



PyPop API Reference

Developer documentation

Release 1.4.2b1

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Apr 29, 2026

Contents

| | | |
|---|--------------------------------|----|
| 1 | API changes | 1 |
| 2 | Package introduction | 2 |
| 3 | Submodules | 3 |
| | PyPop.citation | 3 |
| | PyPop.command_line_interface | 3 |
| | PyPop.datatypes | 5 |
| | PyPop.filters | 7 |
| | PyPop.haplo | 13 |
| | PyPop.hardyweinberg | 16 |
| | PyPop.homozygosity | 19 |
| | PyPop.parsers | 22 |
| | PyPop.popaggregate | 25 |
| | PyPop.popanalysis | 27 |
| | PyPop.popmeta | 28 |
| | PyPop.pypop | 29 |
| | PyPop.randombinning | 29 |
| | PyPop.utils | 30 |
| | PyPop.xslt | 39 |
| 4 | Deprecated Submodules | 40 |
| | PyPop.arlequin | 40 |
| 5 | Attributes | 43 |
| 6 | Exceptions | 43 |
| 7 | Functions | 43 |
| 8 | Package Contents | 43 |
| 9 | GNU Free Documentation License | 44 |
| | Python Module Index | 47 |
| | Index | 49 |

Documenting API for release 1.4.2b1 of PyPop.

Document revision: 1.4.2b1

This API reference guide for PyPop is automatically generated from the 1.4.2b1 source code via [sphinx-autoapi](#)¹.

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References to the *User Guide* can be found in the *PyPop User Guide*: [HTML](#)² | [PDF](#)³.

1 API changes

In PyPop 1.4.0, modules have been renamed to follow the lower-case convention of [PEP8](#)⁴. In addition to lowercasing, some have further renaming to clarify their purpose and follow standard conventions. Backwards-compatible bindings have been created that allow end-user Python scripts using the PyPop API to continue to work with the old module names. However such use will raise a *PyPopModuleRenameDeprecationWarning* (a custom *DeprecationWarning*⁵). In the following minor release, 1.5.0, the warnings will become more visible *UserWarning*⁶. These bindings will be completely removed in the next major release.

Note:

Command-line users of `pypop` will not be affected by these changes, which are completely internal, scripts will continue to work with no changes needed in any configuration files.

Below are the list of all API changes, including removals and any other ongoing API deprecations, and notifications of upcoming removals.

Removed in version 1.4.2

Removed in version 1.4.2: The following modules or classes were removed:

- `PyPop.datatypes.AlleleCounts` The *Genotypes* class now holds allele count data as pseudo-genotype matrix.

Changed in version 1.4.0

Changed in version 1.4.0: The following modules were renamed or refactored:

- `PyPop.CommandLineInterface` → `PyPop.command_line_interface` Lowercased for PEP8 compliance; underscores separate readable words.
- `PyPop.DataTypes` → `PyPop.datatypes` Lowercased for PEP8 compliance and consistency with plural naming for data structures.
- `PyPop.Filter` → `PyPop.filters` Lowercased and clarified plural form since module defines multiple filter functions.
- `PyPop.Haplo` → `PyPop.haplo` Lowercased for PEP8 compliance.
- `PyPop.HardyWeinberg` → `PyPop.hardyweinberg` Lowercased for PEP8 compliance.
- `PyPop.Homozygosity` → `PyPop.homozygosity` Lowercased for PEP8 compliance.
- `PyPop.Main` → `PyPop.popanalysis` Lowercased and renamed for clarity; represents per-population analysis rather than script entry point.
- `PyPop.Meta` → `PyPop.popaggregate` Lowercased and renamed for clarity; aggregates results across populations, not ‘metadata’.
- `PyPop.ParseFile` → `PyPop.parsers` Lowercased for and renamed for clarity: module parses multiple file types, not just one file.
- `PyPop.RandomBinning` → `PyPop.randombinning` Lowercased for PEP8 compliance.
- `PyPop.Utills` → `PyPop.utills` Lowercased for PEP8 compliance.

Removed in version 1.4.0

Removed in version 1.4.0: The following modules or classes were removed:

- `PyPop.GUIApp` Obsolete, never fully implemented a full wxPython UI. Replaced by built-in Tkinter file-picker
- `PyPop.Utills.Index` Obsolete, replaced with `collections.OrderedDict`⁷ with its own `Index` class
- `PyPop.Utills.OrderedDict` Obsolete, replaced with `collections.OrderedDict`⁸

Deprecated since version 1.0.0

Deprecated since version 1.0.0: The following modules were marked deprecated:

- `PyPop.Arlequin` → `PyPop.arlequin` Scheduled for removal in 1.5.0. Lowercased for PEP8 compliance.

2 Package introduction

PyPop is a framework for performing population genetics analyses.

PyPop was originally designed as an end-to-end pipeline that reads configuration files and datasets and produces standardized outputs. While the primary workflow is file-based, most internal functionality is exposed as Python modules and classes.

Important

Updates to PyPop’s API to better expose and streamline “library” access to PyPop’s functionality in end-user programs is still a work-in-progress. Although this API is intended to serve end-users and developers of PyPop, parts of it are not yet optimized for end-users.

Driving PyPop programmatically can be done via the *popanalysis* and *popaggregate* modules. In the example below, we run an simple analysis on a single input `.pop` file and generate output TSV files. There are two main steps:

1. Create the `ConfigParser`⁹ instance (see configuration file section in the *PyPop User Guide* for the description of the configuration options), supply this to the `Main` class, along with an input `.pop` file, to perform the analysis.
2. Next get the name of output XML file from the generated `Main` instance, and pass it to the `Meta` to generate TSV output files.

```

>>> from PyPop.popanalysis import Main
>>> from configparser import ConfigParser
>>>
>>> config = ConfigParser()
>>> config.read_dict({
...     "ParseGenotypeFile": {"validSampleFields": "*a_1\n*a_2"},
...     "HardyWeinberg": {"lumpBelow": "5"}}})
>>>
>>> pop_contents = '''a_1\ta_2
... 01:01\t02:01
... 02:10\t03:01:02'''
>>> with open("my.pop", "w") as f:
...     _ = f.write(pop_contents)
...
>>> application = Main(
...     config=config,
...     fileName="my.pop",
...     version="fake",
... )
LOG: no XSL file, skipping text output
LOG: Data file has no header data block
>>> outXML = application.getXmlOutPath()
>>> from PyPop.popaggregate import Meta
>>> _ = Meta (TSV_output=True, xml_files=[outXML])
./1-locus-hardyweinberg.tsv
./1-locus-summary.tsv
./1-locus-allele.tsv
./1-locus-genotype.tsv

```

See also

The PyPop API examples in the *PyPop User Guide* for a more detailed breakdown of use of the API.

3 Submodules

PyPop.citation

Module for generating citation formats.

Attributes

| | |
|--------------------------------------|---|
| <code>citation_output_formats</code> | Valid citation output formats supported by cffconvert |
|--------------------------------------|---|

Functions

| | |
|---|--|
| <code>convert_citation_formats(build_lib, citation_path)</code> | Generate all supported citation formats. |
|---|--|

Module Contents

`citation_output_formats = ['apalike', 'bibtex', 'endnote', 'ris', 'codemeta', 'cff', 'schema.org', 'zenodo']`

Valid citation output formats supported by cffconvert

`convert_citation_formats(build_lib, citation_path)`

Generate all supported citation formats.

Parameters

- `build_lib` (*str*) – path to build directory when creating package
- `citation_path` (*str*) – path to standard CITATION.cff file

PyPop.command_line_interface

Command-line interface for PyPop scripts.

Classes

| | |
|-----------------------------|---|
| <code>CitationAction</code> | A custom <code>argparse</code> <code>Citation</code> action to read the appropriate citation file format. |
|-----------------------------|---|

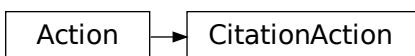
Functions

| | |
|--|---|
| <code>get_parent_cli</code> (<code>[version, copyright_message]</code>) | Command-line options common to all scripts. |
| <code>get_pypop_cli</code> (<code>[version, copyright_message]</code>) | Command-line options for <code>pypop</code> script. |
| <code>get_popmeta_cli</code> (<code>[version, copyright_message]</code>) | Command-line options for <code>popmeta</code> script. |

Module Contents

class `CitationAction`(`option_strings, dest, nargs=None, const=None, default=None, type=None, choices=None, required=False, help=None, metavar=None`)

Bases: `argparse.Action`¹⁰



A custom `argparse` `Citation` action to read the appropriate citation file format.

`__call__`(`parser, _, values, _option_string=None`)

get_parent_cli(`version="", copyright_message=""`)

Command-line options common to all scripts.

Parameters

- **version** (`str`) – Software version.
- **copyright_message** (`str`) – Override the copyright message.

Returns

A tuple of:

- `parent_parser` (`argparse.ArgumentParser`): The base parser.
- `ihwg_args` (`tuple`): Options for the IHWG module.
- `phylip_args` (`tuple`): Options for the Phylip module.
- `common_args` (`tuple`): Common options.
- `prefix_tsv_args` (`tuple`): TSV prefix options.

Return type

`tuple`

get_pypop_cli(`version="", copyright_message=""`)

Command-line options for `pypop` script.

Parameters

- **version** (`str`) – software version
- **copyright_message** (`str`) – override the copyright message

Returns

parser for `pypop`

Return type

`argparse.ArgumentParser`¹¹

get_popmeta_cli(`version="", copyright_message=""`)

Command-line options for `popmeta` script.

Parameters

- **version** (`str`) – software version
- **copyright_message** (`str`) – override the copyright message

Returns
 parser for popmeta

Return type
 argparse.ArgumentParser¹²

PyPop.datatypes

Data structures storing genotype and allele count data.

Classes

| | |
|------------------|--|
| <i>Genotypes</i> | Stores genotypes and caches basic genotype statistics. |
|------------------|--|

Functions

| | |
|--|---|
| <i>checkIfSequenceData</i> (matrix) | Heuristic check to determine whether we are analysing sequence. |
| <i>getMetaLocus</i> (locus, isSequenceData) | Get the overall locus that this sequence belongs to. |
| <i>getLocusPairs</i> (matrix, sequenceData) | Get locus pairs for a given matrix. |
| <i>getLumpedDataLevels</i> (genotypeData, locus, lumpLevels) | Get lumped data for a specific locus. |

Module Contents

class **Genotypes**(*matrix=None, untypedAllele='****', unsequencedSite=None, allowSemiTyped=0*)
 Stores genotypes and caches basic genotype statistics.

Parameters

- **matrix** (*StringMatrix*) – The *StringMatrix* to be converted into a *Genotype* instance
- **untypedAllele** (*str*) – The placeholder for an untyped allele site
- **unsequencedSite** (*bool*) – The identifier used for an unsequenced site (only used for sequence data)
- **allowSemiTyped** (*int*) – Whether or not to allow individuals that are typed at only one allele

getLocusList()

Get the list of loci.

Note

The returned list filters out all loci that consist of individuals that are all untyped. The order of returned list is now fixed for the lifetime of the object.

Returns

The list of loci.

Return type

list

getAlleleCount()

Allele count statistics for all loci.

Returns

a map of tuples where the key is the locus name. Each tuple is a triple, consisting of a map keyed by alleles containing counts, the total count at that locus and the number of untyped individuals.

Return type

dict

getAlleleCountAt(*locus, lumpValue=0*)

Get allele count for given locus.

Parameters

- **locus** (*str*) – locus
- **lumpValue** (*int*) – the specified amount of lumping (Default: 0)

Returns

a tuple consisting of a map keyed by alleles containing counts, the total count at that locus, and number of untyped individuals.

Return type

tuple

serializeSubclassMetadataTo(*stream*)

Serialize subclass-specific metadata.

Specifically, total number of individuals and loci and population name.

Parameters

stream (*TextOutputStream*) – the stream used for output.

serializeAlleleCountDataAt(*stream, locus*)

Serialize locus count data for a specific locus.

Specifically, total number of individuals and loci and population name.

Parameters

- **stream** (*TextOutputStream*) – the stream used for output
- **locus** (*str*) – locus

serializeAlleleCountDataTo(*stream*)

Serialize allele count data for a specific locus.

Parameters

stream (*TextOutputStream*) – the stream used for output

Returns

always returns 1

Return type

int

getLocusDataAt(*locus, lumpValue=0*)

Get the genotyped data for specified locus.

Note

The returned list has filtered out all individuals that are untyped at either chromosome. Data is sorted so that allele1 < allele2, alphabetically

Parameters

- **locus** (*str*) – locus to use
- **lumpValue** (*int*) – the specified amount of lumping (Default: 0).

Returns

a list genotypes consisting of 2-tuples which contain each of the alleles for that individual in the list.

Return type

list

getLocusData()

Get the genotyped data for all loci.

Returns

keyed by locus name of lists of 2-tuples as defined by *getLocusDataAt()*

Return type

dict

getIndividualsData()

Get data for all individuals.

Returns

StringMatrix for all individuals

Return type

StringMatrix

checkIfSequenceData(*matrix*)

Heuristic check to determine whether we are analysing sequence.

Note

The regex matches loci of the form A_32 or A_-32

Parameters

matrix (*StringMatrix*) – matrix to check

Returns

if sequence, return 1, otherwise 0

Return type

int

getMetaLocus(*locus, isSequenceData*)

Get the overall locus that this sequence belongs to.

Parameters

- **locus** (*str*) – Locus of interest.
- **isSequenceData** (*bool*) – whether this locus is sequence data

Returns

The locus name, or None if not sequence data.

Return type

str

getLocusPairs(*matrix, sequenceData*)

Get locus pairs for a given matrix.

Parameters

- **matrix** (*StringMatrix*) – matrix
- **sequenceData** (*bool*) – is this sequence data?

Returns

Returns a list of all pairs of loci from a given *StringMatrix*.

Return type

list

getLumpedDataLevels(*genotypeData, locus, lumpLevels*)

Get lumped data for a specific locus.

Parameters

- **genotypeData** (*Genotypes*) – genotype data to query
- **locus** (*str*) – the locus
- **lumpLevels** (*list*) – a list of integers representing lumping levels

Returns

a dictionary of tuples:

- locusData: keyed by locus
- alleleCount:

Return type

dict

PyPop.filters

Filters for pre-filtering of data files before analysis.

This module includes filters that modify or otherwise transform the input data before being passed to PyPop analysis.

Exceptions

| | |
|----------------------------|--|
| <code>SubclassError</code> | Customized exception if a subclass doesn't implement required methods. |
|----------------------------|--|

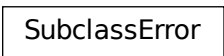
Classes

| | |
|--|--|
| <code>Filter</code> | Abstract base class for all Filters. |
| <code>PassThroughFilter</code> | A filter that doesn't change input data. |
| <code>AnthonyNolanFilter</code> | Filters data via Anthony Nolan's allele call data. |
| <code>BinningFilter</code> | Filters original data into "bins". |
| <code>AlleleCountAnthonyNolanFilter</code> | Filters data with an allelecoun less than a threshold. |

Module Contents

exception SubclassError

Bases: `Exception`¹³



Customized exception if a subclass doesn't implement required methods.

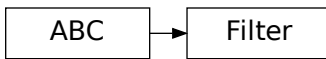
Initialize self. See `help(type(self))` for accurate signature.

`__str__()`

Returns a warning to subclass.

class Filter

Bases: `abc.ABC`¹⁴



Abstract base class for all Filters.

abstractmethod `doFiltering(matrix=None)`

abstractmethod `startFirstPass(locus)`

abstractmethod `checkAlleleName(alleleName)`

abstractmethod `addAllele(alleleName)`

abstractmethod `endFirstPass()`

abstractmethod `startFiltering()`

abstractmethod `filterAllele(alleleName)`

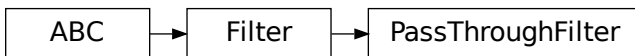
abstractmethod `endFiltering()`

abstractmethod `writeToLog(logstring=None)`

abstractmethod `cleanup()`

class PassThroughFilter

Bases: `Filter`



A filter that doesn't change input data.

doFiltering(`matrix=None`)

startFirstPass(`locus`)

```
checkAlleleName(alleleName)
```

```
addAllele(alleleName)
```

```
endFirstPass()
```

```
startFiltering()
```

```
filterAllele(alleleName)
```

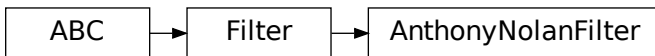
```
endFiltering()
```

```
writeToLog(logstring=None)
```

```
cleanup()
```

```
class AnthonyNolanFilter(directoryName=None, remoteMSF=None, alleleFileFormat='msf', preserveAmbiguousFlag=0, preserveUnknownFlag=0,
                          preserveLowresFlag=0, alleleDesignator='*', logFile=None, untypedAllele='****', unsequencedSite='#',
                          sequenceFileSuffix='_prot', filename=None, numDigits=4, verboseFlag=1, sequenceFilterMethod='strict')
```

Bases: *Filter*



Filters data via Anthony Nolan's allele call data.

Allele call data files can be of either `txt` or `msf` formats.

- `txt` files available at <http://www.anthonynolan.com>
- `msf` files available at <ftp://ftp.ebi.ac.uk/pub/databases/imgt/mhc/hla/>

Base class parameters.

Parameters

- **directoryName** (*str*) – directory that AnthonyNolan allele data is located
- **remoteMSF** (*str*) – Specifies the version (tag) of the remote `msf` directory in the [IMGT-HLA GitHub repo](#)¹⁵. If present, the remote MSF files for the specified version will be downloaded on-demand, and cached for later reuse
- **alleleFileFormat** (*str*, *optional*) – file format, can be `txt` or `msf` (default). Use of `msf` files is required in order to translate allele codes into polymorphic sequence data.
- **preserveAmbiguousFlag** (*int*, *optional*) – If set to 0 (default) then ambiguity is removed (e.g. `010101/0102/010301` will truncate this to `0101`). To preserve the ambiguity, set the option to 1 (for this example, it will result in a filtered allele “name” of `0101/0102/0103`)
- **preserveUnknownFlag** (*int*, *optional*) – If set to 0 (default) replace unknown alleles with the `untypedAllele` designator. To keep unrecognized allele names set to 1.
- **preserveLowresFlag** (*int*, *optional*) – This option is similar to `preserveUnknownFlag`, but only applies to lowres alleles. If set to 1, PyPop will keep allele names that are shorter than the default allele name length, usually 4 digits long. But if `preserveUnknownFlag` is set, this option has no effect, because all unknown alleles are preserved.
- **alleleDesignator** (*str*, *optional*) – the designator used to indicate a locus name (default `*`),
- **logFile** (*str*, *optional*) – log file
- **untypedAllele** (*str*, *optional*) – defaults to `****`
- **unsequencedSite** (*str*, *optional*) – defaults to `#`
- **sequenceFileSuffix** (*str*, *optional*) – Suffix for file names used for finding sequences each allele. (e.g., if the file for locus A is `A_prot.msf`, then keep the default be `_prot`. For nucleotide sequence files, this would be set `_nuc`.)
- **filename** (*str*, *optional*) – Currently not used
- **numDigits** (*int*, *optional*) – Number of digits used for HLA data (default 4)
- **verboseFlag** (*int*, *optional*) – Verbose output (default is on, i.e. 1)
- **sequenceFilterMethod** (*str*, *optional*) – matching alleles to sequence, defaults to `strict`, can also be `greedy`

doFiltering(*matrix=None*)

Do filtering on the provided matrix.

Parameters

matrix (*StringMatrix*) – matrix to be filtered

Returns

returns processed matrix for further downstream processing

Return type

StringMatrix

startFirstPass(*locus*)

Start the first pass of filtering.

Parameters

locus (*str*) – locus to start filtering

 **See also**

Must be paired with a subsequent *endFirstPass()*

checkAlleleName(*alleleName*)

Checks allele name against the database.

Parameters

alleleName (*str*) – allele name

Returns

returns the original *allele* truncated to appropriate number of digits, if it can't be found using any of the heuristics, return it as an *untypedAllele* (normally ****).

Return type

str

addAllele(*alleleName*)

Add allele to be filtered.

Parameters

alleleName (*str*) – process allele to be filtered

endFirstPass()

End first pass of filtering.

 **See also**

Must be paired with a previous *startFirstPass()*

startFiltering()

Start the main filtering.

 **See also**

must be paired with a subsequent *endFiltering()*

filterAllele(*alleleName*)

Filter a specified allele.

Parameters

alleleName (*str*) – allele to filter

Returns

return the translated allele

Return type

dict

endFiltering()

End filtering.

 **See also**

Must be paired with a previous `startFiltering()`

writeToLog(*logstring*='\\n')

Write a string to log.

Parameters

logstring (*str*) – defaults to line feed

cleanup()

Do any cleanups.

makeSeqDictionaries(*matrix*=None, *locus*=None)

Make a sequence dictionary for a given locus.

Parameters

- **matrix** (*StringMatrix*) – matrix to use.
- **locus** (*str*) – locus to use.

Returns

polyseq (dict): Keyed on locus*allele of all allele sequences, containing **ONLY** the polymorphic positions.

polyseqpos (dict): Keyed on locus of the positions of the polymorphic residues which you find in polyseq.

Return type

tuple

Raises

RuntimeError¹⁶ – If the alignment length could not be found in the MSF header.

translateMatrix(*matrix*=None)

Translate the whole matrix (all loci).

Parameters

matrix (*StringMatrix*) – matrix to translate

Returns

new instance with sequence data in columns

Return type

StringMatrix

class BinningFilter(*customBinningDict*=None, *logFile*=None, *untypedAllele*='****', *filename*=None, *binningDigits*=4)

Filters original data into “bins”.

This can be done through either digits (for HLA alleles) or custom rules defined a file for each locus.

Parameters

- **customBinningDict** (*dict*, *optional*) – a custom binning dict, this is keyed by locus, but each key consists of a series of lines, each line containing ruleset of which alleles belong in a given bin
- **logFile** (*str*, *optional*) – output logfile, must be set
- **untypedAllele** (*str*, *optional*) – defaults to ****
- **filename** (*str*, *optional*) – filename (**unused**), defaults to None
- **binningDigits** (*int*, *optional*) – defaults to 4

doDigitBinning(*matrix*=None)

Do the **digit** binning on specified matrix.

 **Note**

Digit binning is done only if `binningDigits` is set.

Parameters

matrix (*StringMatrix*) – matrix to modify

Returns
the modified matrix

Return type
StringMatrix

doCustomBinning(*matrix=None*)

Do the **custom** binning on specified matrix.

Note

Custom binning is done only if `customBinningDict` is set.

Parameters
matrix (*StringMatrix*) – matrix to modify

Returns
the modified matrix

Return type
StringMatrix

lookupCustomBinning(*testAllele, locus*)

Apply custom binning rules to a allele and locus pair.

Parameters

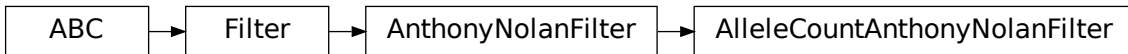
- **testAllele** (*str*) – allele to check
- **locus** (*str*) – locus to check

Returns
binned (or not) allele

Return type
str

class AlleleCountAnthonyNolanFilter(*lumpThreshold=None, **kw*)

Bases: *AnthonyNolanFilter*



Filters data with an allelecoun less than a threshold.

Parameters
lumpThreshold (*int*) – set threshold

Base class parameters.

Parameters

- **directoryName** (*str*) – directory that AnthonyNolan allele data is located
- **remoteMSF** (*str*) – Specifies the version (tag) of the remote `msf` directory in the [IMGT-HLA GitHub repo](#)¹⁷. If present, the remote MSF files for the specified version will be downloaded on-demand, and cached for later reuse
- **alleleFileFormat** (*str, optional*) – file format, can be `txt` or `msf` (default). Use of `msf` files is required in order to translate allele codes into polymorphic sequence data.
- **preserveAmbiguousFlag** (*int, optional*) – If set to `0` (default) then ambiguity is removed (e.g. `010101/0102/010301` will truncate this to `0101`). To preserve the ambiguity, set the option to `1` (for this example, it will result in a filtered allele “name” of `0101/0102/0103`)
- **preserveUnknownFlag** (*int, optional*) – If set to `0` (default) replace unknown alleles with the `untypedAllele` designator. To keep unrecognized allele names set to `1`.
- **preserveLowresFlag** (*int, optional*) – This option is similar to `preserveUnknownFlag`, but only applies to lowres alleles. If set to `1`, PyPop will keep allele names that are shorter than the default allele name length, usually 4 digits long. But if `preserveUnknownFlag` is set, this option has no effect, because all unknown alleles are preserved.
- **alleleDesignator** (*str, optional*) – the designator used to indicate a locus name (default `*`),
- **logFile** (*str, optional*) – log file

- **untypedAllele** (*str*, *optional*) – defaults to ****
- **unsequencedSite** (*str*, *optional*) – defaults to #
- **sequenceFileSuffix** (*str*, *optional*) – Suffix for file names used for finding sequences each allele. (e.g., if the file for locus A is A_prot.msxf, then keep the default be _prot. For nucleotide sequence files, this would be set _nuc.
- **filename** (*str*, *optional*) – Currently not used
- **numDigits** (*int*, *optional*) – Number of digits used for HLA data (default 4)
- **verboseFlag** (*int*, *optional*) – Verbose output (default is on, i.e. 1)
- **sequenceFilterMethod** (*str*, *optional*) – matching alleles to sequence, defaults to strict, can also be greedy

endFirstPass()

End first pass and then lump alleles.

First process regular *AnthonyNolanFilter* then modify all alleles with a count < lumpThreshold to lump.

PyPop.haplo

Module for estimating haplotypes and linkage disequilibrium measures.

Currently there are two implementations: *Emhaplofreq* and *Haplostats*.

Classes

| | |
|----------------------|---|
| <i>Haplo</i> | Estimating haplotypes given genotype data. |
| <i>Emhaplofreq</i> | Haplotype and linkage disequilibrium (LD) estimation via emhaplofreq. |
| <i>Haplostats</i> | Haplotype and LD estimation implemented via haplo.stats. |
| <i>HaploArlequin</i> | Performs haplotype estimation via Arlequin. |

Module Contents

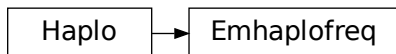
class Haplo

Estimating haplotypes given genotype data.

This is abstract stub class (currently has no methods).

class Emhaplofreq(locusData, untypedAllele='****', stream=None, testMode=False)

Bases: *Haplo*



Haplotype and linkage disequilibrium (LD) estimation via emhaplofreq.

This is essentially a wrapper to a Python extension built on top of the emhaplofreq command-line program. Will refuse to estimate haplotypes longer than that defined by emhaplofreq.

Parameters

- **locusData** (*StringMatrix*) – a StringMatrix
- **untypedAllele** (*str*) – defaults to ****
- **stream** (*TextOutputStream*) – output file
- **testMode** (*bool*) – default is False

serializeStart()

Serialize start of XML output to the currently defined XML stream.

➡ See also

must be paired with a subsequent *Emhaplofreq.serializeEnd()*

serializeEnd()

Serialize end of XML output to the currently defined XML stream.

➔ See also

must be paired with a previous `Emhaplofreq.serializeStart()`

estHaplotypes(*locusKeys=None, numInitCond=None*)

Estimate haplotypes for listed loci in locusKeys.

Parameters

- **locusKeys** (*str*) – format is a string consisting of
 - comma (,) separated haplotypes blocks for which to estimate haplotypes
 - within each “block”, each locus is separated by colons (:)
- **numInitCond** (*int*) – number of initial conditions to use

Example

*DQA1:*DPB1,*DRB1:*DQB1, means to estimate haplotypes for DQA1 and DPB1 loci followed by estimation of haplotypes for DRB1 and DQB1 loci.

estLinkageDisequilibrium(*locusKeys=None, permutationPrintFlag=0, numInitCond=None, numPermutations=None, numPermuInitCond=None*)

Estimate linkage disequilibrium (LD) for listed loci.

Parameters

- **locusKeys** (*str*) – see `estHaplotypes()`
- **permutationPrintFlag** (*int*) – print all permutations (default 0)
- **numInitCond** (*int*) – number of initial conditions (default None)
- **numPermutations** (*int*) – number of permutations (default None)
- **numPermuInitCond** (*int*) – number of initial conditions for each permutation (default None)

Example

See `estHaplotypes()` for an example that estimates LD

allPairwise(*permutationPrintFlag=0, numInitCond=None, numPermutations=None, numPermuInitCond=None, haploSuppressFlag=None, haplosToShow=None, mode=None*)

Estimate pairwise statistics for a given set of loci.

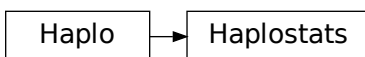
Depending on the flags passed, this can be used to estimate both LD (linkage disequilibrium) and HF (haplotype frequencies), an optional permutation test on LD can be run.

Parameters

- **permutationPrintFlag** (*int*) – sets whether the result from permutation output run will be included in the output XML. Default: 0 (disabled).
- **numInitCond** (*int*) – sets number of initial conditions before performing the permutation test. Default: None.
- **numPermutations** (*int*) – sets number of permutations that will be performed. Default: None.
- **numPermuInitCond** (*int*) – sets number of initial conditions tried per-permutation. Default: None.
- **haploSuppressFlag** (*int*) – sets whether haplotype information is generated in the output. Default: None
- **haplosToShow** (*list*) – list of haplotypes to show in output
- **mode** (*str*) – mode for haplotype output

class Haplostats(*locusData, untypedAllele='**', stream=None, testMode=False*)

Bases: `Haplo`



Haplotype and LD estimation implemented via `haplo.stats`.

This is a wrapper to a portion of the `haplo.stats` R package.

Parameters

- **locusData** (*StringMatrix*) – a *StringMatrix*
- **untypedAllele** (*str*) – defaults to ****
- **stream** (*TextOutputStream*) – output file
- **testMode** (*bool*) – default is `False`

serializeStart()

Serialize start of XML output to currently defined XML stream.

➔ **See also**

must be paired with a subsequent *Haplostats.serializeEnd()*

serializeEnd()

Serialize end of XML output to currently defined XML stream.

➔ **See also**

must be paired with a previous *Haplostats.serializeStart()*

estHaplotypes(*locusKeys=None, weight=None, control=None, numInitCond=10, testMode=False*)

Estimate haplotypes for listed loci in *locusKeys*.

If *locusKeys* is `None`, assume entire matrix. LD is also estimated if there are *locusKeys* consisting of only two loci.

⚠ **Warning**

FIXME: this does *not* yet remove missing data before haplotype estimations

Parameters

- **locusKeys** (*str*) – see *Emhaplofreq.estHaplotypes()* for format
- **weight** (*list*) – set weights (default `None`, which sets all weights equal)
- **control** (*dict*) – a dictionary of control parameters
- **numInitCond** (*int*) – number of initial conditions (default `None`)
- **testMode** (*bool*) – run in test mode default is `False`

Returns

multiple statistics

Return type

tuple

allPairwise(*weight=None, control=None, numInitCond=10*)

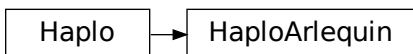
Estimate pairwise statistics for all pairs of loci.

Parameters

- **weight** (*list*) – see *Haplostats.estHaplotypes()*
- **control** (*dict*) – see *Haplostats.estHaplotypes()*
- **numInitCond** (*int*) – see *Haplostats.estHaplotypes()*

class HaploArlequin(*arpFilename, idCol, prefixCols, suffixCols, windowSize, mapOrder=None, untypedAllele='0', arlequinPrefix='arl_run'*)

Bases: *Haplo*



Performs haplotype estimation via Arlequin.

Deprecated since version 1.0.0

Deprecated since version 1.0.0.

Outputs Arlequin format data files and runtime info, also runs and parses the resulting Arlequin data so it can be made available programmatically to rest of Python framework.

Delegates all calls Arlequin to an internally instantiated ArlequinBatch Python object called 'batch'.

Parameters

- **arpFilename** (*str*) – Arlequin filename (must have .arp file extension)
- **idCol** (*str*) – column in input file that contains the individual id.
- **prefixCols** (*int*) – number of columns to ignore before allele data starts
- **suffixCols** (*int*) – number of columns to ignore after allele data stops
- **windowSize** (*int*) – size of sliding window
- **mapOrder** (*list*) – list order of columns if different to column order in file (defaults to order in file)
- **untypedAllele** (*str*) – (defaults to 0)
- **arlequinPrefix** (*str*) – prefix for all Arlequin run-time files (defaults to arl_run).

outputArlequin(*data*)

Outputs the specified .arp sample file.

Parameters

data (*list*) – list of strings containing the .arp sample file

runArlequin()

Run the Arlequin haplotyping program.

Generates the expected .txt set-up files for Arlequin, then forks a copy of arlecore.exe, which must be on PATH to actually generate the haplotype estimates from the generated .arp file.

genHaplotypes()

Parses Arlequin output to retrieve estimated haplotypes.

Returns

a list of the sliding windows which consists of tuples. Each tuple consists of:

- freqs (dict): dictionary entry (the haplotype-frequency) key-value pairs.
- popName (str): population name (original .arp file prefix)
- sampleCount (int): sample count (number of samples for that window)
- lociList (list): ordered list of loci considered

Return type

list

PyPop.hardyweinberg

Computing Hardy-Weinberg statistics on genotype data.

Attributes

use_scipy

If True use *scipy* to compute pvalue, rather than internal *pval*

Classes

HardyWeinberg

Calculate Hardy-Weinberg statistics for a single locus.

HardyWeinbergGuoThompson

Use Guo & Thompson (1992) algorithm for calculating statistics.

HardyWeinbergEnumeration

HW testing with Maldonado Torres' exact enumeration test.

HardyWeinbergGuoThompsonArlequin

Arlequin implementation of the Guo & Thompson algorithm.

Functions

| | |
|-------------------------------|--------------------|
| <code>pval(chisq, dof)</code> | Calculate p-value. |
|-------------------------------|--------------------|

Module Contents

`use_scipy = False`

If True use `scipy` to compute pvalue, rather than internal `pval`

class `HardyWeinberg`(*locusData=None, alleleCount=None, lumpBelow=5, flagChenTest=0*)

Calculate Hardy-Weinberg statistics for a single locus.

Given the observed genotypes for a locus, calculate the expected genotype counts based on Hardy Weinberg proportions for individual genotype values, and test for fit.

Parameters

- `locusData` (*list*) – list of tuples of genotype (`allele1`, `allele2`)
- `alleleCount` (*tuple*) – a tuple consisting of a dictionary of counts, total count and number of untyped individuals as returned by `PyPop.DataTypes.Genotypes.getLocusDataAt()`
- `lumpBelow` (*int, optional*) – lump alleles with frequency less than this threshold as if they were in same class (Default: 5)
- `flagChenTest` (*int, optional*) – if enabled (1) do Chen’s chi-square-based “corrected” p-value (Default: 0, disabled)

`serializeTo`(*stream, allelelump=0*)

Serialize output to specified XML stream.

Parameters

- `stream` (`XMLOutputStream`) – write to specified XML stream (generally a file)
- `allelelump` (*int*) – record the allele lumping value

`serializeXMLTableTo`(*stream*)

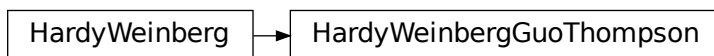
Serialize the genotype table.

Parameters

`stream` (`XMLOutputStream`) – XML stream

class `HardyWeinbergGuoThompson`(*locusData=None, alleleCount=None, runMCMCTest=0, runPlainMCTest=0, dememorizationSteps=2000, samplingNum=1000, samplingSize=1000, maxMatrixSize=250, monteCarloSteps=1000000, testing=False, **kw*)

Bases: `HardyWeinberg`



Use Guo & Thompson (1992) algorithm for calculating statistics.

This Python class wraps the functionality of the Guo & Thompson program `gthwe`. In addition to the arguments for the base class, this class accepts the following additional keywords:

Parameters

- `locusData` (*list*) – list of tuples of genotype (`allele1`, `allele2`)
- `alleleCount` (*tuple*) – a tuple consisting of a dictionary of counts, total count and number of untyped individuals as returned by `PyPop.DataTypes.Genotypes.getLocusDataAt()`
- `runMCMCTest` (*int*) – If enabled (1) run the Monte Carlo-Markov chain (MCMC) version of the test (what is normally referred to as “Guo & Thompson”), default disabled (0)
- `runPlainMCTest` (*int*) – If enabled (1) run a plain Monte Carlo/randomization without the Markov-chain version of the test (this is also described in the original Guo & Thompson *Biometrics* paper, but was not in their original program)
- `dememorizationSteps` (*int*) – number of “dememorization” initial steps for random number generator (default 2000).
- `samplingNum` (*int*) – the number of chunks for random number generator (default 1000).
- `samplingSize` (*int*) – size of each chunk (default 1000).
- `maxMatrixSize` (*int*) – maximum size of *flattened’ lower-triangular matrix of observed alleles* (default ‘250’).
- `monteCarloSteps` (*int*) – number of steps for the plain Monte Carlo randomization test (without Markov-chain)

- **testing** (*bool*) – testing mode, default `False`

generateFlattenedMatrix()

Generated a flattened version of the genotype matrix.

dumpTable(*locusName, stream, allelump=0*)

Output table to stream.

Parameters

- **locusName** (*str*) – locus to output table
- **stream** (*XMLOutputStream*) – name of XML stream
- **allelump** (*int*) – record allele lumping level (default `0`)

Returns

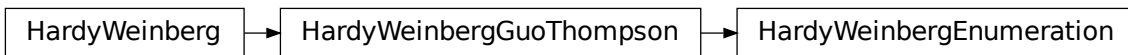
if an empty tag

Return type

None

class HardyWeinbergEnumeration(*locusData=None, alleleCount=None, doOverall=0, **kw*)

Bases: *HardyWeinbergGuoThompson*



HW testing with Maldonado Torres' exact enumeration test.

Warning

This requires the Enumeration C code to be compiled as a module using SWIG. By default this is currently disabled.

Parameters

- **locusData** (*list*) – list of tuples of genotype (*allele1, allele2*)
- **alleleCount** (*tuple*) – a tuple consisting of a dictionary of counts, total count and number of untyped individuals as returned by `PyPop.DataTypes.Genotypes.getLocusDataAt()`
- **doOverall** (*int*) – if set to true (1), then do overall *p*-value test default is false (0)

serializeTo(*stream, allelump=0*)

Serialize enumeration test output to stream.

Parameters

- **stream** (*XMLOutputStream*) – XML stream to use
- **allelump** (*int*) – record allele lumping level (default `0`)

class HardyWeinbergGuoThompsonArlequin(*matrix=None, locusName=None, arlequinExec='arlecure.exe', markovChainStepsHW=100000, markovChainDememorisationStepsHW=1000, untypedAllele='****')*

Arlequin implementation of the Guo & Thompson algorithm.

Deprecated since version 1.0.0

Deprecated since version 1.0.0.

This class extracts the Hardy-Weinberg (HW) statistics using the Arlequin implementation of the HW exact test, by the following:

1. creates a subdirectory `arlequinRuns` in which all the Arlequin specific files are generated;
2. then the specified arlequin executable is run, generating the Arlequin output HTML files (`*.htm`);
3. the Arlequin output is then parsed for the relevant statistics;
4. lastly, the `arlequinRuns` directory is removed.

Since the directory name `arlequinRuns` is currently hardcoded, this has the consequence that this class cannot be invoked concurrently.

Parameters

- **matrix** (*StringMatrix*) – matrix to extract locus from

- **locusName** (*str*) – locus to use
- **arlequinExec** (*str*) – name of Arlequin executable
- **markovChainStepsHW** (*int*) – number of steps to use in Markov chain (default: 100000).
- **markovChainDememorisationStepsHW** (*int*) – “Burn-in” time for Markov chain (default: 1000).
- **untypedAllele** (*str*) – untyped allele identifier

serializeTo(*stream*)

Serialize output to stream.

Parameters

stream (*XMLOutputStream*) – stream to serialize to

pval(*chisq, dof*)

Calculate p-value.

Parameters

- **chisq** (*float*) – Chi-square value
- **dof** (*int*) – degrees of freedom

Returns

p-value

Return type

float

PyPop.homozygosity

Computing homozygosity statistics on genotype or allele counts.

Classes

| | |
|---|--|
| <i>Homozygosity</i> | Calculate homozygosity statistics. |
| <i>HomozygosityEWSlatkinExact</i> | Compute homozygosity using the Ewens-Watterson-Slatkin "exact test". |
| <i>HomozygosityEWSlatkinExactPairwise</i> | Compute pairwise homozygosity using the Ewens-Watterson-Slatkin. |

Functions

| | |
|--|------------------------------------|
| <i>getObservedHomozygosityFromAlleleData</i> (<i>alleleData</i>) | Get homozygosity from allele data. |
|--|------------------------------------|

Module Contents

class **Homozygosity**(*alleleData, rootPath='.'*)

Calculate homozygosity statistics.

Given allele count data for a given locus, calculates the observed homozygosity and returns the approximate expected homozygosity statistics taken from previous simulation runs.

Parameters

- **alleleData** (*list*) – list of allele counts
- **rootPath** (*str*) – path to the root of the directory where the pre-calculated expected homozygosity statistics can be found.

getObservedHomozygosity()

Calculate and return observed homozygosity.

Available even if expected stats cannot be calculated.

Returns

observed homozygosity

Return type

float

canGenerateExpectedStats()

Can expected homozygosity stats be calculated?

Returns 1 if expected homozygosity statistics can be calculated. Should be called before attempting to get any expected homozygosity statistics.

Returns

1 if can be calculated, otherwise 0

Return type

int

getPValueRange()

Gets lower and upper bounds for p-value.

Only meaningful if `canGenerateExpectedStats()` returns true.

Returns

(lower, upper) bounds.

Return type

tuple

getCount()

Number of runs used to calculate statistics.

Only meaningful if `canGenerateExpectedStats()` returns 1.

Returns

number of runs

Return type

int

getExpectedHomozygosity()

Gets mean of expected homozygosity.

This is the estimate of the *expected* homozygosity. Only meaningful if `canGenerateExpectedStats()` returns true.

Returns

mean of expected homozygosity

Return type

float

getVarExpectedHomozygosity()

Gets variance of expected homozygosity.

This is the estimate of the variance *expected* homozygosity. Only meaningful if `canGenerateExpectedStats()` returns true.

Returns

variance of expected homozygosity

Return type

float

getNormDevHomozygosity()

Gets normalized deviate of homozygosity.

Only meaningful if `canGenerateExpectedStats()` returns true.

Returns

normalized deviate of homozygosity

Return type

float

serializeHomozygosityTo(stream)

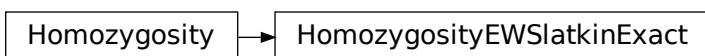
Serialize homozygosity to a stream.

Parameters

stream (`XMLOutputStream`) – stream to save to

class `HomozygosityEWSlatkinExact`(*alleleData=None, numReplicates=10000*)

Bases: `Homozygosity`



Compute homozygosity using the Ewens-Watterson-Slatkin “exact test”.

Parameters

- **alleleData** (*list*) – list of allele counts
- **numReplicates** (*int*) – number or replicates for simulation.

doCalcs(*alleleData*)

Run the computations.

Parameters

alleleData (*list*) – list of allele counts

getHomozygosity()

Get the homozygosity statistics.

Returns

tuple consisting of:

- theta
- prob_ewens
- prob_homozygosity
- mean_homozygosity
- obsv_homozygosity
- var_homozygosity

Return type

tuple

serializeHomozygosityTo(*stream*)

Serialize homozygosity to a stream.

Parameters

stream (*XMLOutputStream*) – stream to save to

returnBulkHomozygosityStats(*alleleCountDict=None, binningMethod=None*)

Get bulk homozygosity statistics for multiple allele counts.

This function is designed to work with the `PyPop.RandomBinning` submodule.

Parameters

- **alleleCountDict** (*dict*) – dictionary of lists of allele counts
- **binningMethod** (*str*) – record the binning method used

Returns

dictionary of statistics

Return type

dict

class **HomozygosityEWSlatkinExactPairwise**(*matrix=None, numReplicates=10000, untypedAllele='****')*

Compute pairwise homozygosity using the Ewens-Watterson-Slatkin.

Parameters

- **matrix** (*StringMatrix*) – matrix with multiple loci columns for pairwise comparison
- **numReplicates** (*int, optional*) – number or replicates for simulation.
- **untypedAllele** (*str, optional*) – untyped allele

serializeTo(*stream*)

Serialize to a stream.

Parameters

stream (*XMLOutputStream*) – stream to save to

getObservedHomozygosityFromAlleleData(*alleleData*)

Get homozygosity from allele data.

Parameters

alleleData (*list*) – list of allele counts

Returns
observed homozygosity

Return type
float

PyPop.parsers

Parsing input population data files.

Includes *ParseGenotypeFile* for parsing individuals genotyped at multiple loci and *ParseAlleleCountFile* for parsing literature data which only includes allele counts.

Both file formats are assumed to have a population header information with, consisting of a line of column headers (population metadata) followed by a line with the actual data, followed by the column headers for the samples (sample metadata) followed by the sample data itself (either individuals in the genotyped case, or alleles in the allele count case).

Classes

| | |
|-----------------------------|--|
| <i>ParseFile</i> | Common functionality for reading the two file formats. |
| <i>ParseGenotypeFile</i> | Class to parse standard datafile in genotype form. |
| <i>ParseAlleleCountFile</i> | Class to parse datafile in allele count form. |

Module Contents

class ParseFile(*filename*, *validPopFields=None*, *validSampleFields=None*, *separator='\t'*, *fieldPairDesignator='_1:_2'*, *alleleDesignator='*'*, *popNameDesignator='+'*)

Common functionality for reading the two file formats.

Base class.

Parameters

- **filename** (*str*) – filename for the file to be parsed.
- **validPopFields** (*str*) – valid headers (one per line) for overall population data (no default)
- **validSampleFields** (*str*) – valid headers (one per line) for lines of sample data. (no default)
- **separator** (*str*, *optional*) – separator for adjacent fields (default: a tab stop, '\t').
- **fieldPairDesignator** (*str*, *optional*) – consists of additions to the allele *stem* for fields grouped in pairs (*allele fields*) [e.g. for `HLA-A`, and `HLA-A(2)`, then we use `:(2)`, for `DQA1_1` and `DQA1_2`, then use `_1:_2`, the latter case distinguishes both fields from the stem] (default: `:(2)`)
- **alleleDesignator** (*str*, *optional*) – first character of the key which determines whether this column contains allele data. Defaults to `*`
- **popNameDesignator** (*str*, *optional*) – first character of the key which determines whether this column contains the population name. Defaults to `+`

getPopData()

Returns a dictionary of population data.

Returns

keyed by types specified in population metadata file

Return type

dict

getSampleMap()

Returns dictionary of sample data.

Returns

each entry contains either a 2-tuple of column position or a single column position keyed by field originally specified in sample metadata file

Return type

dict

getFileData()

Returns the file data.

Returns

- a 2-tuple “wrapper”:
- `str`: raw sample lines, *without* header metadata.
- `str`: the field separator.

Return type

tuple

genSampleOutput(*fieldList*)

Prints the data specified in ordered field list.

Deprecated since version 0.7.0

Deprecated since version 0.7.0.

serializeMetadataTo(*stream*)

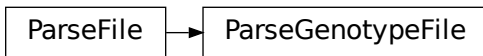
Write metadata to stream.

Parameters

stream (*XMLStreamOutput*) – output stream

class ParseGenotypeFile(*filename*, *untypedAllele*=‘****’, ***kw*)

Bases: *ParseFile*



Class to parse standard datafile in genotype form.

Processes files that consist specifically of data with individual genotyped for one or more loci.

Parameters

- **filename** (*str*) – filename for the file to be parsed.
- **untypedAllele** (*str*, *optional*) – The designator for an untyped locus. Defaults to ****.

Base class.

Parameters

- **filename** (*str*) – filename for the file to be parsed.
- **validPopFields** (*str*) – valid headers (one per line) for overall population data (no default)
- **validSampleFields** (*str*) – valid headers (one per line) for lines of sample data. (no default)
- **separator** (*str*, *optional*) – separator for adjacent fields (default: a tab stop, ‘\t’).
- **fieldPairDesignator** (*str*, *optional*) – consists of additions to the allele *stem* for fields grouped in pairs (*allele fields*) [e.g. for ‘HLA-A’, and HLA-A(2), then we use : (2), for DQA1_1 and DQA1_2, then use _1:_2, the latter case distinguishes both fields from the stem] (default: :(2))
- **alleleDesignator** (*str*, *optional*) – first character of the key which determines whether this column contains allele data. Defaults to *
- **popNameDesignator** (*str*, *optional*) – first character of the key which determines whether this column contains the population name. Defaults to +

genValidKey(*field*, *fieldList*)

Check and validate key.

- ‘field’: string with field name.
- ‘fieldList’: a dictionary of valid fields.

Check to see whether ‘field’ is a valid key, and generate the appropriate ‘key’. Returns a 2-tuple consisting of ‘isValidKey’ boolean and the ‘key’.

Note: this is explicitly done in the subclass of the abstract ‘ParseFile’ class (i.e. since this subclass should have ‘knowledge’ about the nature of fields, but the abstract class should not have)

getMatrix()

Returns the genotype data.

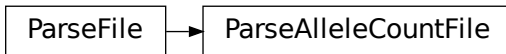
Returns the genotype data in a 'StringMatrix' NumPy array.

serializeSubclassMetadataTo(stream)

Serialize subclass-specific metadata.

class ParseAlleleCountFile(filename, **kw)

Bases: *ParseFile*



Class to parse datafile in allele count form.

Input files consist of allele counts across a whole population. Currently only handles one locus per population. Example:

```
<metadata-line1>
<metadata-line2>
DQA1 count
0102 20
0103 33
...
```

Base class.

Parameters

- **filename** (*str*) – filename for the file to be parsed.
- **validPopFields** (*str*) – valid headers (one per line) for overall population data (no default)
- **validSampleFields** (*str*) – valid headers (one per line) for lines of sample data. (no default)
- **separator** (*str*, *optional*) – separator for adjacent fields (default: a tab stop, '\t').
- **fieldPairDesignator** (*str*, *optional*) – consists of additions to the allele *stem* for fields grouped in pairs (*allele fields*) [e.g. for `HLA-A`, and `HLA-A(2)`, then we use `:(2)`, for `DQA1_1` and `DQA1_2`, then use `_1:_2`, the latter case distinguishes both fields from the stem] (default: `:(2)`)
- **alleleDesignator** (*str*, *optional*) – first character of the key which determines whether this column contains allele data. Defaults to `*`
- **popNameDesignator** (*str*, *optional*) – first character of the key which determines whether this column contains the population name. Defaults to `+`

genValidKey(*field*, *fieldList*)

Checks validity of a field.

Parameters

- **field** (*str*) – field to check
- **fieldList** (*str*) – list that `field` is checked against

Returns

2-tuple of:

- boolean: whether key is valid
- str: key

Return type

tuple

Note

The first element in the `fieldList` is a locus name, which may contain many loci (delimited by colons `:`). If `field` in the input file match *any* of these keys, this method will return the field and a valid match.

Example

If the first element of `fieldList` is `DQA1:DRA:DQB1`, then calling this function with `field` set to `DRA`, this would return `(True, DRA)`

`serializeSubclassMetadataTo(stream)`

Serialize subclass specific metadata.

Parameters

stream (*XMLOutputStream*) – output stream

`getAlleleTable()`

Get the current allele table.

Returns

keyed by allele name with value count

Return type

dict

`getLocusName()`

Get the locus name.

Returns

locus name

Return type

str

`getMatrix()`

Get the full genotype data.

Returns

containing all the genotype data

Return type

StringMatrix

PyPop.popaggregate

Module for collecting multiple population outputs.

Classes

| | |
|-------------|--|
| <i>Meta</i> | Aggregates output from multiple population runs. |
|-------------|--|

Functions

| | |
|--|---|
| <code>translate_string_to_stdout(xslFilename, inString[, ...])</code> | Transform XML string using XSLT and save to stdout. |
| <code>translate_string_to_file(xslFilename, inString, outFile)</code> | Transform XML string using XSLT and save to file. |
| <code>translate_file_to_stdout(xslFilename, inFile[, ...])</code> | Transform XML file using XSLT and save to stdout. |
| <code>translate_file_to_file(xslFilename, inFile, outFile[, ...])</code> | Transform XML file using XSLT and save to a file. |

Module Contents

class `Meta`(*popmetabinpath=None, datapath=None, metaXSLTDirectory=None, dump_meta=False, TSV_output=True, prefixTSV=None, PHYLIP_output=False, ihwg_output=False, batchsize=0, outputDir=None, xml_files=None*)

Aggregates output from multiple population runs.

Transform a specified list of `.xml` output files to `.tsv` tab-separated values (TSV) form.

Parameters

- **popmetabinpath** (*str*) – the directory for where meta sources are kept
- **datapath** (*str*) – data where XSLT and other meta sources may be kept
- **metaXSLTDirectory** (*str*) – fallback XSLT directory
- **dump_meta** (*bool*) – create the `meta.xml` file (default to `False`.)
- **TSV_output** (*bool*) – output `.tsv` tables by default (enabled by default). (such tables can be used by R)

- **prefixTSV** (*str*) – prefix to use for all .tsv files
- **PHYLIP_output** (*bool*) – create PHYLIP output (disabled by default)
- **ihwg_output** (*bool*) – by default, don't enable the 13th IHWG format headers
- **batchsize** (*int*) – size of batches to process separately (default batchsize=0, a separate batch for each file)
- **outputDir** (*str*) – output directory to write XML files to
- **xml_files** (*list*) – list of generate XML files

translate_string_to_stdout(*xslFilename, inString, outputDir=None, params=None*)

Transform XML string using XSLT and save to stdout.

Parameters

- **xslFilename** (*str*) – name of XSLT file
- **inString** (*str*) – XML string
- **outputDir** (*str, optional*) – name of output directory
- **params** (*list, optional*) – list of XSLT parameters

translate_string_to_file(*xslFilename, inString, outFile, outputDir=None, params=None*)

Transform XML string using XSLT and save to file.

Parameters

- **xslFilename** (*str*) – name of XSLT file
- **inString** (*str*) – XML string
- **outFile** (*str*) – name of output file
- **outputDir** (*str*) – name of output directory
- **params** (*list*) – list of XSLT parameters

translate_file_to_stdout(*xslFilename, inFile, inputDir=None, params=None*)

Transform XML file using XSLT and save to stdout.

Parameters

- **xslFilename** (*str*) – name of XSLT file
- **inFile** (*str*) – name of input XML file
- **inputDir** (*str, optional*) – name of input directory
- **params** (*list, optional*) – list of XSLT parameters

Returns

consisting of a bool (transformation successful) and str (output)

Return type

tuple

translate_file_to_file(*xslFilename, inFile, outFile, inputDir=None, outputDir=None, params=None*)

Transform XML file using XSLT and save to a file.

Parameters

- **xslFilename** (*str*) – name of XSLT file
- **inFile** (*str*) – name of input XML file
- **outFile** (*str*) – name of output file
- **inputDir** (*str, optional*) – name of input directory
- **outputDir** (*str, optional*) – name of output directory
- **params** (*list, optional*) – list of XSLT parameters

Returns

transformation successful

Return type

bool

PyPop.popanalysis

Primary access to PyPop's population genetics statistics modules.

This module handles processing `configparser.ConfigParser`¹⁸ instance. The `Main` class coordinates running the analysis packages specified in this `configparser.ConfigParser`¹⁹ instance which can be:

- created from a filename passed from command-line argument `oar`;
- from values populated by the GUI (for example, selected from an `.ini` file,
- created programmatically as part of an external Python program

Here is an example of calling `Main` programmatically, explicitly specifying the `untypedAllele` and `alleleDesignator` in the `.pop` file:

```
>>> from PyPop.popanalysis import Main
>>> from configparser import ConfigParser
>>>
>>> config = ConfigParser()
>>> config.read_dict({
...     "ParseGenotypeFile": {"untypedAllele": "****",
...                             "alleleDesignator": "*",
...                             "validSampleFields": "%a_1\n*a_2"}})
>>>
>>> pop_contents = '''a_1\ta_2
... ****\t****
... 01:01\t02:01
... 02:10\t03:01:02'''
>>> with open("my.pop", "w") as f:
...     _ = f.write(pop_contents)
...
>>> application = Main(
...     config=config,
...     fileName="my.pop",
...     version="fake",
... )
LOG: no XSL file, skipping text output
LOG: Data file has no header data block
```

Classes

| | |
|-------------------|--------------------------------------|
| <code>Main</code> | Main interface to the PyPop modules. |
|-------------------|--------------------------------------|

Functions

| | |
|---|---|
| <code>getConfigInstance(configFilename, altpath)</code> | Create and return <code>ConfigParser</code> instance. |
| <code>get_sequence_directory(directory_str)</code> | Get the directory for the <code>PyPop.Filter</code> . <code>AnthonyNolanFilter</code> . |

Module Contents

class `Main`(`config=None`, `xslFilename=None`, `xslFilenameDefault=None`, `fileName=None`, `datapath=None`, `thread=None`, `outputDir=None`, `version=None`, `testMode=False`)

Main interface to the PyPop modules.

Runs the analyses specified in the configuration object provided to the `config` parameter, and an input `fileName`, and generates an output XML file. The XML output file name, appends `-out.xml` on to the stem of the provided `fileName`. For example, if `fileName="MyPopulation.pop"` is provided as a parameter, the output XML file will be `MyPopulation-out.xml`.

Changed in version 1.4.0

Changed in version 1.4.0: If an `xslFilename` or `xslFilenameDefault` is provided, also generate a plain text output. Otherwise no text output is generated. Previous to this version, if neither were provided, the program would exit with an error.

Parameters

- **config** (`configparser.ConfigParser`²⁰) – configure object
- **xslFilename** (`str`, *optional*) – XSLT file to use
- **xslFilenameDefault** (`str`, *optional*) – fallback file name
- **fileName** (`str`) – input `.pop` file
- **datapath** (`str`, *optional*) – root of data path

- **thread** (*str*, *optional*) – specified thread
- **outputDir** (*str*, *optional*) – use a different output directory than default
- **version** (*str*, *optional*) – current Python version for output
- **testMode** (*bool*, *optional*) – enable testing mode

getXmlOutPath()

Get name of XML file.

Returns

return XML file name

Return type

XMLOutputStream

getTxtOutPath()

Get name of .txt output file.

Returns

return txt file name

Return type

TextOutputStream

getConfigInstance(*configFilename=None, altpath=None*)

Create and return ConfigParser instance.

Parameters

- **configFilename** (*str*) – a specified .ini filename
- **altpath** (*str*) – an alternative path to search if no .ini filename provided in configFilename

Returns

configuration object

Return type

*configparser.ConfigParser*²¹

get_sequence_directory(*directory_str*)

Get the directory for the `PyPop.Filter.AnthonyNolanFilter`.

Parameters

directory_str (*str*) – directory to search

Returns

path to sequence files

Return type

str

PyPop.popmeta

Command-line interface for popmeta.

Functions

| | |
|---------------------------|---------------------------------|
| <code>main([argv])</code> | Entry point for popmeta script. |
|---------------------------|---------------------------------|

Module Contents

main(*argv=sys.argv*)

Entry point for popmeta script.

Parameters

argv (*list*) – list of command-line options (default is `sys.argv`)

PyPop.pypop

Command-line interface for pypop.

Functions

| | |
|---------------------------------------|--|
| <code>main([argv])</code> | Entry point for pypop script. |
| <code>main_interactive([argv])</code> | Entry point for interactive mode script pypop-interactive. |

Module Contents

main(*argv=sys.argv*)

Entry point for pypop script.

Parameters

argv (*list*) – list of command-line options (default is `sys.argv`)

main_interactive(*argv=sys.argv*)

Entry point for interactive mode script pypop-interactive.

Parameters

argv (*list*) – list of command-line options (default is `sys.argv`)

PyPop.randombinning

Generating randomized sets allele counts for statistical analyses.

Classes

| | |
|--|---|
| <code>RandomBinsForHomozygosity</code> | Generate randomized sets of bins for homozygosity analysis. |
|--|---|

Module Contents

class RandomBinsForHomozygosity(*logFile=None, untypedAllele='***', filename=None, numReplicates=10000, binningReplicates=100, locus=None, xmlfile=None, randomResultsFileName=None*)

Generate randomized sets of bins for homozygosity analysis.

Parameters

- **logFile** (*str*) – output log file
- **untypedAllele** (*str, optional*) – untyped allele (default `***`)
- **filename** (*str*) – input filename
- **numReplicates** (*int, optional*) – replicates (default `10000`)
- **binningReplicates** (*int, optional*) – replicates for binning (default `100`)
- **locus** (*str*) – locus name
- **xmlfile** (*XMLOutputStream, optional*) – output stream
- **randomResultsFileName** (*str*) – output file for the randomized results

randomMethod(*alleleCountsBefore=None, alleleCountsAfter=None*)

Do binning replicates with random-based method.

Parameters

- **alleleCountsBefore** (*list*) – allele counts before binning
- **alleleCountsAfter** (*list*) – allele counts after binning

sequenceMethod(*alleleCountsBefore=None, alleleCountsAfter=None, polyseq=None, polyseqpos=None*)

Do binning replicates with sequence-based method.

Parameters

- **alleleCountsBefore** (*list*) – allele counts before binning
- **alleleCountsAfter** (*list*) – allele counts after binning

- **polyseq** (*dict*) – Keyed on locus*allele of all allele sequences, containing **ONLY** the polymorphic positions.
- **polyseqpos** (*dict*) – Keyed on locus of the positions of the polymorphic residues which you find in polyseq.

PyPop.utils

Module for common utility classes and functions.

Contains convenience classes for output of text and XML files.

Attributes

| | |
|----------------------------------|-----------------------------|
| <code>GENOTYPE_SEPARATOR</code> | Separator between genotypes |
| <code>GENOTYPE_TERMINATOR</code> | Terminator of genotypes |

Classes

| | |
|-------------------------------|--|
| <code>TextOutputStream</code> | Output stream for writing text files. |
| <code>XMLOutputStream</code> | Output stream for writing XML files. |
| <code>StringMatrix</code> | Matrix of strings and other metadata from input file to PyPop. |
| <code>Group</code> | Group list or sequence into non-overlapping chunks. |

Functions

| | |
|--|--|
| <code>critical_exit(message, *args)</code> | Log a CRITICAL message and exit with status 1. |
| <code>getStreamType(stream)</code> | Get the type of stream. |
| <code>glob_with_pathlib(pattern)</code> | Use globbing with <code>pathlib</code> . |
| <code>natural_sort_key(s[, _nsre])</code> | Generate a key for natural (human-friendly) sorting. |
| <code>unique_elements(li)</code> | Gets the unique elements in a list. |
| <code>appendTo2dList(aList[, appendStr])</code> | Append a string to each element in a list. |
| <code>convertLineEndings(file, mode)</code> | Convert line endings based on platform. |
| <code>fixForPlatform(filename[, txt_ext])</code> | Fix for some Windows/MS-DOS platforms. |
| <code>copyfileCustomPlatform(src, dest[, txt_ext])</code> | Copy file to file with fixes. |
| <code>copyCustomPlatform(file, dist_dir[, txt_ext])</code> | Copy file to directory with fixes. |
| <code>checkXSLFile(xslFilename[, path, subdir, abort, msg])</code> | Check XSL filename and return full path. |
| <code>getUserFilenameInput(prompt, filename)</code> | Get user filename input. |
| <code>splitIntoNGroups(alist[, n])</code> | Divides a list up into n parcels (plus whatever is left over). |

Module Contents

`GENOTYPE_SEPARATOR = '~'`

Separator between genotypes

Example

In a haplotype `01:01~13:01~04:02`

`GENOTYPE_TERMINATOR = '~'`

Terminator of genotypes

Example

``02:01:01:01~`

`class TextOutputStream(file)`

Output stream for writing text files.

Parameters

`file (file)` – file handle

`write(str)`

Write to stream.

Parameters

`str (str)` – string to write

writeln(*str*='\n')

Write a newline to stream.

Parameters
str (*str*, *optional*) – defaults to newline

close()

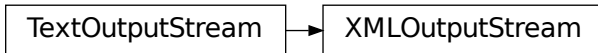
Close stream.

flush()

Flush to disk.

class XMLOutputStream(*file*)

Bases: *TextOutputStream*



Output stream for writing XML files.

opentag(*tagname*, ***kw*)

Write an open XML tag to stream.

Tag attributes passed as optional named keyword arguments.

Example

```
opentag('tagname', role=something, id=else)
```

produces the result:

```
<tagname role="something" id="else">
```

Attribute and values are optional:

```
opentag('tagname')
```

Produces:

```
<tagname>
```

➔ See also

Must be followed by a [closetag\(\)](#).

Parameters
tagname (*str*) – name of XML tag

emptytag(*tagname*, ***kw*)

Write an empty XML tag to stream.

This follows the same syntax as [opentag\(\)](#) but without XML content (but can contain attributes).

Example

```
`emptytag('tagname', attr='val')
```

produces:

```
<tagname attr="val"/>
```

Parameters
tagname (*str*) – name of XML tag

closetag(*tagname*)

Write a closing XML tag to stream.

Example

```
closetag('tagname')
```

Generate a tag in the form:

```
</tagname>
```

See also

Must be preceded by a `opentag()`.

Parameters

tagname (*str*) – name of XML tag

tagContents(*tagname*, *content*, ***kw*)

Write XML tags around contents to a stream.

Example

```
tagContents('tagname', 'foo bar')
```

produces:

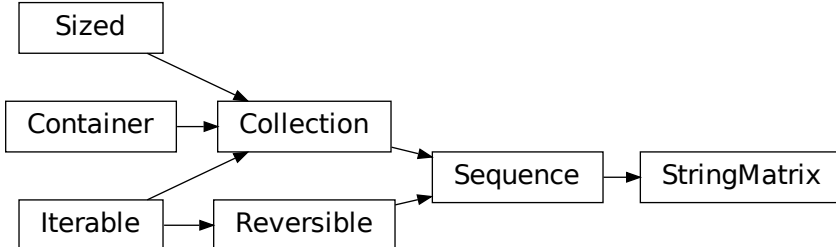
```
<tagname>foo bar</tagname>
```

Parameters

- **tagname** (*str*) – name of XML tag
- **content** (*str*) – must only be a string. &, < and > are converted into valid XML equivalents.

class StringMatrix(*rowCount=None*, *colList=None*, *extraList=None*, *colSep='\t'*, *headerLines=None*)

Bases: `collections.abc.Sequence`²²



Matrix of strings and other metadata from input file to PyPop.

`StringMatrix` is a subclass of `collections.abc.Sequence`²³ and represents genotype or locus-based data in a row-oriented matrix structure with NumPy-style indexing and sequence semantics. Rows correspond to individuals, and columns correspond to loci.

The object supports indexing, assignment, copying, and printing using standard Python and NumPy idioms.

Parameters

- **rowCount** (*int*) – number of rows in matrix
- **colList** (*list*) – list of locus keys in a specified order
- **extraList** (*list*) – other non-matrix metadata
- **colSep** (*str*) – column separator
- **headerLines** (*list*) – list of lines in the header of original file

Note

- `len(matrix)` returns the number of rows.
- Indexing retrieves data by locus or locus combinations.
- Assignment updates genotype or metadata values in place.

- Slicing over rows (e.g., `matrix[i:j]`) is not currently supported.
- Deep copying produces a fully independent matrix.

Examples

Create a matrix of two individuals with two loci and assign genotype data:

```
>>> matrix = StringMatrix(2, ["A", "B"])
>>> matrix [0, "A"] = ("A0_1", "A0_2")
>>> matrix [1, "A"] = ("A1_1", "A1_2")
>>> matrix [0, "B"] = ("B0_1", "B0_2")
>>> matrix [1, "B"] = ("B1_1", "B1_2")
```

Length of matrix is defined as the number of individuals in the matrix:

```
>>> len(matrix)
2
```

Retrieve data for a single locus:

```
>>> matrix["A"]
[['A0_1', 'A0_2'], ['A1_1', 'A1_2']]
```

String representation:

```
>>> print (matrix)
StringMatrix([[ 'A0_1', 'A0_2', 'B0_1', 'B0_2'],
               ['A1_1', 'A1_2', 'B1_1', 'B1_2']], dtype=object)
```

Copying the matrix:

```
>>> import copy
>>> m2 = copy.deepcopy(matrix)
>>> m2 is matrix
False
```

`__repr__()`

Override default representation.

Returns

new string representation

Return type

str

`__len__()`

Get number of rows (individuals) in the matrix.

This allows `StringMatrix` instances to be used with `len()`, iteration, and other Python sequence protocols.

Returns

number of rows in the matrix

Return type

int

`__deepcopy__(memo)`

Create a deepcopy for `copy.deepcopy`.

This simply calls `self.copy()` to allow `copy.deepcopy(matrixInstance)` to work out of the box.

Parameters

memo (*dict*) – opaque object

Returns

copy of the matrix

Return type

StringMatrix

`__getslice__(i, j)`

Get slice (overrides built-in).

Warning

Currently not supported for *StringMatrix*

`__getitem__(key)`

Get the item at given key (overrides built-in numpy).

Parameters

key (*str*) – locus key

Returns

a list (a single column vector if only one position specified), or list of lists: (a set of column vectors if several positions specified) of tuples for key

Return type

list

Raises

KeyError²⁴ – if key is not found, or of wrong type

`__setitem__(index, value)`

Set the value at an index (override built in).

Parameters

- **index** (*tuple*) – index into matrix
- **value** (*tuple|str*) – can set using a tuple of strings, or a single string (for metadata)

Raises

- **IndexError**²⁵ – if index is not a tuple
- **ValueError**²⁶ – if value is not a tuple or string
- **KeyError**²⁷ – if the index can't be found

`dump(locus=None, stream=sys.stdout)`

Write file to a stream in original format.

Parameters

- **locus** (*str, optional*) – write just specified locus, if omitted, default to all loci
- **stream** (*TextOutputStream/XMLOutputStream/stdout*) – output stream

`copy()`

Make a (deep) copy.

Returns

a deep copy of the current object

Return type

StringMatrix

`getNewStringMatrix(key)`

Create new StringMatrix containing specified loci.

Note

The format of the keys is identical to `__getitem__()` except that it returns a full *StringMatrix* instance which includes all metadata

Parameters

key (*str*) – a string representing the loci, using the locus1:locus2 format

Returns

full instance

Return type

StringMatrix

Raises

KeyError²⁸ – if locus can not be found.

getUniqueAlleles(*key*)

Get naturally sorted list of unique alleles.

Parameters

key (*str*) – loci to get

Returns

list of unique integers sorted by allele name using natural sort

Return type

list

convertToInts()

Convert the matrix to integers.

Note

This function is used by the *PyPop.haplo.Haplostats* class. Note that integers start at 1 for compatibility with haplo-stats module

Returns

matrix where the original allele names are now represented by integers

Return type

StringMatrix

countPairs()

Count all possible pairs of haplotypes for each matrix row.

Warning

This does *not* do any involved handling of missing data as per *geno.count.pairs* from R *haplo.stats* module.

Returns

each element is the number of pairs in row order

Return type

list

flattenCols()

Flatten columns into a single list.

Important

Currently assumes entries are integers.

Returns

all alleles, the two genotype columns concatenated for each locus

Return type

list

filterOut(*key*, *blankDesignator*)

Get matrix rows filtered by a designator.

Parameters

- **key** (*str*) – locus to filter
- **blankDesignator** (*str*) – string to exclude

Returns

the rows of the matrix that *do not* contain *blankDesignator* at any rows

Return type

list

getSuperType(key)

Get a matrix grouped by specified key.

Example

Return a new matrix with the column vector with the alleles for each genotype concatenated like so:

```
>>> matrix = StringMatrix(2, ["A", "B"])
>>> matrix[0, "A"] = ("A01", "A02")
>>> matrix[1, "A"] = ("A11", "A12")
>>> matrix[0, "B"] = ("B01", "B02")
>>> matrix[1, "B"] = ("B11", "B12")
>>> print(matrix)
StringMatrix([[ 'A01', 'A02', 'B01', 'B02'],
               [ 'A11', 'A12', 'B11', 'B12']], dtype=object)
>>> matrix.getSuperType("A:B")
StringMatrix([[ 'A01:B01', 'A02:B02'],
               [ 'A11:B11', 'A12:B12']], dtype=object)
```

Parameters

key (*str*) – loci to group

Returns

a new matrix with the columns concatenated

Return type

StringMatrix

class Group(li, size)

Group list or sequence into non-overlapping chunks.

Example

```
>>> for pair in Group('aabbccdde', 2):
...     print(pair)
...
aa
bb
cc
dd
ee
```

```
>>> a = Group('aabbccdde', 2)
>>> a[0]
'aa'
>>> a[3]
'dd'
```

Parameters

- **li** (*str/list*) – string or list
- **size** (*int*) – size of grouping

__getitem__(group)

Get the item by position.

Parameters

group (*int*) – get the item by position

Returns

the value at that position

Return type

str|list

Raises

IndexError²⁹ – if group is out of bounds

critical_exit(message, *args)

Log a CRITICAL message and exit with status 1.

Added in version 1.4.0

Added in version 1.4.0.

Parameters

message (*str*) – Logging format string.

getStreamType(*stream*)

Get the type of stream.

Parameters

stream (*TextOutputStream/XMLOutputStream*) – stream to check

Returns

either `xml` or `text`.

Return type

string

glob_with_pathlib(*pattern*)

Use globbing with `pathlib`.

Parameters

pattern (*str*) – globbing pattern

Returns

of `pathlib` globs

Return type

list

natural_sort_key(*s*, *_nsre=re.compile('[0-9]+')*)

Generate a key for natural (human-friendly) sorting.

This function splits a string into text and number components so that numbers are compared by value instead of lexicographically. It is intended for use as the `key` function in `list.sort()` or `sorted()`.

Example

```
>>> items = ["item2", "item10", "item1"]
>>> sorted(items, key=natural_sort_key)
['item1', 'item2', 'item10']
```

Parameters

- **s** (*str*) – The string to split into text and number components.
- **_nsre** (*Pattern*) – Precompiled regular expression used internally to split the string into digit and non-digit chunks. This is not intended to be overridden in normal use.

Returns

A list of strings and integers to be used as a sort key.

Return type

list

unique_elements(*li*)

Gets the unique elements in a list.

Parameters

li (*list*) – a list

Returns

unique elements

Return type

list

appendTo2dList(*aList*, *appendStr=':'*)

Append a string to each element in a list.

Parameters

- **aList** (*list*) – list to append to
- **appendStr** (*str*) – string to append

Returns

a list with string appended to each element

Return type

list

convertLineEndings(*file, mode*)

Convert line endings based on platform.

Parameters

- **file** (*str*) – file name to convert
- **mode** (*int*) – Conversion mode, one of
 - 1 Unix to Mac
 - 2 Unix to DOS

fixForPlatform(*filename, txt_ext=0*)

Fix for some Windws/MS-DOS platforms.

Parameters

- **filename** (*str*) – path to file
- **txt_ext** (*int, optional*) – if enabled (1) add a .txt extension

copyfileCustomPlatform(*src, dest, txt_ext=0*)

Copy file to file with fixes.

Parameters

- **src** (*str*) – source file
- **dest** (*str*) – source file
- **txt_ext** (*int, optional*) – if enabled (1) add a .txt extension

copyCustomPlatform(*file, dist_dir, txt_ext=0*)

Copy file to directory with fixes.

Parameters

- **file** (*str*) – source file
- **dist_dir** (*str*) – source directory
- **txt_ext** (*int, optional*) – if enabled (1) add a .txt extension

checkXSLFile(*xslFilename, path="", subdir="", abort=False, msg=""*)

Check XSL filename and return full path.

Parameters

- **xslFilename** (*str*) – name of the XSL file
- **path** (*str*) – root path to check
- **subdir** (*str*) – subdirectory under **path** to check
- **abort** (*bool*) – if enabled (True) file isn't found, exit with an error. Default is False
- **msg** (*str*) – output message on abort

Returns

checked and validated path

Return type

str

getUserFilenameInput(*prompt, filename*)

Get user filename input.

Read user input for a filename, check its existence, continue requesting input until a valid filename is entered.

Parameters

- **prompt** (*str*) – description of file
- **filename** (*str*) – default filename

Returns

name of file eventually selected

Return type

str

splitIntoNGroups(*alist*, *n=1*)

Divides a list up into n parcels (plus whatever is left over).

Example

```
>>> a = ['A', 'B', 'C', 'D', 'E']
>>> splitIntoNGroups(a, 2)
[['A', 'B'], ['C', 'D'], ['E']]
```

Parameters

- **alist** (*list*) – list to divide up
- **n** (*int*) – parcel size

Returns

list of lists

Return type

list

PyPop.xslt

Python XSLT extensions for handling things outside the scope of XSLT 1.0.

Attributes

| | |
|-----------|---|
| <i>ns</i> | Function namespace for custom PyPop XSLT extension functions. |
|-----------|---|

Functions

| | |
|---|-------------------------------------|
| <i>num_zeros</i> (decimal) | Count zeroes. |
| <i>exponent_len</i> (num) | Calculate space taken for exponent. |
| <i>format_number_fixed_width</i> (<i>_context</i> , *args) | Format number to fixed width. |

Package Contents**ns**

Function namespace for custom PyPop XSLT extension functions.

This namespace allows registering Python functions that can be called directly from XSLT stylesheets.

prefixThe namespace prefix used in XSLT stylesheets. Here it is set to "es", so extension functions are invoked as `es:format_number_fixed_width(...)`. See example in `format_number_fixed_width()`**Type**

str

num_zeros(*decimal*)

Count zeroes.

Parameters**decimal** (*float*) – number to check**Returns**number of zeroes in floating point number, or `inf` if number is zero**Return type**

int

exponent_len(*num*)

Calculate space taken for exponent.

Example

```
>>> exponent_len(1e-03)
2
>>> exponent_len(1e-10)
3
```

Parameters

num (*float*) – input number

Returns

length of exponent

Return type

int

format_number_fixed_width(*_context*, *args)

Format number to fixed width.

Example

```
>>> ns["format_number_fixed_width"] = format_number_fixed_width
>>> root = etree.XML("<a><b>0.0000043</b></a>")
>>> doc = etree.ElementTree(root)
>>> xslt = etree.XSLT(etree.XML('''
... <stylesheet version="1.0" xmlns="http://www.w3.org/1999/XSL/Transform" xmlns:es="http://pypop.org/lxml/functions">
... <output method="text" encoding="ASCII"/>
... <template match="/">
... <text>Yep [</text>
... <value-of select="es:format_number_fixed_width(string(/a/b), 5)"/>
... <text></text>
... </template>
... </stylesheet>
... '''))
>>> print(xslt(doc))
Yep [4.3e-6]
```

Note

arguments from XSLT file: num and places are encoded in *args.

Parameters

_context (*obj*) – not used

Returns

formatted number to fixed width

Return type

str

4 Deprecated Submodules

PyPop.arlequin

Provides Arlequin functionality in Python.

Deprecated since version 1.0.0

Deprecated since version 1.0.0: Only works for an obsolete version of Arlequin.

Attributes

usage_message

Classes

| | |
|-------------------------------------|--|
| ArlequinWrapper | Wraps the functionality of the Arlequin ³⁰ program. |
| ArlequinExactHWTest | Wraps the Arlequin Hardy-Weinberg exact functionality. |
| ArlequinBatch | A wrapper for running Arlequin from the command-line. |

Module Contents

class ArlequinWrapper (*matrix=None, arlequinPrefix='arl_run', arlequinExec='arlecore.exe', untypedAllele='***', arpFilename='output.arp', arsFilename='arl_run.ars'*)

Wraps the functionality of the Arlequin³¹ program.

Parameters

- **matrix** (*StringMatrix*) – matrix
- **arlequinPrefix** (*str, optional*) – directory prefix (default arl_run)
- **arlequinExec** (*str, optional*) – executable program (default arlecore.exe)
- **untypedAllele** (*str, optional*) – untyped allele designator (default ***)
- **arpFilename** (*str, optional*) – default output file name (default output.arp)
- **arsFilename** (*str, optional*) – default run file name (default arl_run.ars)

outputArpFile (*group*)

Output the .arp file.

Parameters

group (*list*) – list of loci to pass to Arlequin

outputArsFile (*arsFilename, arsContents*)

Outputs the run-time Arlequin program file.

Parameters

- **arsFilename** (*str*) – name of file
- **arsContents** (*str*) – contents of file

outputRunFiles ()

Generates the expected '.txt' set-up files for Arlequin.

runArlequin ()

Run the Arlequin haplotyping program.

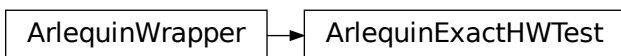
Forks a copy of arlecore.exe, which must be on PATH to actually generate the desired statistics estimates from the generated .arp file.

cleanup ()

Remove the working Arlequin subdirectory.

class ArlequinExactHWTest (*matrix=None, lociList=None, markovChainStepsHW=100000, markovChainDememorisationStepsHW=1000, **kw*)

Bases: [ArlequinWrapper](#)



Wraps the Arlequin Hardy-Weinberg exact functionality.

Run Hardy-Weinberg exact test on list specified in lociList.

hwExactTest

standard config options for Arlequin

Type

str

Parameters

- **matrix** (*StringMatrix*) – StringMatrix for testing
- **lociList** (*list*) – list of loci
- **markovChainStepsHW** (*int, optional*) – Number of steps to use in Markov chain (default: 100000)

- **markovChainDememorisationStepsHW** (*int*, *optional*) – “Burn-in” time for Markov chain (default: 1000).

getHWExactTest()

Returns a dictionary of loci.

Returns

Each dictionary element contains a tuple of the results from the Arlequin implementation of the Hardy-Weinberg exact test, namely:

- number of genotypes,
- observed heterozygosity,
- expected heterozygosity,
- the p-value,
- the standard deviation,
- number of steps,

If locus is monomorphic, the HW exact test can't be run, and the contents of the dictionary element simply contains the string `monomorphic`, rather than the tuple of values.

Return type

`dict`

```
class ArlequinBatch(arpFilename, arsFilename, idCol, prefixCols, suffixCols, windowSize, mapOrder=None, untypedAllele='0',
                   arlequinPrefix='arl_run')
```

A wrapper for running Arlequin from the command-line.

Given a delimited text file of multi-locus genotype data: provides methods to output Arlequin format data files and runtime info and execution of Arlequin itself. Used to provide a “batch” (i.e. command line) mode for generating appropriate Arlequin input files and for forking Arlequin itself.

Parameters

- **arpFilename** (*str*) – Arlequin filename (must have `.arp` file extension)
- **arsFilename** (*str*) – Arlequin settings filename (must have `.ars` file extension)
- **idCol** (*str*) – column in input file that contains the individual id.
- **prefixCols** (*int*) – number of columns to ignore before allele data starts
- **suffixCols** (*int*) – number of columns to ignore after allele data stops
- **windowSize** (*int*) – size of sliding window
- **mapOrder** (*list*, *optional*) – list order of columns if different to column order in file (defaults to order in file)
- **untypedAllele** (*str*, *optional*) – (defaults to `0`)
- **arlequinPrefix** (*str*, *optional*) – prefix for all Arlequin run-time files (defaults to `arl_run`).

outputArlequin(data)

Outputs the specified `.arp` sample file.

Parameters

data (*list*) – list of lines of data.

outputRunFiles()

Generates the expected set-up files for Arlequin.

Includes `.txt` and `.ars` file names.

runArlequin()

Run the Arlequin haplotyping program.

Forks a copy of `arlecore.exe`, which must be on `PATH` to actually generate the desired statistics estimates from the generated `.arp` file.

usage_message = **Multiline-String**

```
"""Usage: Arlequin.py [OPTION] INPUTFILE ARPFIL ARSFILE
Process a tab-delimited INPUTFILE of alleles to produce an data files
(including ARPFIL), using parameters from ARSFILE for the Arlequin population
genetics program.

-i, --idcol=NUM      column number of identifier (first column is zero)
-l, --ignorelines=NUM number of header lines to ignore in in file
-c, --cols=POS1,POS2 number of leading columns (POS1) before start and
```

(continues on next page)

```

        number of trailing columns before the end (POS2) of
        allele data (including IDCOL)
-k, --sort=POS1,.. specify order of loci if different from column order
                   in file (must not repeat a locus)
-w, --windowsize=NUM number of loci involved in window size
                   (note that this is half the number of allele columns)
-u, --untyped=STR  the string that represents 'untyped' alleles
                   (defaults to '****')
-x, --execute      execute the Arlequin program
-h, --help         this message
-d, --debug        switch on debugging

INPUTFILE  input text file
ARPFILe    output Arlequin '.arp' project file
ARSFILE    input Arlequin '.ars' settings file""

```

5 Attributes

| | |
|--------------------------------|--|
| <code>logger</code> | Package-wide logger used throughout a PyPop run. |
| <code>__version__</code> | PyPop version. If installed, this is the package version, otherwise it returns repository version. |
| <code>copyright_message</code> | copyright information used in <code>--help</code> screens and elsewhere |
| <code>platform_info</code> | platform information used in <code>--help</code> screens and elsewhere |

6 Exceptions

| | |
|--|---|
| <code>PyPopModuleRenameDeprecationWarning</code> | Deprecation warning for PyPop module renames. |
|--|---|

7 Functions

| | |
|--|--|
| <code>setup_logger([level, filename, doctest_mode])</code> | Configure the 'pypop' logger with stdout/file handler, optional debug verbosity, and doctest mode. |
|--|--|

8 Package Contents

exception `PyPopModuleRenameDeprecationWarning`

Bases: `DeprecationWarning`³²

`PyPopModuleRenameDeprecationWarning`

Deprecation warning for PyPop module renames.

Added in version 1.4.0

Added in version 1.4.0.

Initialize self. See `help(type(self))` for accurate signature.

logger

Package-wide logger used throughout a PyPop run.

Added in version 1.4.0

Added in version 1.4.0.

`__version__`

PyPop version. If installed, this is the package version, otherwise it returns repository version.

copyright_message = Multiline-String

```
"""Copyright (C) 2003-2006 Regents of the University of California.  
Copyright (C) 2007-2026 PyPop team.  
This is free software. There is NO warranty; not even for  
MERCHANTABILITY or FITNESS FOR A PARTICULAR PURPOSE."""
```

copyright information used in `--help` screens and elsewhere

platform_info

platform information used in `--help` screens and elsewhere

setup_logger(level=logging.INFO, filename=None, doctest_mode=True)

Configure the 'pypop' logger with stdout/file handler, optional debug verbosity, and doctest mode.

Added in version 1.4.0

Added in version 1.4.0.

Parameters

- **level** (*str*, *optional*) – INFO (default), DEBUG (more detailed), WARNING, CRITICAL
- **filename** (*str*, *optional*) – Optional file to log to. If None, logs to stdout.
- **doctest_mode** (*bool*, *optional*) – If True, forcibly rebinds the logger to sys.stdout and disables propagation so doctests see output.

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''''

Python Module Index

p

- PyPop, 2
- PyPop.arlequin, 40
- PyPop.citation, 3
- PyPop.command_line_interface, 3
- PyPop.datatypes, 5
- PyPop.filters, 7
- PyPop.haplo, 13
- PyPop.hardyweinberg, 16
- PyPop.homozygosity, 19
- PyPop.parsers, 22
- PyPop.popaggregate, 25
- PyPop.popananalysis, 27
- PyPop.popmeta, 28
- PyPop.pypop, 29
- PyPop.randombinning, 29
- PyPop.utils, 30
- PyPop.xslt, 39

Notes

1. <https://github.com/readthedocs/sphinx-autoapi>
2. <http://pypop.org/docs>
3. <http://pypop.org/pypop-guide-1.4.2b1.pdf>
4. <https://peps.python.org/pep-0008/#package-and-module-names>
5. <https://docs.python.org/3/library/exceptions.html#DeprecationWarning>
6. <https://docs.python.org/3/library/exceptions.html#UserWarning>
7. <https://docs.python.org/3/library/collections.html#collections.OrderedDict>
8. <https://docs.python.org/3/library/collections.html#collections.OrderedDict>
9. <https://docs.python.org/3/library/configparser.html#configparser.ConfigParser>
10. <https://docs.python.org/3/library/argparse.html#argparse.Action>
11. <https://docs.python.org/3/library/argparse.html#argparse.ArgumentParser>
12. <https://docs.python.org/3/library/argparse.html#argparse.ArgumentParser>
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15. <https://github.com/ANHIG/IMGTHLA/>
16. <https://docs.python.org/3/library/exceptions.html#RuntimeError>
17. <https://github.com/ANHIG/IMGTHLA/>
18. <https://docs.python.org/3/library/configparser.html#configparser.ConfigParser>
19. <https://docs.python.org/3/library/configparser.html#configparser.ConfigParser>
20. <https://docs.python.org/3/library/configparser.html#configparser.ConfigParser>
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22. <https://docs.python.org/3/library/collections.abc.html#collections.abc.Sequence>
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Index

Symbols

`__call__()` (*CitationAction* method), 4
`__deepcopy__()` (*StringMatrix* method), 33
`__getitem__()` (*Group* method), 36
`__getitem__()` (*StringMatrix* method), 34
`__getslice__()` (*StringMatrix* method), 33
`__len__()` (*StringMatrix* method), 33
`__repr__()` (*StringFilter* method), 33
`__setitem__()` (*StringMatrix* method), 34
`__str__()` (*SubclassError* method), 8
`__version__` (*in module PyPop*), 43

A

`addAllele()` (*AnthonyNolanFilter* method), 10
`addAllele()` (*Filter* method), 8
`addAllele()` (*PassThroughFilter* method), 9
`AlleleCountAnthonyNolanFilter` (*class in PyPop.filters*), 12
`allPairwise()` (*Emhaplofreq* method), 14
`allPairwise()` (*Haplostats* method), 15
`AnthonyNolanFilter` (*class in PyPop.filters*), 9
`appendTo2dList()` (*in module PyPop.utils*), 37
`ArlequinBatch` (*class in PyPop.arlequin*), 42
`ArlequinExactHWTTest` (*class in PyPop.arlequin*), 41
`ArlequinWrapper` (*class in PyPop.arlequin*), 41

B

`BinningFilter` (*class in PyPop.filters*), 11

C

`canGenerateExpectedStats()` (*Homozygosity* method), 19
`checkAlleleName()` (*AnthonyNolanFilter* method), 10
`checkAlleleName()` (*Filter* method), 8
`checkAlleleName()` (*PassThroughFilter* method), 8
`checkIfSequenceData()` (*in module PyPop.datatypes*), 6
`checkXSLFile()` (*in module PyPop.utils*), 38
`citation_output_formats` (*in module PyPop.citation*), 3
`CitationAction` (*class in PyPop.command_line_interface*), 4
`cleanup()` (*AnthonyNolanFilter* method), 11
`cleanup()` (*ArlequinWrapper* method), 41
`cleanup()` (*Filter* method), 8
`cleanup()` (*PassThroughFilter* method), 9
`close()` (*TextOutputStream* method), 31
`closetag()` (*XMLOutputStream* method), 31
`convert_citation_formats()` (*in module PyPop.citation*), 3
`convertLineEndings()` (*in module PyPop.utils*), 38
`convertToInts()` (*StringMatrix* method), 35
`copy()` (*StringMatrix* method), 34
`copyCustomPlatform()` (*in module PyPop.utils*), 38
`copyfileCustomPlatform()` (*in module PyPop.utils*), 38
`copyright_message` (*in module PyPop*), 43
`countPairs()` (*StringMatrix* method), 35
`critical_exit()` (*in module PyPop.utils*), 36

D

`doCalcs()` (*HomozygosityEWSlatkinExact* method), 21
`doCustomBinning()` (*BinningFilter* method), 12
`doDigitBinning()` (*BinningFilter* method), 11
`doFiltering()` (*AnthonyNolanFilter* method), 9
`doFiltering()` (*Filter* method), 8
`doFiltering()` (*PassThroughFilter* method), 8
`dump()` (*StringMatrix* method), 34
`dumpTable()` (*HardyWeinbergGuoThompson* method), 18

E

`Emhaplofreq` (*class in PyPop.haplo*), 13
`emptytag()` (*XMLOutputStream* method), 31
`endFiltering()` (*AnthonyNolanFilter* method), 10
`endFiltering()` (*Filter* method), 8
`endFiltering()` (*PassThroughFilter* method), 9
`endFirstPass()` (*AlleleCountAnthonyNolanFilter* method), 13
`endFirstPass()` (*AnthonyNolanFilter* method), 10
`endFirstPass()` (*Filter* method), 8
`endFirstPass()` (*PassThroughFilter* method), 9
`estHaplotypes()` (*Emhaplofreq* method), 14
`estHaplotypes()` (*Haplostats* method), 15
`estLinkageDisequilibrium()` (*Emhaplofreq* method), 14
`exponent_len()` (*in module PyPop.xslt*), 39

F

`Filter` (*class in PyPop.filters*), 8
`filterAllele()` (*AnthonyNolanFilter* method), 10
`filterAllele()` (*Filter* method), 8
`filterAllele()` (*PassThroughFilter* method), 9
`filterOut()` (*StringMatrix* method), 35
`fixForPlatform()` (*in module PyPop.utils*), 38
`flattenCols()` (*StringMatrix* method), 35
`flush()` (*TextOutputStream* method), 31
`format_number_fixed_width()` (*in module PyPop.xslt*), 40

G

`generateFlattenedMatrix()` (*HardyWeinbergGuoThompson* method), 18
`genHaplotypes()` (*HaploArlequin* method), 16
`GENOTYPE_SEPARATOR` (*in module PyPop.utils*), 30
`GENOTYPE_TERMINATOR` (*in module PyPop.utils*), 30
`Genotypes` (*class in PyPop.datatypes*), 5
`genSampleOutput()` (*ParseFile* method), 23
`genValidKey()` (*ParseAlleleCountFile* method), 24
`genValidKey()` (*ParseGenotypeFile* method), 23
`get_parent_cli()` (*in module PyPop.command_line_interface*), 4
`get_popmeta_cli()` (*in module PyPop.command_line_interface*), 4
`get_pypop_cli()` (*in module PyPop.command_line_interface*), 4
`get_sequence_directory()` (*in module PyPop.popanalisys*), 28
`getAlleleCount()` (*Genotypes* method), 5
`getAlleleCountAt()` (*Genotypes* method), 5
`getAlleleTable()` (*ParseAlleleCountFile* method), 25
`getConfigInstance()` (*in module PyPop.popanalisys*), 28
`getCount()` (*Homozygosity* method), 20
`getExpectedHomozygosity()` (*Homozygosity* method), 20
`getFileData()` (*ParseFile* method), 22
`getHomozygosity()` (*HomozygosityEWSlatkinExact* method), 21
`getHWExactTest()` (*ArlequinExactHWTTest* method), 42
`getIndividualsData()` (*Genotypes* method), 6
`getLocusData()` (*Genotypes* method), 6
`getLocusDataAt()` (*Genotypes* method), 6
`getLocusList()` (*Genotypes* method), 5
`getLocusName()` (*ParseAlleleCountFile* method), 25
`getLocusPairs()` (*in module PyPop.datatypes*), 7
`getLumpedDataLevels()` (*in module PyPop.datatypes*), 7
`getMatrix()` (*ParseAlleleCountFile* method), 25
`getMatrix()` (*ParseGenotypeFile* method), 23
`getMetalocus()` (*in module PyPop.datatypes*), 7
`getNewStringMatrix()` (*StringMatrix* method), 34
`getNormDevHomozygosity()` (*Homozygosity* method), 20
`getObservedHomozygosity()` (*Homozygosity* method), 19
`getObservedHomozygosityFromAlleleData()` (*in module PyPop.homozygosity*), 21
`getPopData()` (*ParseFile* method), 22
`getPValueRange()` (*Homozygosity* method), 20

getSampleMap() (*ParseFile method*), 22
 getStreamType() (*in module PyPop.utils*), 37
 getSuperType() (*StringMatrix method*), 35
 getTxtOutPath() (*Main method*), 28
 getUniqueAlleles() (*StringMatrix method*), 35
 getUserFilenameInput() (*in module PyPop.utils*), 38
 getVarExpectedHomozygosity() (*Homozygosity method*), 20
 getXmlOutPath() (*Main method*), 28
 glob_with_pathlib() (*in module PyPop.utils*), 37
 Group (*class in PyPop.utils*), 36

H

Haplo (*class in PyPop.haplo*), 13
 HaploArlequin (*class in PyPop.haplo*), 15
 Haplostats (*class in PyPop.haplo*), 14
 HardyWeinberg (*class in PyPop.hardyweinberg*), 17
 HardyWeinbergEnumeration (*class in PyPop.hardyweinberg*), 18
 HardyWeinbergGuoThompson (*class in PyPop.hardyweinberg*), 17
 HardyWeinbergGuoThompsonArlequin (*class in PyPop.hardyweinberg*), 18
 Homozygosity (*class in PyPop.homozygosity*), 19
 HomozygosityEWSlatkinExact (*class in PyPop.homozygosity*), 20
 HomozygosityEWSlatkinExactPairwise (*class in PyPop.homozygosity*), 21
 hwExactTest (*ArlequinExactHWTest attribute*), 41

L

logger (*in module PyPop*), 43
 lookupCustomBinning() (*BinningFilter method*), 12

M

Main (*class in PyPop.popanalisys*), 27
 main() (*in module PyPop.popmeta*), 28
 main() (*in module PyPop.pyppop*), 29
 main_interactive() (*in module PyPop.pyppop*), 29
 makeSeqDictionaries() (*AnthonyNolanFilter method*), 11
 Meta (*class in PyPop.popaggregate*), 25
 module
 PyPop, 2
 PyPop.arlequin, 40
 PyPop.citation, 3
 PyPop.command_line_interface, 3
 PyPop.datatypes, 5
 PyPop.filters, 7
 PyPop.haplo, 13
 PyPop.hardyweinberg, 16
 PyPop.homozygosity, 19
 PyPop.parsers, 22
 PyPop.popaggregate, 25
 PyPop.popanalisys, 27
 PyPop.popmeta, 28
 PyPop.pyppop, 29
 PyPop.randombinning, 29
 PyPop.utils, 30
 PyPop.xslt, 39

N

natural_sort_key() (*in module PyPop.utils*), 37
 ns (*in module PyPop.xslt*), 39
 num_zeros() (*in module PyPop.xslt*), 39

O

opentag() (*XMLOutputStream method*), 31
 outputArlequin() (*ArlequinBatch method*), 42
 outputArlequin() (*HaploArlequin method*), 16
 outputArpFile() (*ArlequinWrapper method*), 41
 outputArsFile() (*ArlequinWrapper method*), 41
 outputRunFiles() (*ArlequinBatch method*), 42

outputRunFiles() (*ArlequinWrapper method*), 41

P

ParseAlleleCountFile (*class in PyPop.parsers*), 24
 ParseFile (*class in PyPop.parsers*), 22
 ParseGenotypeFile (*class in PyPop.parsers*), 23
 PassThroughFilter (*class in PyPop.filters*), 8
 platform_info (*in module PyPop*), 44
 prefix (*in module PyPop.xslt*), 39
 pval() (*in module PyPop.hardyweinberg*), 19
 PyPop
 module, 2
 PyPop.arlequin
 module, 40
 PyPop.citation
 module, 3
 PyPop.command_line_interface
 module, 3
 PyPop.datatypes
 module, 5
 PyPop.filters
 module, 7
 PyPop.haplo
 module, 13
 PyPop.hardyweinberg
 module, 16
 PyPop.homozygosity
 module, 19
 PyPop.parsers
 module, 22
 PyPop.popaggregate
 module, 25
 PyPop.popanalisys
 module, 27
 PyPop.popmeta
 module, 28
 PyPop.pyppop
 module, 29
 PyPop.randombinning
 module, 29
 PyPop.utils
 module, 30
 PyPop.xslt
 module, 39
 PyPopModuleRenameDeprecationWarning, 43

R

RandomBinsForHomozygosity (*class in PyPop.randombinning*), 29
 randomMethod() (*RandomBinsForHomozygosity method*), 29
 returnBulkHomozygosityStats() (*HomozygosityEWSlatkinExact method*), 21
 runArlequin() (*ArlequinBatch method*), 42
 runArlequin() (*ArlequinWrapper method*), 41
 runArlequin() (*HaploArlequin method*), 16

S

sequenceMethod() (*RandomBinsForHomozygosity method*), 29
 serializeAlleleCountDataAt() (*Genotypes method*), 6
 serializeAlleleCountDataTo() (*Genotypes method*), 6
 serializeEnd() (*Emhaplofreq method*), 13
 serializeEnd() (*Haplostats method*), 15
 serializeHomozygosityTo() (*Homozygosity method*), 20
 serializeHomozygosityTo() (*HomozygosityEWSlatkinExact method*), 21
 serializeMetadataTo() (*ParseFile method*), 23
 serializeStart() (*Emhaplofreq method*), 13
 serializeStart() (*Haplostats method*), 15
 serializeSubclassMetadataTo() (*Genotypes method*), 6
 serializeSubclassMetadataTo() (*ParseAlleleCountFile method*), 25
 serializeSubclassMetadataTo() (*ParseGenotypeFile method*), 24

serializeTo() (*HardyWeinberg method*), 17
serializeTo() (*HardyWeinbergEnumeration method*), 18
serializeTo() (*HardyWeinbergGuoThompsonArlequin method*), 19
serializeTo() (*HomozygosityEWSlatkinExactPairwise method*), 21
serializeXMLTableTo() (*HardyWeinberg method*), 17
setup_logger() (*in module PyPop*), 44
splitIntoGroups() (*in module PyPop.utils*), 39
startFiltering() (*AnthonyNolanFilter method*), 10
startFiltering() (*Filter method*), 8
startFiltering() (*PassThroughFilter method*), 9
startFirstPass() (*AnthonyNolanFilter method*), 10
startFirstPass() (*Filter method*), 8
startFirstPass() (*PassThroughFilter method*), 8
StringMatrix (*class in PyPop.utils*), 32
SubclassError, 8

T

tagContents() (*XMLOutputStream method*), 32
TextOutputStream (*class in PyPop.utils*), 30
translate_file_to_file() (*in module PyPop.popaggregate*), 26
translate_file_to_stdout() (*in module PyPop.popaggregate*), 26
translate_string_to_file() (*in module PyPop.popaggregate*), 26
translate_string_to_stdout() (*in module PyPop.popaggregate*), 26
translateMatrix() (*AnthonyNolanFilter method*), 11

U

unique_elements() (*in module PyPop.utils*), 37
usage_message (*in module PyPop.arlequin*), 42
use_scipy (*in module PyPop.hardyweinberg*), 17

W

write() (*TextOutputStream method*), 30
writeln() (*TextOutputStream method*), 30
writeToLog() (*AnthonyNolanFilter method*), 11
writeToLog() (*Filter method*), 8
writeToLog() (*PassThroughFilter method*), 9

X

XMLOutputStream (*class in PyPop.utils*), 31