[![Build Status](data:image/svg+xml;charset=utf-8;base64,)](http://18.194.224.158:8080/job/antigen.garnish/lastBuild/consoleFull) [codecov.io](https://codecov.io/github/andrewrech/antigen.garnish?branch=master) ![](data:image/svg+xml;charset=utf-8;base64,)

# antigen.garnish

Ensemble neoepitope prediction from DNA variants in R.



## Description

An R package for [neoepitope](http://science.sciencemag.org/content/348/6230/69) analysis that takes human or murine DNA missense mutations, insertions, deletions, and gene fusions and performs neoepitope prediction. Input is a VCF file or table of peptides. Output is neoepitopes and a summary of neoepitope load and fitness by sample. [More information.](http://antigen-garnish-presentation.s3-website-us-east-1.amazonaws.com)

### Advantages

1. **Thoroughness**: + missense mutations, insertions, deletions, and gene fusions + human and mouse + ensemble MHC class I/II binding prediction using [mhcflurry](https://github.com/hammerlab/mhcflurry), [mhcnuggets](https://github.com/KarchinLab/mhcnuggets), [netMHC](http://www.cbs.dtu.dk/services/NetMHC/), [netMHCII](http://www.cbs.dtu.dk/services/NetMHCII/), [netMHCpan](http://www.cbs.dtu.dk/services/NetMHCpan/) and [netMHCIIpan](http://www.cbs.dtu.dk/services/NetMHCIIpan/i) + rank by dissimilarity to the normal peptidome / similarity to known immunogenic antigens
2. **Speed and simplicity**: + 1000 variants are ranked in a single step in less than five minutes
3. **Integration with R/Bioconductor** + upstream/VCF processing + exploratory data analysis, visualization

## Installation

### Requirements

* Linux
* R ≥ 3.4
* python-pip

### Install prediction tools and antigen.garnish

curl -fsSL http://get.rech.io/antigen.garnish.sh | sudo sh

## [Package documentation](http://get.rech.io/antigen.garnish.pdf)

* garnish\_variants: process missense / indel VCF variants from [SnpEff](http://snpeff.sourceforge.net/)
* garnish\_jaffa: process gene fusions from [JAFFA](https://github.com/Oshlack/JAFFA)
* garnish\_predictions: perform ensemble neoepitope prediction
* garnish\_summary: summarize and rank results
* garnish\_plot: generate summary plots
* list\_mhc: list all supported MHC allele syntax

### [Vignette](http://get.rech.io/antigen.garnish.pdf)

### Examples

#### Predict neoepitopes from missense mutations, insertions, and deletions

library(magrittr)  
library(antigen.garnish)  
  
 # download an example VCF  
 dt <- "antigen.garnish\_example.vcf" %T>%  
 utils::download.file("http://get.rech.io/antigen.garnish\_example.vcf", .) %>%  
  
 # extract variants  
 garnish\_variants %>%  
  
 # add space separated MHC types  
 # see list\_mhc() for nomenclature of supported alleles  
 # separate murine and human alleles into separate rows, even if same sample\_id.  
  
 .[, MHC := c("HLA-A\*02:01 HLA-DRB1\*14:67",  
 "H-2-Kb H-2-IAd",  
 "HLA-A\*01:47 HLA-DRB1\*03:08")] %>%  
  
 # predict neoepitopes  
 garnish\_predictions  
  
 # summarize predictions  
 dt %>%  
 garnish\_summary %T>%  
 print  
  
 # generate summary graphs  
 dt %>% garnish\_plot

#### Predict neoepitopes from gene fusions

library(magrittr)  
library(antigen.garnish)  
  
 # load example jaffa output  
 path <- "antigen.garnish\_jaffa\_results.csv" %T>%  
 utils::download.file("http://get.rech.io/antigen.garnish\_jaffa\_results.csv", .)  
 fasta\_path <- "antigen.garnish\_jaffa\_results.fasta" %T>%  
 utils::download.file("http://get.rech.io/antigen.garnish\_jaffa\_results.fasta", .)  
  
 # get predictions  
 dt <- garnish\_jaffa(path, db = "GRCm38", fasta\_path) %>%  
  
 # add MHC info with list\_mhc() compatible names  
 .[, MHC := "H-2-Kb"] %>%  
  
 # get predictions  
 garnish\_predictions %>%  
  
 # summarize predictions  
 garnish\_summary %T>%  
 print

### Tests

#### Automated testing

library(testthat)  
 testthat::test\_package("antigen.garnish")

#### How are peptides generated?

library(magrittr)  
  
 # generate a fake peptide  
 dt <- data.table::data.table(  
 pep\_base = "Y\_\_\_\*\_\_\_THIS\_IS\_\_\_\_\_\_\_\_\_\*\_\_\_A\_CODE\_TEST!\_\_\_\_\_\_\*\_\_X",  
 mutant\_index = c(5, 25, 47, 50),  
 pep\_type = "test",  
 var\_uuid = c(  
 "front\_truncate",  
 "middle",  
 "back\_truncate",  
 "end")) %>%  
 # create nmers  
 make\_nmers %T>% print

## Bugs

## Authors

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## Contributing

We welcome contributions and feedback via Github or [email](mailto:andrewrech@gmail.com).

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