

PeptoVar USER'S MANUAL

PeptoVar (**Peptides of Variations**) is a pure Python3 program for personalized and population-wide peptidome generation. PeptoVar can be used for *in-silico* prediction of new minor histocompatibility antigen (MiHa), simulation of stem cells transplantation or as peptide database generator for shotgun proteomic studies of immunopeptidome.

The main idea of PeptoVar is to decrease computational complexity of the task of translation of nucleotide sequence with a substantial number of polymorphisms and determine their translation dependencies (allele combinations of frame shifts and closely located polymorphisms that are the diversity factors for translation products). The program can handle both phased and unphased variation data.

REQUIREMENTS

Platforms:

Linux, Mac OS

Dependencies:

python >= 3.5

pysam module >= 0.11.2.2

INSTALLATION

1) install pysam module with pip:

```
pip3 install pysam
```

2) download latest stable PeptoVar build from the project page:

<https://open-projects.github.io/PeptoVar/>

and unzip the archive

or clone PeptoVar using git:

```
git clone https://github.com/open-projects/PeptoVar
```

3) add resulting folder to your ``PATH`` variable

or add symbolic link for ``PeptoVar`` script to your ``bin`` folder

or use PeptoVar directly by specifying full path to the executable script

INPUT DATA AND FORMATS

- genome annotation

PeptoVar uses genome annotation data in GFF3 format (<http://gmod.org/wiki/GFF3>). Note that only records with CDS type are processed and grouped by Parent identifiers.

- set of genomic variations

VCF files with genetic variation data must be compressed with bgzip (block compression/decompression utility) and indexed with tabix (generic indexer for TAB-delimited genome position files). The both utilities are parts of Samtools - a suite of programs for interacting with high-throughput sequencing data (<http://www.htslib.org>).

USAGE

```
PeptoVar.py [-h] [-gff file.gff] [-fasta file.fasta] [-vcf filevcf.gz]
            [-tmpdir dirpath] [-samples sample_name1 [sample_name2]]
            [-minaf THRESHOLD] [-var all | used] [-nopt]
            [-peptlen LENGTH1 [LENGTH2 ...]] [-outdir dirpath]
            [-indir dirpath] [-trnlist transcriptID [transcriptID ...]] [-trnfile transcriptID.txt]
```

-h show this help message and exit

-gff GFF input file

-fasta FASTA input file (use if GFF file has no sequences)

-vcf VCF input file (requirements see in INPUT FILE FORMAT paragraph)

-tmpdir TEMP directory

-samples a sample name or a pair of names in VCF file; for two samples (donor/recipient) only unique peptides will be represented

-tagaf allele frequency tag in VCF file (for example EUR_AF, SAS_AF, AMR_AF etc.); used with '-minaf' argument, default=AF

-minaf allele frequency (AF) threshold; alleles with AF < THRESHOLD will be ignored (AF=0 will be set for alleles with no AF data); **NOTE: ignoring -minaf at all can cause high memory usage and increasing computational time**

-var (all | used) save translated polymorphisms (all or only the ones used to make peptides)

-nopt do not use optimization, i.e synonymous and non-synonymous variations will be used (may cause high CPU load and memory usage)

-peptlen lengths of peptides (0 - full-length proteins)

-outdir output directory (will be created if not exists, default: ./output)
-indir input directory for files *.vcf.gz, *.vcf.gz.tbi, *.gff and *.fasta (if no sequences in GFF file);
the files MUST have the same name for each locus (chromosome)
-trnlist list of transcriptID for processing
-trnfile one column text file with the transcriptID list for processing

MAIN APPLICATIONS AND EXAMPLES

1. To make personalized peptidomes for selected samples (sample mode):

```
PeptoVar.py -samples SAMPLE01 -peptlen 9 -var used \  
-gff ./testdata/test.gff -vcf ./testdata/test.vcf.gz
```

or

```
PeptoVar.py -samples SAMPLE01 -peptlen 9 -var used -indir ./testdata
```

2. To get unique peptides for a sample in a pair of samples (transplantation mode). Note that unique peptides are calculated for each sample, i. e. for transplantation in both directions):

```
PeptoVar.py -samples SAMPLE01 SAMPLE02 -peptlen 9 -var used \  
-gff ./testdata/test.gff -vcf ./testdata/test.vcf.gz
```

or

```
PeptoVar.py -samples SAMPLE01 SAMPLE02 -peptlen 9 -var used \  
-indir ./testdata
```

3. To generate peptides for all combinations of genome variations in a population (population mode):

```
PeptoVar.py -peptlen 9 -var used -gff ./testdata/test.gff \  
-vcf ./testdata/test.vcf.gz
```

or

```
PeptoVar.py -peptlen 9 -var used -indir ./testdata
```

OUTPUT FILE FORMATS

PeptoVar creates four files in CSV format (TAB-delimited) in the output directory: the file for peptides (if -peptlen option has a value more than 0), the file for proteins (if -peptlen option has 0 value), the file for polymorphisms (if -var option is utilized) and the file for warnings.

Data fields in the file for peptides (sample_name.pept.csv):

chrom – chromosome number (or locus name)

transcript_id – transcript ID

sample – sample name

sample_allele1 – presence in allele 1 ('0' - not in allele 1; '1' - in allele 1)

sample_allele2 – presence in allele 2 ('0' - not in allele 2; '1' - in allele 2)

beg – start genome position of the peptide*

end – end genome position of the peptide*

upstream_fshifts – frame shifts in upstream of the peptide

variations(positions_in_matrix) - polymorphisms inside the peptide and their nucleotide positions

peptide – peptide sequence

matrix – genome sequence of translation to the peptide

* - if peptide translation starts and/or ends on a genome insertion the peptide genome positions are calculated as:

beg = leftmost_translated_reference_position – number_of_translated_insertion_nucleotides

end = rightmost_translated_reference_position + number_of_translated_insertion_nucleotides

Data fields in the file for proteins (sample_name.prot.csv):

chrom – chromosome number (or locus name)

transcript_id – transcript ID

sample – sample name

sample_allele1 – presence in allele 1 ('0' - not in allele 1; '1' - in allele 1)

sample_allele2 – presence in allele 2 ('0' - not in allele 2; '1' - in allele 2)

beg – start genome position of the protein

end – end genome position of the protein

variations(positions_in_matrix) - polymorphisms inside the protein and their nucleotide positions

peptide – protein sequence

matrix – genome sequence of translation to the protein

Data fields in the file for polymorphisms (variations.csv):

transcript_id – transcript ID

variation_id – polymorphism ID

beg – start genome position of the polymorphism

end – end genome position of the polymorphism

allele_id – allele ID (polymorphism_ID:polymorphism_sequence=allele_frequency(ref|alt), where ‘=allele_frequency’ is reported only for defined values in VCF files; ref - reference sequence, alt - alternative sequence)

sample – sample name

sample_allele1 – presence in allele 1 (‘0’ - not in allele 1; ‘1’ - in allele 1)

sample_allele2 – presence in allele 2 (‘0’ - not in allele 2; ‘1’ - in allele 2)

synonymous – ‘1’ if the polymorphism is synonymous, else ‘0’

upstream_fshifts – frame shifts in upstream of the polymorphism

prefix_alleles – polymorphisms in the polymorphism prefix

prefix – sequence of the polymorphism prefix (the nucleotide sequence from the start of current codon to the start of polymorphism)

allele – sequence of the polymorphism

suffix – sequence of the polymorphism suffix (the nucleotide sequence from the end of the polymorphism to the end of current codon)

suffix_alleles – polymorphisms in the polymorphism suffix

translation – translation of the polymorphism with the suffix and the prefix

NOTE: ID of synonymous polymorphism alleles are enclosed in square brackets

File with warnings (warnings.csv):

PeptoVar inspect records in the VCF and the GFF files for collisions.

The most important ones:

- multiple polymorphisms with the same ID
- multiple polymorphisms with the same genome positions but different ID
- intersection of a polymorphism and an exon border (in this case it is unknown if the polymorphism changes the site of splicing)
- no data for the sample in the VCF file
- no genome sequence in the exon position range

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