 1240K|HumanOrigins|Other \
  -o path/to/new_package_name

```

102 requires the paths to the respective files (--genoFile --snpFile --indFile | --bedFile --bimFile
 103 --famFile | --vcfFile), and optionally the “shape” of these files (--snpSet), so if they cover the 1240K, the
 104 HumanOrigins or an Other SNP set.

105 A simpler interface is available with -p (+ --snpSet), which only requires a path to one of the genotype data
 106 files and automatically discovers the others if they share the same base name:

```

trident init \
  -p path/to/genoFile \
  --snpSet 1240K|HumanOrigins|Other \
  -o path/to/new_package_name

```

107 The following file extensions are expected:

	EIGENSTRAT	PLINK	VCF
genoFile	.geno	.bed	.vcf
snpFile	.snp	.bim	—
indFile	.ind	.fam	—

108 The output package created by `init` is located in a new directory `-o`, which should not already exist when `init`
 109 is called, and gets the package title corresponding to the basename of `-o`. You can also set the title explicitly
 110 with `-n`.

111 The `--minimal` flag causes `init` to create a minimal package with a very basic POSEIDON.yml and no `.bib`
 112 and `.janno` files.

113 4 Fetch command

114 `fetch` allows to download Poseidon packages from a remote Poseidon server via a Web API. This server provides
 115 all packages in the Poseidon public archives.

116 Command line details

```

Usage: trident fetch (-d|--baseDir DIR)
        (--downloadAll |
        (--fetchFile FILE | (-f|--fetchString DSL)))
        [--remoteURL URL] [--archive STRING]

```

Download data from a remote Poseidon repository

Available options:

<code>-h,--help</code>	Show this help text
<code>-d,--baseDir DIR</code>	A base directory to search for Poseidon packages.
<code>--downloadAll</code>	Download all packages the server is offering.
<code>--fetchFile FILE</code>	A file with a list of packages. Works just as <code>-f</code> , but multiple values can also be separated by newline, not just by comma. <code>-f</code> and <code>--fetchFile</code> can be combined.
<code>-f,--fetchString DSL</code>	List of packages to be downloaded from the remote server. Package names should be wrapped in asterisks: <code>*package_title*</code> . You can combine multiple values with comma, so for example: <code>"*package_1*, *package_2*, *package_3*"</code> . <code>fetchString</code> uses the same parser as <code>forgeString</code> , but does not allow excludes. If groups

	or individuals are specified, then packages which include these groups or individuals are included in the download.
<code>--remoteURL URL</code>	URL of the remote Poseidon server. (default: "https://server.poseidon-adna.org")
<code>--archive STRING</code>	The name of the Poseidon package archive that should be queried. If not given, then the query falls back to the default archive of the server selected with <code>--remoteURL</code> . See the archive documentation at https://www.poseidon-adna.org/#/archive_overview for a list of archives currently available from the official Poseidon Web API. (default: Nothing)

117 It works with

```
trident fetch -d ... -d ... \
  -f "*package_title_1*,*package_title_2-1.0.1*,group_name,<individual1>"
```

118 and the entities you want to download must be listed either in a simple string of comma-separated values, which
119 can be passed via `-f/--fetchString`, or in a text file (`--fetchFile`). Entities are then combined from these
120 sources.

121 Entities are specified using a special syntax (see also the documentation of `forge` below): packages are
122 wrapped in asterisks, with or without a version number appended after a dash (e.g. `*package_title*` or
123 `*package_title-1.2.3`), group names are spelled as is, and individual names are wrapped in angular brackets
124 (e.g. `<individual1>`). Fetch will figure out which packages need to be downloaded to include all specified entities.

125 `--downloadAll`, which can be given instead of `-f` and `--fetchFile`, causes fetch to download all packages from
126 the server. The downloaded packages are added in the first (!) `-d` directory (which gets created if it doesn't
127 exist), but downloads are only performed if the respective packages are not already present in the latest version
128 in any of the `-d` directories.

129 Note that `trident fetch` is usually used in a workflow with `trident list --remote`: First one inspects what
130 is available on the server with `list`, to then compile a custom, targeted `fetch` command.

131 `fetch` has the optional arguments `--remote https://...` to name an alternative Poseidon server and
132 `--archive` to select a specific Poseidon archive on the server.

133 5 Forge command

134 `forge` creates new Poseidon packages by extracting and merging packages, populations and individuals/samples
135 from Poseidon repositories.

136 Command line details

```
Usage: trident forge ((-d|--baseDir DIR) |
  ((-p|--genoOne FILE) | --genoFile FILE --snpFile FILE
  --indFile FILE |
  --bedFile FILE --bimFile FILE --famFile FILE |
  --vcfFile FILE) [--snpSet SET])
```



```

[--forgeFile FILE | (-f|--forgeString DSL)]
[--selectSnps FILE] [--intersect] [--outFormat FORMAT]
[--onlyGeno | --minimal | --preservePym1] [-z|--zip]
(-o|--outPackagePath DIR) [-n|--outPackageName STRING]
[--packagewise] [--outPlinkPopName MODE] [--ordered]

```

Select packages, groups or individuals and create a new Poseidon package from them

Available options:

<code>-h,--help</code>	Show this help text
<code>-d,--baseDir DIR</code>	A base directory to search for Poseidon packages.
<code>-p,--genoOne FILE</code>	One of the input genotype data files. Expects .bed, .bed.gz, .bim, .bim.gz or .fam for PLINK, .geno, .geno.gz, .snp, .snp.gz or .ind for EIGENSTRAT, or .vcf or .vcf.gz for VCF. In case of EIGENSTRAT and PLINK, the two other files must be in the same directory and must have the same base name. If a gzipped file is given, it is assumed that the file pairs (.geno.gz, .snp.gz) or (.bim.gz, .bed.gz) are both zipped, but not the .fam or .ind file. If a .ind or .fam file is given, it is assumed that none of the file triples is zipped.
<code>--genoFile FILE</code>	Eigenstrat genotype matrix, optionally gzipped. Accepted file endings are .geno, .geno.gz
<code>--snpFile FILE</code>	Eigenstrat snp positions file, optionally gzipped. Accepted file endings are .snp, .snp.gz
<code>--indFile FILE</code>	Eigenstrat individual file. Accepted file endings are .ind
<code>--bedFile FILE</code>	Plink genotype matrix, optionally gzipped. Accepted file endings are .bed, .bed.gz
<code>--bimFile FILE</code>	Plink snp positions file, optionally gzipped. Accepted file endings are .bim, .bim.gz
<code>--famFile FILE</code>	Plink individual file. Accepted file endings are .fam
<code>--vcfFile FILE</code>	VCF (Variant Call Format) file, optionall gzipped. Accepted file endings are .vcf, .vcf.gz
<code>--snpSet SET</code>	The snpSet of the package: 1240K, HumanOrigins or Other. Only relevant for data input with -p --genoOne or --genoFile + --snpFile + --indFile, because the packages in a -d --baseDir already have this information in their respective POSEIDON.yml files. (default: Other)
<code>--forgeFile FILE</code>	A file with a list of packages, groups or individual samples. Works just as -f, but multiple values can also be separated by newline, not just by comma.

	<p>Empty lines are ignored and comments start with "#", so everything after "#" is ignored in one line.</p> <p>Multiple instances of -f and --forgeFile can be given. They will be evaluated according to their input order on the command line.</p>
-f,--forgeString DSL	<p>List of packages, groups or individual samples to be combined in the output package. Packages follow the syntax <code>*package_title*</code>, populations/groups are simply <code>group_id</code> and individuals <code><individual_id></code>. You can combine multiple values with comma, so for example: <code>"*package_1*, <individual_1>, <individual_2>, group_1"</code>. Duplicates are treated as one entry.</p> <p>Negative selection is possible by prepending "-" to the entity you want to exclude (e.g. <code>"*package_1*, -<individual_1>, -group_1"</code>). <code>forge</code> will apply excludes and includes in order. If the first entity is negative, then <code>forge</code> will assume you want to merge all individuals in the packages found in the <code>baseDirs</code> (except the ones explicitly excluded) before the exclude entities are applied. An empty <code>forgeString</code> (and no <code>--forgeFile</code>) will therefore merge all available individuals. If there are individuals in your input packages with equal individual id, but different main group or source package, they can be specified with the special syntax <code>"<package:group:individual>"</code>.</p>
--selectSnps FILE	<p>To extract specific SNPs during this <code>forge</code> operation, provide a Snp file. Can be either Eigenstrat (file ending must be <code>'.snp'</code> or <code>'.snp.gz'</code>) or Plink (file ending must be <code>'.bim'</code> or <code>'.bim.gz'</code>). When this option is set, the output package will have exactly the SNPs listed in this file. Any SNP not listed in the file will be excluded. If option <code>'--intersect'</code> is also set, only the SNPs overlapping between the SNP file and the forged packages are output.</p> <p>(default: Nothing)</p>
--intersect	<p>Whether to output the intersection of the genotype files to be forged. The default (if this option is not set) is to output the union of all SNPs, with genotypes defined as missing in those packages which do not have a SNP that is present in another package. With this option set, the forged dataset will typically have fewer SNPs, but less missingness.</p>
--outFormat FORMAT	<p>The format of the output genotype data: EIGENSTRAT or PLINK. (default: "PLINK")</p>

<code>--onlyGeno</code>	Should only the resulting genotype data be returned? This means the output will not be a Poseidon package.
<code>--minimal</code>	Should the output Poseidon package be reduced to a necessary minimum?
<code>--preservePym1</code>	Should the output Poseidon package mimic the input package? With this option some fields of the source package's POSEIDON.yml file, its README file and its CHANGELOG file (if available) are copied to the output package. Only works for a singular source package.
<code>-z,--zip</code>	Should the resulting genotype- and snp-files be gzipped?
<code>-o,--outPackagePath DIR</code>	Path to the output package directory.
<code>-n,--outPackageName STRING</code>	The output package name. This is optional: If no name is provided, then the package name defaults to the basename of the (mandatory) <code>--outPackagePath</code> argument. (default: Nothing)
<code>--packagewise</code>	Skip the within-package selection step in forge. This will result in outputting all individuals in the relevant packages, and hence a superset of the requested individuals/groups. It may result in better performance in cases where one wants to forge entire packages or almost entire packages. Details: Forge conceptually performs two types of selection: First, it identifies which packages in the supplied base directories are relevant to the requested forge, i.e. whether they are either explicitly listed using <code>*PackageName*</code> , or because they contain selected individuals or groups. Second, within each relevant package, individuals which are not requested are removed. This option skips only the second step, but still performs the first.
<code>--outPlinkPopName MODE</code>	Where to write the population/group name into the FAM file in Plink-format. Three options are possible: <code>asFamily</code> (default) <code>asPhenotype</code> <code>asBoth</code> . See also <code>--inPlinkPopName</code> .
<code>--ordered</code>	With this option, the output of forge is ordered according to the entities given.

137 forge can be used with

```
trident forge -d ... -d ... \
-f "*package_name*, group_id, <individual_id>" \
-o path/to/new_package_name
```

138 where the entities (packages, groups/populations, individuals/samples) you want in the output package can be
139 denoted either as a string on the command line (`-f/--forgeString`), or in an input text file (`--forgeFile`).
140 See the section below for the syntax of this selection language. Do not forget to wrap the `--forgeString` query
141 in quotes.

142 Including one or multiple Poseidon packages with `-d` is not the only way to include data for a forge operation. It is
143 also possible to consider unpackaged genotype data directly with `-p` (+ `--snpSet`), `--genoFile` + `--snpFile`
144 + `--indFile` (+ `--snpSet`) (for EIGENSTRAT data), `--bedFile` + `--bimFile` + `--famFile` (+ `--snpSet`)
145 (for PLINK data) or `--vcfFile` (+ `--snpSet`) (for VCF data). This makes the following example possible, where
146 we merge data from one Poseidon package and two unpackaged genotype datasets to get a new EIGENSTRAT
147 dataset.

```
trident forge \  
-d 2017_GonzalesFortesCurrentBiology \  
-p 2018_VeeramahPNAS/2018_VeeramahPNAS.fam \  
--bedFile 2017_HaberAJHG/2017_HaberAJHG.bed \  
--bimFile 2017_HaberAJHG/2017_HaberAJHG.bim \  
--famFile 2017_HaberAJHG/2017_HaberAJHG.fam \  
-f "<STR241.SG>,<ERS1790729.SG>,Iberia_HG.SG" \  
-o testpackage \  
--outFormat EIGENSTRAT \  
--onlyGeno
```

148 5.1 The forge selection language

149 The text in `--forgeString` and `--forgeFile` (and with a reduced syntax also in `--fetchString` and
150 `--fetchFile`) are parsed as a domain specific query language that describes precisely which entities should be
151 compiled in the output package of a given `forge` operation. The language has multiple syntactic elements and a
152 specific evaluation logic.

153 In general a `--forgeString` query consists of multiple entities, separated by `,.` The main entities are Poseidon
154 packages, groups/populations and individuals/samples:

- 155 • Each package title is surrounded by `*`: `*package*`. That means if you want all individuals of the Poseidon
156 package 2019_Jeong_InnerEurasia in the output package you would add `*2019_Jeong_InnerEurasia*`
157 to the query.
- 158 • Groups/populations are not specially marked: `group`. So to get all individuals of the group
159 `Swiss_Roman_Period`, you would simply add `Swiss_Roman_Period`.
- 160 • Individuals/samples are surrounded by `<` and `>`: `<individual>`. ALA026 therefore becomes `<ALA026>`. A sec-
161 ond way to denote individuals is with the more verbose and specific syntax `<package:group:individual>`.
162 Such defined individuals take precedence over differently defined ones (so directly with `<individual>` or
163 as a subset of `*package*` or `group`). This allows to resolve duplication issues precisely – at least in cases
164 where the duplicated individuals differ in source package or primary group.
- 165 • Package versions can be appended to package names, such as `*package-1.2.3*`.
- 166 • This also works with the verbose individual syntax: `<package-1.2.3:group:individual>`.

167 In the `--forgeFile` each line is treated as a separate `forgeString`, empty lines are ignored and `#` symbols start
168 comments. So this is a valid example of a `forgeFile`:

```

# Packages
*pac1*, *pac2-1.2.3*

# Groups and individuals from other packages beyond pac1 and pac2
group1, <ind1>, group2, <ind2>, <pac3:group3:ind3>

# pac2 has two outlier individuals that should be ignored
-<ind4>           # This one has very low coverage
-<pac2:group4:ind5> # This one is from a different time period

```

By prepending `-` to entities, we can exclude them from the forged package (this feature is not available for `fetch`). `forge` figures out the final list of samples to include by interpreting all forge-entities in order. So an entity list `*pac1*, -<ind1>, group1` may result in a different outcome than `*pac1*, group1, -<ind1>`, depending on whether `<ind1>` belongs to `group1` or not.

If the forge entity list starts with a negative entity, or if the entity list is empty, `forge` will implicitly assume you want to include all individuals in all **latest** versions of packages found in the base directories (except the ones explicitly excluded, of course).

The specific semantics of the various ways to include or exclude entities are as follows:

5.1.1 Inclusion queries

- `*pac1*`: Select all individuals in the latest version of package “pac1”
- `*pac1-1.0.1*`: Select all individuals in package “pac1” with version “1.0.1”
- `group1`: Select all individuals associated with “group1” in all latest versions of all packages
- `<ind1>`: Select the individual named “ind1”, searching in all latest packages.
- `<pac1:group1:ind1>`: Select the individual named “ind1” associated with “group1” in the latest version of package “pac1”
- `<pac1-1.0.1:group1:ind1>`: Select the individual named “ind1” associated with “group1” in the package “pac1” with version “1.0.1”

5.1.2 Exclusion queries

- `-*pac1*`: Remove all individuals in all versions of package “pac1”
- `-*pac1-1.0.1*`: Remove only individuals in package “pac1” with version “1.0.1” (but leave other versions in)
- `-group1`: Remove all individuals associated with “group1” in all versions of all packages (not just the latest)
- `-<ind1>`: Remove all individuals named “ind1” in all versions of all packages (not just the latest)
- `-<pac1:group1:ind1>`: Remove the individual named “ind1” associated with “group1”, searching in all versions of package “pac1”
- `-<pac1-1.0.1:group1:ind1>`: Remove the individual named “ind1” associated with “group1”, but only if they are in “pac1” with version “1.0.1”

If a query results in multiple individuals with the same name, `forge` will throw an error.

5.2 Ordered output

By default the order of samples in a Poseidon package created with **forge** depends on the order in which the relevant source packages are discovered by **trident** (e.g. when it crawls for packages in the **-d** base directories) and then the sample order within these packages.

The option **--ordered** gives more control over the output order. It causes **trident** to output the resulting package with samples ordered according to the selection in **-f** or **--forgeFile**. This works through an alternative, slower sample selection algorithm that loops through the list of entities and checks for each entity which samples it adds or removes respectively to and from the final selection.

For simple, positive selection, packages, groups and samples are added as expected. Negative selection removes samples from the list again. If an entity is selected twice via positive selection, then its first occurrence is considered for the ordering.

5.2.1 Reordering samples in a package

One particular application of **--ordered** is the reordering of samples in an existing Poseidon package, here for example **MyPac**. We suggest the following workflow for this application:

1. Generate a **--forgeFile** with the desired order of the samples in **MyPac**. This can be done manually or with any suitable tool. Here is an example, where we employ **qjanno** to generate a **forge** selection so that the samples are ordered alphabetically by their **Poseidon_ID**:

```
qjanno "SELECT '<||Poseidon_ID||>' FROM d(MyPac) ORDER BY Poseidon_ID" \  
--raw --noOutHeader > myOrder.txt
```

2. Use **trident forge** with **--ordered** and **--preservePysql** (see below) to create the package with the specified order:

```
trident forge -d MyPac --forgeFile myOrder.txt -o MyPac2 --ordered --preservePysql
```

3. Apply **trident rectify** to increment the package version number and document the reordering:

```
trident rectify -d MyPac2 --packageVersion Minor \  
--logText "reordered the samples alphabetically by Poseidon_ID"
```

MyPac2 then acts as a stand-in replacement for **MyPac** that only differs in the order of samples (and maybe the order of variables/fields in the **POSEIDON.yml**, **.janno**, **.ssf** or **.bib** files).

5.3 Treatment of the genotype data while merging

Forge performs a series of steps to merge the genotype data of multiple source files:

1. Genotype data from each package is streamed in parallel. Because our packages may have different SNP locations (specified by chromosome-position pairs) listed in their **.bim/.snp** or **.vcf** file, we first perform a zipping-operation, whose behaviour depends on whether **--intersect** is set or not. Without **--intersect**, any SNP position listed in any package will be forwarded to the output, with missing values being filled in in all packages that do not list that particular SNP. With **--intersect**, only SNP positions that are present in all packages are considered. Note that relevant for this step is only whether a given SNP position is part of the genotype data, not whether the actual genotypes are missing or not.
2. At each SNP, the consensus alleles are selected, by collecting all reference and alternative alleles from all sources. If more than two non-dummy alleles (alleles different from **N**) are present in that collection, an

error is thrown. If exactly two non-dummy alleles are present (which should be the case for binary SNPs), the two alleles are declared “reference” and “alternative” alleles for the output. If only one non-dummy allele is present, it is set to be the reference allele, and “N” is set to be the alternative.

3. All source genotype data is then read and recoded in terms of the two chosen consensus alleles. This will make sure that source data with flipped reference and alternative allele gets correctly merged in.
4. SNP IDs, as part of PLINK `.bim` and `.vcf` files are checked across the source files. If all SNP IDs for a given SNP are missing, then the result will also be missing. If there is only one SNP ID present in some or all source packages, that ID gets forwarded to the output. In the (unusual) case that there are multiple different non-missing SNP IDs (of the form “rs” followed by a number), then a debug warning is output (which gets printed to the screen when `--debug` is selected), and simply the first value is chosen to be output into the forged `.bim` file. We decided not to throw an error in that case, because we consider the physical position of the SNP (specified by Chromosome and position) to be definitive, and the SNP ID to be of secondary importance.
5. Genetic positions, as part of PLINK `.bim` files are checked in a similar manner, with “0.0” being interpreted as missing.

5.4 Treatment of the `.janno` file while merging

`forge` merges and subsets `.janno` files along with the genotype data. If a package lacks a `.janno` file, then a basic one will be created internally on-the-fly based on the information in the genotype data, and used for the output. Missing columns across packages will be filled with `n/a`.

For merging two `.janno` files **A** and **B** the following rules apply regarding undefined, arbitrary additional columns:

- If **A** has an additional column which is not in **B** then empty cells in the rows imported from **B** are filled with `n/a`.
- If **A** and **B** share additional columns with identical column name, then they are treated as semantically identical units and merged accordingly.
- In the resulting `.janno` file, all additional columns from both **A** and **B** are sorted alphabetically and appended after the normal, specified variables.

The following example illustrates the described behaviour:

A.janno

Poseidon_ID	Group_Name	Genetic_Sex	AdditionalColumn1	AdditionalColumn2
XXX011	POP1	M	A	D
XXX012	POP2	F	B	E
XXX013	POP1	M	C	F

B.janno

Poseidon_ID	Group_Name	Genetic_Sex	AdditionalColumn3	AdditionalColumn2
YYY022	POP5	F	G	J
YYY023	POP5	F	H	K
YYY024	POP5	M	I	L

Poseidon_ID	Group_Name	Genetic_Sex	AdditionalColumn1	AdditionalColumn2	AdditionalColumn3
XXX011	POP1	M	A	D	n/a
XXX012	POP2	F	B	E	n/a
XXX013	POP1	M	C	F	n/a
YYY022	POP5	F	n/a	J	G
YYY023	POP5	F	n/a	K	H
YYY024	POP5	M	n/a	L	I

262 **5.5 Treatment of the .ssf file while merging**

263 The Sequencing Source File (short **.ssf** file) is forged in exactly the same way as the **.janno** file. **.ssf** files
264 that are present are included in the forge product, following selection of those entities which are listed in the
265 **poseidon_IDs** columns. Columns that are only present in some packages, including those not defined in the
266 Poseidon package specification, are also included in the forged product in the same way as described for **.janno**
267 files above.

268 **5.6 Treatment of the .bib file while merging**

269 In the forge process all relevant samples for the output package are determined. This includes their **.janno**
270 entries and therefore the information on the publication keys documented for them in the **.janno Publication**
271 column. The output **.bib** file compiles only the relevant references for the samples in the output package. It
272 includes the references exactly once and is sorted alphabetically by key.

273 **5.7 Output modes**

274 The output package of **forge** is created as a new directory **-o**. The title can also be explicitly defined with **-n**.
275 **forge** by default returns a new output package with a generic **POSEIDON.yml** file, the genotype data as created
276 from the input and the selection, and a **.janno** file. If the input includes **.bib** or **.ssf** files, the output will as
277 well.

278 Other output formats can be selected with these mutually exclusive flags:

279 **--onlyGeno:**

280 Only the genotype data is returned without any Poseidon package wrapping around it. This is especially useful
281 for data analysis pipelines, where only the genotype data is required.

282 **--minimal:**

283 A minimal output package without **.janno**, **.bib** and **.ssf**. This wraps the genotype data in a very basic
284 Poseidon package.

285 **--preservePyaml:**

286 A full Poseidon package just as the default, but with various settings copied from the source package. This only
287 works in case of a single source package.

288 For the specific task of sub-setting or reordering (see above) a singular, existing Poseidon package it can be useful
289 to preserve some fields of the **POSEIDON.yml** file of this input package, as well as supplementary information in

the README.md and the CHANGELOG.md file. These are typically discarded by **forge**, but can be copied over to the output package with the new **--preservePysql** output mode.

--preservePysql specifically preserves the following POSEIDON.yml fields:

- **description**
- **contributor**
- **packageVersion**
- **lastModified**
- **readmeFile**
- **changelogFile**

This does not include the package **title**, which can be easily set to be identical to the source with **-n** or **-o** if it is desired. The **poseidonVersion** field is also not copied, because **trident** can only ever produce output packages with the latest Poseidon schema version.

With **-z|--zip** the genotype data output (independent of the selected output mode) can be wrapped in gzipped archives with the additional file extension **.gz**. **trident** can seamlessly interact with genotype data in this format.

5.8 Other options

forge has a an optional flag **--intersect**, that defines, if the genotype data from different packages should be merged with a union or an intersect operation. See *Treatment of the genotype data while merging* above.

--intersect also influences the automatic determination of the **snpSet** field in the POSEIDON.yml file for the resulting package. If the **snpSets** of all input packages are identical, then the resulting package will just inherit this configuration. Otherwise **forge** applies the following pairwise merging logic:

Input snpSet A	Input snpSet B	--intersect	Ouput snpSet
Other	*	*	Other
1240K	HumanOrigins	True	HumanOrigins
1240K	HumanOrigins	False	1240K

--selectSnps allows to provide **forge** with a SNP file in EIGENSTRAT (**.snp**) or PLINK (**.bim**) format to create a package with a specific selection. When this option is set, the output package will have exactly the SNPs listed in this file. Any SNP not listed in the file will be excluded. If **--intersect** is also set, only the SNPs overlapping between the SNP file and the forged packages are output.

With **--packagewise** the within-package selection step in **forge** can be skipped. This will result in outputting all individuals in the relevant packages, and hence a superset of the requested individuals/groups. It may result in better performance in cases where one wants to forge entire packages.

6 Genoconvert command

genoconvert converts the genotype data in a Poseidon package to a different file format. The respective entries in the POSEIDON.yml file are changed accordingly.

Command line details

```
Usage: trident genoconvert ((-d|--baseDir DIR) |
    ((-p|--genoOne FILE) | --genoFile FILE
    --snpFile FILE --indFile FILE |
    --bedFile FILE --bimFile FILE --famFile FILE |
    --vcfFile FILE) [--snpSet SET])
--outFormat FORMAT [-o|--outPackagePath DIR]
[--removeOld] [--outPlinkPopName MODE] [--onlyLatest]
[-z|--zip]
```

Convert the genotype data in a Poseidon package to a different file format

Available options:

-h,--help	Show this help text
-d,--baseDir DIR	A base directory to search for Poseidon packages.
-p,--genoOne FILE	One of the input genotype data files. Expects .bed, .bed.gz, .bim, .bim.gz or .fam for PLINK, .geno, .geno.gz, .snp, .snp.gz or .ind for EIGENSTRAT, or.vcf or .vcf.gz for VCF. In case of EIGENSTRAT and PLINK, the two other files must be in the same directory and must have the same base name. If a gzipped file is given, it is assumed that the file pairs (.geno.gz, .snp.gz) or (.bim.gz, .bed.gz) are both zipped, but not the .fam or .ind file. If a .ind or .fam file is given, it is assumed that none of the file triples is zipped.
--genoFile FILE	Eigenstrat genotype matrix, optionally gzipped. Accepted file endings are .geno, .geno.gz
--snpFile FILE	Eigenstrat snp positions file, optionally gzipped. Accepted file endings are .snp, .snp.gz
--indFile FILE	Eigenstrat individual file. Accepted file endings are .ind
--bedFile FILE	Plink genotype matrix, optionally gzipped. Accepted file endings are .bed, .bed.gz
--bimFile FILE	Plink snp positions file, optionally gzipped. Accepted file endings are .bim, .bim.gz
--famFile FILE	Plink individual file. Accepted file endings are .fam
--vcfFile FILE	VCF (Variant Call Format) file, optionall gzipped. Accepted file endings are .vcf, .vcf.gz
--snpSet SET	The snpSet of the package: 1240K, HumanOrigins or Other. Only relevant for data input with -p --genoOne or --genoFile + --snpFile + --indFile, because the packages in a -d --baseDir already have this information in their respective POSEIDON.yml files. (default: Other)
--outFormat FORMAT	the format of the output genotype data: EIGENSTRAT or

	PLINK.
<code>-o,--outPackagePath DIR</code>	Path for the converted genotype files to be written to. If a path is provided, only the converted genotype files are written out, with no change of the original package. If no path is provided, genotype files will be converted in-place, including a change in the POSEIDON.yml file to yield an updated valid package (default: Nothing)
<code>--removeOld</code>	Remove the old genotype files when creating the new ones.
<code>--outPlinkPopName MODE</code>	Where to write the population/group name into the FAM file in Plink-format. Three options are possible: asFamily (default) asPhenotype asBoth. See also <code>--inPlinkPopName</code> .
<code>--onlyLatest</code>	Consider only the latest versions of packages, or the groups and individuals within the latest versions of packages, respectively.
<code>-z,--zip</code>	Should the resulting genotype- and snp-files be gzipped?

322 With the default setting

```
trident genoconvert -d ... -d ... --outFormat EIGENSTRAT|PLINK
```

323 all packages in `-d` will be converted to the desired `--outFormat` (either EIGENSTRAT or PLINK), if the data is
324 not already in this format. This includes updating the respective POSEIDON.yml files.

325 The “old” data is not deleted, but kept around. That means conversion can result in a package with both PLINK
326 and EIGENSTRAT data, but only one is linked in the POSEIDON.yml file, and that is what will be used by
327 **trident**. To delete the old data in the conversion you can add the `--removeOld` flag.

328 `-p` (+ `--snpSet`), `--genoFile` + `--snpFile` + `--indFile` (+ `--snpSet`) (for EIGENSTRAT data),
329 `--bedFile` + `--bimFile` + `--famFile` (+ `--snpSet`) (for PLINK data) or `--vcfFile` (+ `--snpSet`) (for
330 VCF data) allow to directly convert genotype data that is not wrapped in a Poseidon package and store it to a
331 directory given in `-o`. See this example:

```
trident genoconvert \
  -p 2018_Mittnik_Baltic/Mittnik_Baltic.bed \
  --outFormat EIGENSTRAT \
  -o my_directory
```

332 With `-z|--zip` the genotype data output can be wrapped in gzipped archives with the additional file extension
333 `.gz`.

334 7 Jannocoalesce command

335 **jannocoalesce** merges information from one or multiple source `.janno` files into a target `.janno` file.

336 Command line details

```
Usage: trident jannocoalesce ((-s|--sourceFile FILE) | (-d|--baseDir DIR))
                                (-t|--targetFile FILE) [-o|--outFile FILE]
                                [--includeColumns ARG | --excludeColumns ARG]
                                [-f|--force] [--sourceKey ARG] [--targetKey ARG]
                                [--stripIdRegex ARG]
```

Coalesce information from one or multiple janno files to another one

Available options:

<code>-h,--help</code>	Show this help text
<code>-s,--sourceFile FILE</code>	The source .janno file.
<code>-d,--baseDir DIR</code>	A base directory to search for Poseidon packages.
<code>-t,--targetFile FILE</code>	The target .janno file to fill.
<code>-o,--outFile FILE</code>	An optional file to write the results to. If not specified, change the target file in place. (default: Nothing)
<code>--includeColumns ARG</code>	A comma-separated list of .janno column names to coalesce. If not specified, all columns that can be found in the source and target will get filled.
<code>--excludeColumns ARG</code>	A comma-separated list of .janno column names NOT to coalesce. All columns that can be found in the source and target will get filled, except the ones listed here.
<code>-f,--force</code>	With this option, potential non-missing content in target columns gets overridden with non-missing content in source columns. By default, only missing data gets filled-in.
<code>--sourceKey ARG</code>	The .janno column to use as the source key. (default: "Poseidon_ID")
<code>--targetKey ARG</code>	The .janno column to use as the target key. (default: "Poseidon_ID")
<code>--stripIdRegex ARG</code>	An optional regular expression to identify parts of the IDs to strip before matching between source and target. Uses POSIX Extended regular expressions.

337 A most basic run may just include two arguments:

```
trident jannocoalesce \
  --sourceFile path/to/source.janno \
  --targetFile path/to/target.janno
```

338 jannocoalesce generally works by reading a source .janno file with `-s|--sourceFile` (or all .janno files in a
339 `-d|--baseDir`) and a target .janno file with `-t|--targetFile`.

340 It then merges these files by a key column, which can be selected with `--sourceKey` and `--targetKey`. The
341 default for both of these key columns is the `Poseidon_ID`. In case the entries in the key columns slightly and
342 systematically differ, e.g. because the `Poseidon_ID`s in either have a special suffix (for example `_SG`), then the

343 `--stripIdRegex` option allows to strip these with a regular expression to thus match the keys.

344 `jannocoalesce` generally attempts to fill **all** empty cells in the target `.janno` file with information from the

345 source. `--includeColumns` and `--excludeColumns` allow to select specific columns for which this should be

346 done. In some cases it may be desirable to not just fill empty fields in the target, but overwrite the information

347 already there with the `-f|--force` option. If the target file should be preserved, then the output can be directed

348 to a new output `.janno` file with `-o|--outFile`.

349 8 Rectify command

350 `rectify` automatically harmonizes POSEIDON.yml files of one or multiple packages. This is not an automatic

351 update from one Poseidon version to the next, but rather a clean-up wizard after manual modifications. It also

352 includes additional, automatic package editing features.

353 Command line details

```
Usage: trident rectify (-d|--baseDir DIR) [--ignorePoseidonVersion]
      [--poseidonVersion ??.?]
      [--packageVersion VPART [--logText STRING]]
      [--checksumAll | [--checksumGeno] [--checksumJanno]
      [--checksumSSF] [--checksumBib]]
      [--newContributors DSL] [--jannoRemoveEmpty]
      [--onlyLatest]
```

Adjust POSEIDON.yml files automatically to package changes

Available options:

<code>-h,--help</code>	Show this help text
<code>-d,--baseDir DIR</code>	A base directory to search for Poseidon packages.
<code>--ignorePoseidonVersion</code>	Read packages even if their poseidonVersion is not compatible with trident.
<code>--poseidonVersion ??.?</code>	Poseidon version the packages should be updated to: e.g. "2.5.3".
<code>--packageVersion VPART</code>	Part of the package version number in the POSEIDON.yml file that should be updated: Major, Minor or Patch (see https://semver.org).
<code>--logText STRING</code>	Log text for this version in the CHANGELOG file.
<code>--checksumAll</code>	Update all checksums.
<code>--checksumGeno</code>	Update genotype data checksums.
<code>--checksumJanno</code>	Update .janno file checksum.
<code>--checksumSSF</code>	Update .ssf file checksum
<code>--checksumBib</code>	Update .bib file checksum.
<code>--newContributors DSL</code>	Contributors to add to the POSEIDON.yml file in the form "[Firstname Lastname](Email address);...".
<code>--jannoRemoveEmpty</code>	Reorder the .janno file and remove empty columns. Remember to pair this option with <code>--checksumJanno</code> to also update the checksum.

```
--onlyLatest          Consider only the latest versions of packages, or the
                        groups and individuals within the latest versions of
                        packages, respectively.
```

It can be called with a lot of optional arguments. Note that `rectify` by default does **not** apply any changes if none of these arguments are set. Each change requires explicit opt-in.

```
trident rectify -d ... -d ... \
  --poseidonVersion "X.X.X" \
  --packageVersion Major|Minor|Patch \
  --logText "short description of the update" \
  --checksumAll \
  --newContributors "[Firstname Lastname](Email address);..." \
  --jannoRemoveEmpty
```

The following arguments determine which fields of the POSEIDON.yml file should be modified:

- `--poseidonVersion` allows a simple change of the `poseidonVersion` field in the POSEIDON.yml file.
- `--packageVersion` increments the package version number in the first, the second or the third position. It can optionally be called with `--logText`, which appends an entry to the CHANGELOG file for the respective package version update. `--logText` also creates a new CHANGELOG.md file if it does not exist yet.
- `--checksumGeno`, `--checksumJanno`, `--checksumSSF` and `--checksumBib` add or modify the respective checksum fields in the POSEIDON.yml file. `--checksumAll` is a wrapper to call all of them at once.
- `--newContributors` adds new contributors.

As `rectify` reads and rewrites POSEIDON.yml files, it may change their inner order, layout or even content (e.g. if they have fields which are not in the POSEIDON.yml specification). Create a backup of the POSEIDON.yml file before running `rectify` if you are uncertain if this might affect you negatively.

`--jannoRemoveEmpty` is the first option that does not edit POSEIDON.yml, but .janno files. It allows to remove empty columns from .janno files, so columns that only feature empty strings or n/a values. As part of this process it reorders the columns of the .janno file. Remember to pair this option with `--checksumJanno` or `checksumAll` to automatically update the .janno checksum in the POSEIDON.yml file afterwards.

9 List command

`list` lists packages, groups, individuals and bibliography entries of local Poseidon package datasets, or of packages available in the archives on the web server.

Command line details

```
Usage: trident list ((-d|--baseDir DIR) | --remote [--remoteURL URL]
                    [--archive STRING])
                    (--packages | --groups | --individuals
                    [--fullJanno | [-j|--jannoColumn COLNAME]] |
                    --bibliography [--fullBib | [-b|--bibField BIB-FIELD]])
                    [--raw] [--onlyLatest]
```

List packages, groups or individuals from local or remote Poseidon repositories

Available options:

<code>-h,--help</code>	Show this help text
<code>-d,--baseDir DIR</code>	A base directory to search for Poseidon packages.
<code>--remote</code>	List packages from a remote server instead the local file system.
<code>--remoteURL URL</code>	URL of the remote Poseidon server. (default: "https://server.poseidon-adna.org")
<code>--archive STRING</code>	The name of the Poseidon package archive that should be queried. If not given, then the query falls back to the default archive of the server selected with <code>--remoteURL</code> . See the archive documentation at https://www.poseidon-adna.org/#/archive_overview for a list of archives currently available from the official Poseidon Web API. (default: Nothing)
<code>--packages</code>	List all packages.
<code>--groups</code>	List all groups, ignoring any group names after the first as specified in the .janno-file.
<code>--individuals</code>	List all individuals/samples.
<code>--fullJanno</code>	output all Janno Columns
<code>-j,--jannoColumn COLNAME</code>	List additional fields from the janno files, using the .janno column heading name, such as "Country", "Site", "Date_C14_Uncal_BP", etc... Can be given multiple times
<code>--bibliography</code>	output bibliography information for packages
<code>--fullBib</code>	output all bibliography fields found in any bibliography item
<code>-b,--bibField BIB-FIELD</code>	List information from the given bibliography field, for example "abstract" or "publisher". Can be given multiple times.
<code>--raw</code>	Return the output table as tab-separated values without header. This is useful for piping into grep or awk.
<code>--onlyLatest</code>	Consider only the latest versions of packages, or the groups and individuals within the latest versions of packages, respectively.

376 To list packages from your local repositories, as seen above you can run

```
trident list -d ... -d ... --packages
```

377 This will yield a nicely formatted table of all packages, their version and the number of individuals in them.

378 You can use `--remote` to show packages on the remote server. For example

```
trident list --packages --remote --archive "community-archive"
```

will result in a view of all packages available in one of the public Poseidon archives. Just as for **fetch**, the **--archive** flag allows to choose which public archive to query.

Independent of whether you query a local or an online archive, you can not just list packages, but also groups, as defined in the third column of EIGENSTRAT **.ind** files (or the first/last column of a PLINK **.fam** file), and individuals with the flags **--groups** and **--individuals** (instead of **--packages**). **--bibliography** returns publication-wise bibliography information.

The **--individuals** flag additionally provides a way to immediately access information from **.janno** files on the command line. This works with the **-j|--jannoColumn** option. For example adding **-j Country -j Date_C14_Uncal_BP** to the commands above will add the **Country** and the **Date_C14_Uncal_BP** columns to the respective output tables. **--fullJanno** outputs all available columns.

Analogously, with **--bibliography** additional fields from the **.bib** files can be added to the output table with **-b|--bibField ...** and **--fullBib**. **-b journal**, for example, adds a column with the publication's journal.

Note that if you want a less ornate table, for example because you want to load this into Excel, or pipe into another command that cannot deal with the table layout, you can use the **--raw** option to output that table as a simple tab-delimited stream.

10 Summarise command

summarise prints some general summary statistics for a given Poseidon dataset taken from the **.janno** files.

Command line details

Usage: **trident summarise** (**-d|--baseDir DIR**) [**--raw**]

Get an overview over the content of one or multiple Poseidon packages

Available options:

-h,--help	Show this help text
-d,--baseDir DIR	A base directory to search for Poseidon packages.
--raw	Return the output table as tab-separated values without header. This is useful for piping into grep or awk .

You can run it with

```
trident summarise -d ... -d ...
```

which will show you context information like – among others – the number of individuals in the dataset, their sex distribution, the mean age of the samples or the mean coverage on the 1240K SNP array in a table. **summarise** depends on complete **.janno** files and will silently ignore missing information.

You can use the **--raw** option to output the summary table in a simple, tab-delimited layout.

402 11 Survey command

403 `survey` tries to indicate package completeness (mostly focused on `.janno` files) for Poseidon datasets.

404 Command line details

```
Usage: trident survey (-d|--baseDir DIR) [--raw] [--onlyLatest]
```

Survey the degree of context information completeness for 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>--raw</code>	Return the output table as tab-separated values without header. This is useful for piping into <code>grep</code> or <code>awk</code> .
<code>--onlyLatest</code>	Consider only the latest versions of packages, or the groups and individuals within the latest versions of packages, respectively.

405 Running

```
trident survey -d ... -d ...
```

406 will yield a table with one row for each package. See `trident survey -h` for a legend which cell of this table
407 means what.

408 Again you can use the `--raw` option to output the survey table in a tab-delimited format.

409 12 Validate command

410 `validate` checks Poseidon packages and individual package components for structural correctness.

411 Command line details

```
Usage: trident validate ((-d|--baseDir DIR) [--ignoreGeno] [--fullGeno]
                        [--ignoreDuplicates] [-c|--ignoreChecksums]
                        [--ignorePoseidonVersion] |
                        --pyml FILE | (-p|--genoOne FILE) | --genoFile FILE
                        --snpFile FILE --indFile FILE |
                        --bedFile FILE --bimFile FILE --famFile FILE |
                        --vcfFile FILE | --janno FILE | --ssf FILE |
                        --bib FILE) [--noExitCode] [--onlyLatest]
```

Check Poseidon packages or package components for structural correctness

Available options:

<code>-h,--help</code>	Show this help text
<code>-d,--baseDir DIR</code>	A base directory to search for Poseidon packages.
<code>--ignoreGeno</code>	Ignore snp and geno file.

<code>--fullGeno</code>	Test parsing of all SNPs (by default only the first 100 SNPs are probed).
<code>--ignoreDuplicates</code>	Do not stop on duplicated individual names in the package collection.
<code>-c,--ignoreChecksums</code>	Whether to ignore checksums. Useful for speedup in debugging.
<code>--ignorePoseidonVersion</code>	Read packages even if their poseidonVersion is not compatible with trident.
<code>--pyml FILE</code>	Path to a POSEIDON.yml file.
<code>-p,--genoOne FILE</code>	One of the input genotype data files. Expects .bed, .bed.gz, .bim, .bim.gz or .fam for PLINK, .geno, .geno.gz, .snp, .snp.gz or .ind for EIGENSTRAT, or.vcf or .vcf.gz for VCF. In case of EIGENSTRAT and PLINK, the two other files must be in the same directory and must have the same base name. If a gzipped file is given, it is assumed that the file pairs (.geno.gz, .snp.gz) or (.bim.gz, .bed.gz) are both zipped, but not the .fam or .ind file. If a .ind or .fam file is given, it is assumed that none of the file triples is zipped.
<code>--genoFile FILE</code>	Eigenstrat genotype matrix, optionally gzipped. Accepted file endings are .geno, .geno.gz
<code>--snpFile FILE</code>	Eigenstrat snp positions file, optionally gzipped. Accepted file endings are .snp, .snp.gz
<code>--indFile FILE</code>	Eigenstrat individual file. Accepted file endings are .ind
<code>--bedFile FILE</code>	Plink genotype matrix, optionally gzipped. Accepted file endings are .bed, .bed.gz
<code>--bimFile FILE</code>	Plink snp positions file, optionally gzipped. Accepted file endings are .bim, .bim.gz
<code>--famFile FILE</code>	Plink individual file. Accepted file endings are .fam
<code>--vcfFile FILE</code>	VCF (Variant Call Format) file, optional all gzipped. Accepted file endings are .vcf, .vcf.gz
<code>--janno FILE</code>	Path to a .janno file.
<code>--ssf FILE</code>	Path to a .ssf file.
<code>--bib FILE</code>	Path to a .bib file.
<code>--noExitCode</code>	Do not produce an explicit exit code.
<code>--onlyLatest</code>	Consider only the latest versions of packages, or the groups and individuals within the latest versions of packages, respectively.

412 You can run it with

```
trident validate -d ... -d ...
```

413 to check packages and it will either report a success (Validation passed) or failure with specific error messages.

414 Instead of validating entire packages with `-d` you can also apply it to individual files and package compo-
415 nents: `--pym1` (POSEIDON.yml), `-p | --genoFile + --snpFile + --indFile | --bedFile + --bimFile`
416 `+ --famFile | --vcfFile` (genotype data), `--janno` (.janno file), `--ssf` (.ssf file) or `--bib` (.bib file). In this
417 case `validate` attempts to read and parse the respective files individually and reports any issues it encounters.
418 Note that this considers the files in isolation and does not include any cross-file consistency checks.

419 When applied to packages, `validate` tries to ensure that each package adheres to the Poseidon package
420 specification. Here is a list of what is checked:

- 421 • Structural correctness of the POSEIDON.yml file.
- 422 • Presence of all files references in the POSEIDON.yml file.
- 423 • Full structural correctness of .janno, .ssf and .bib file.
- 424 • Superficial correctness of genotype data files by parsing the first 100 SNPs. A full check that parses all
425 SNPs can be triggered with the `--fullGeno` option. `--ignoreGeno`, on the other hand, causes `validate`
426 to ignore the genotype data entirely, which speeds up the validation significantly.
- 427 • Correspondence of BibTeX keys in .bib and .janno
- 428 • Correspondence of sample IDs in .janno and .ssf.
- 429 • Correspondence of sample and group IDs in .janno and genotype data files.

430 In fact much of this validation already runs as part of the general package reading pipeline invoked for other
431 `trident` subcommands (e.g. `forge`). `validate` is meant to be more thorough and brittle, though, and will
432 explicitly fail if even a single package is broken. For special cases more flexibility can be enabled with the options
433 `--ignoreDuplicates`, `--ignoreChecksums` and `--ignorePoseidonVersion`.

434 Remember to run `validate` with `--debug` to get more information in case the default output is not sufficient to
435 analyse an issue.