CassOpt is a program for optimization of mini-genes which are translated to proteins with particular immunogenic peptides. The mini-genes are used in immunology to research an immune response to particular peptides binded to MHC (the major histocompatibility complex). To create an unbiased mini-gene sequence, the translation of the joined peptide coding subsequences should not originate unnecessary immunogenic peptides in addition to the peptides of interest. The main idea of CassOpt is to find the shortest combination of peptide flanks (the flanks are parts of the native proteins which originate the peptides of interest) that do not originate unnecessary peptides with ability to bind to MHC. To estimate peptide binding CassOpt uses predictions of netMHCpan program (http://www.cbs.dtu.dk/services/NetMHCpan/). Rearrangement of the initial subsequences in couple with variation of theirs flank lengths gives the best results for mini-gene sequence optimization (Figure 1).

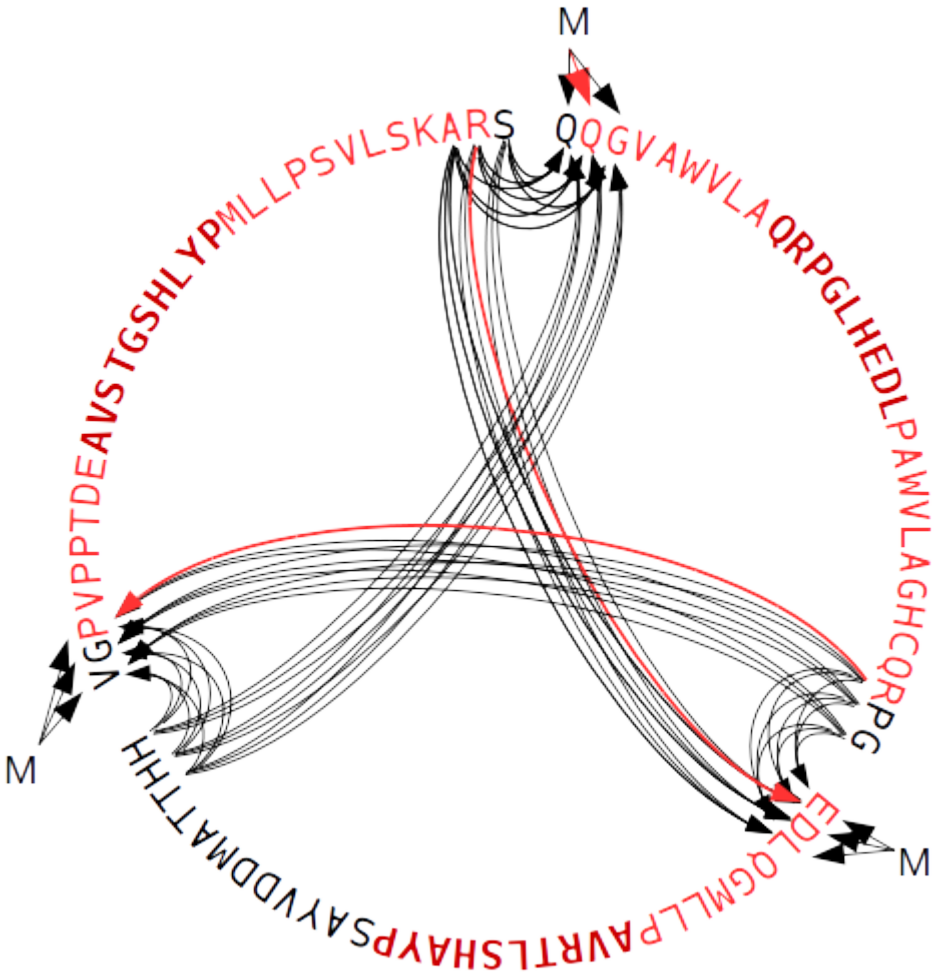


**Figure 1.** The diagram explains how the program arranges three peptides (a bold font) with flanks in order of the optimized protein sequence without immunogenic junctions (red sequence). Arrows represent possible paths of rearrangements, the optimal path is shown with red arrows. The program starts from each of the three start positions (“M”) and iterates over all combinations of the peptide arrangements using the shortest flanks. If two peptides can not be joined with a nonimmunogenic junction, the longer peptide flanks will be used. A junction is nonimmunogenic if there are no any immunogenic peptides which overlap the junction. Immunogenicity of the peptides is verified with netMHCpan program.

## Program usage

**CassOpt.py -f fasta_file [-o output_file]**

fasta_file – a file of peptide sequences with flanks in FASTA file format (http://genetics.bwh.harvard.edu/pph/FASTA.html).

output_file – an output file with the arranged peptide sequences with optimized flanks

## Dependencies

* Linux or MacOS
* python >= 3.5

## Examples of usage

**CassOpt.py -f test/input.fasta -o output.csv**

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