

# SecretSanta

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flexible pipelines for scalable secretome prediction

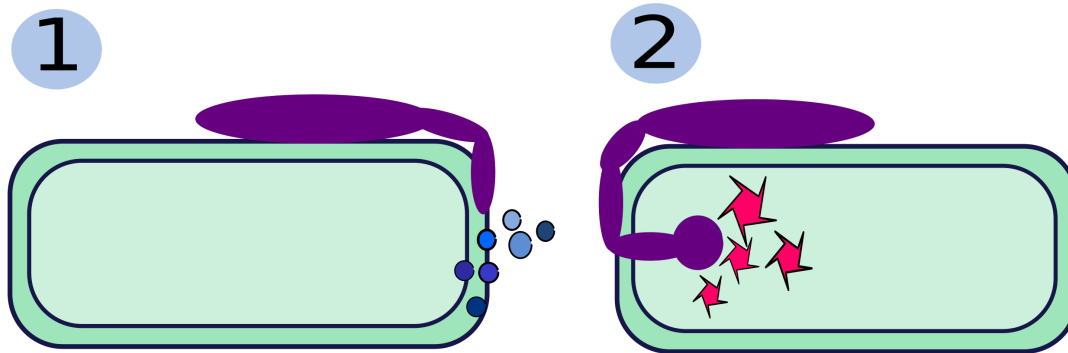
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2017-12-06

# What is a secretome?

- a collection of macromolecules secreted by a cell
- vital for cell-cell communication
- widely exploited by pathogens

secretomes in plant-pathogen interactions

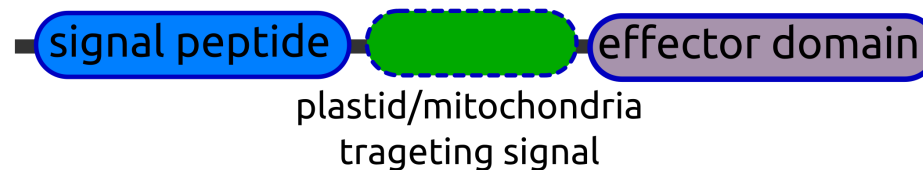
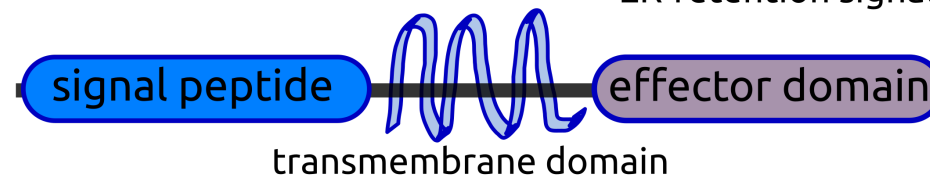
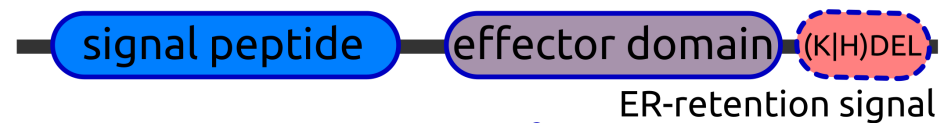


# How to spot secreted proteins

secreted protein:



complications:

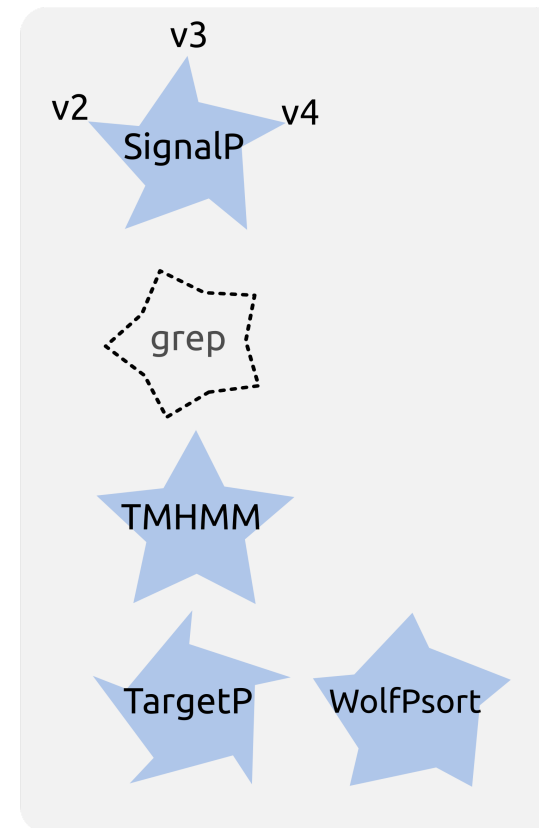
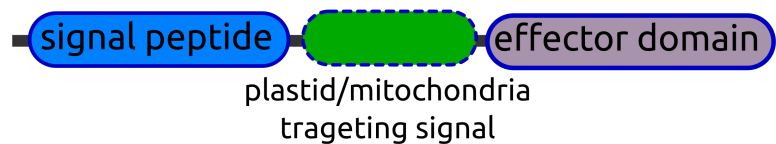
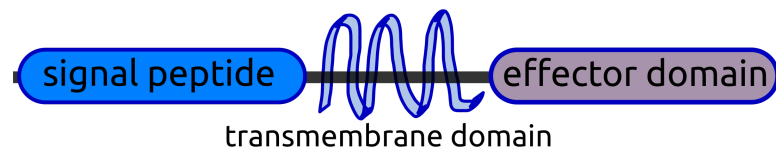
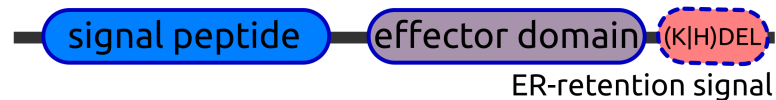


# Tools for prediction of individual motifs

secreted protein:



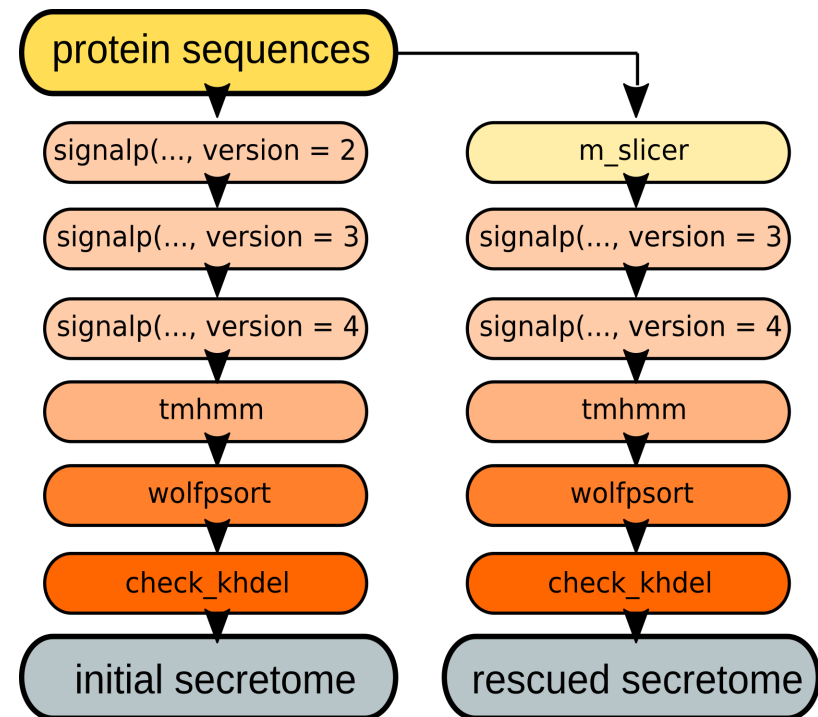
complications:



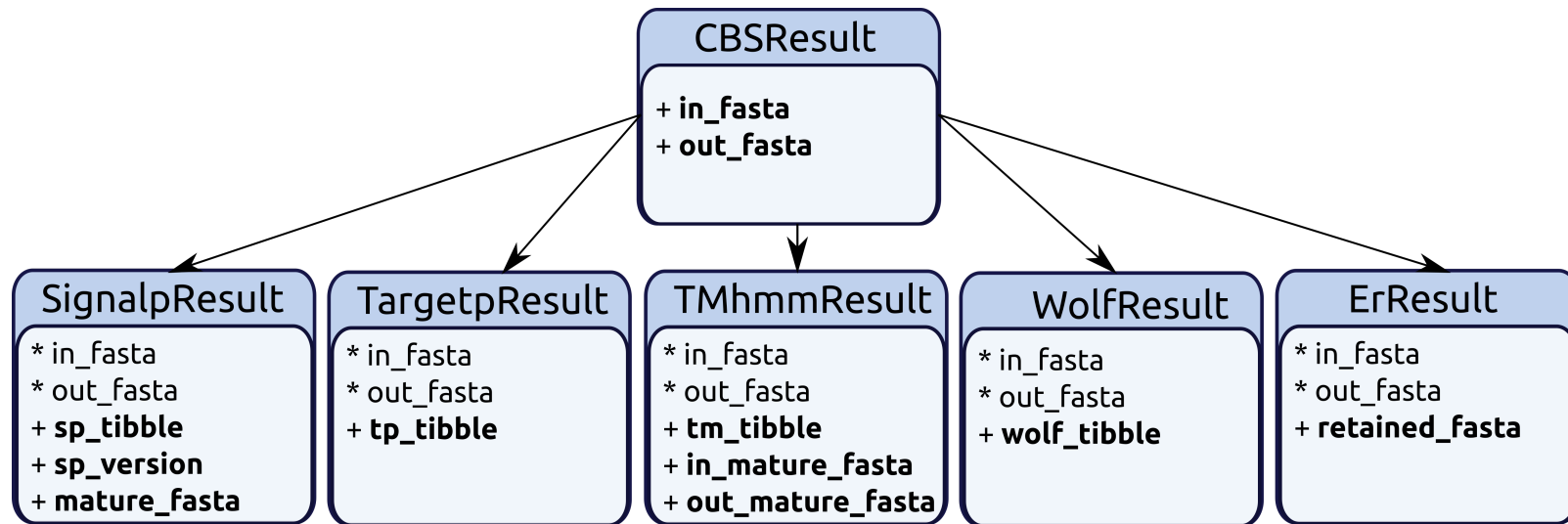
# Tidy secretome prediction

Main functions:

- `manage_paths()`
- `signalp()`
- `targetp()`
- `wolfpsort()`
- `tmhmm()`
- `check_khdel()`
- `m_slicer()`



# SecretSanta S4 class structure



# SecretSanta in action

```
library(devtools)
install_github("gogleva/SecretSanta")
library(SecretSanta)

aa <- readAAStringSet(system.file("extdata", "sample_prot_100.fasta",
                                package = "SecretSanta"))

pipeline <- signalp(CBSResult(in_fasta = aa),
                    version = 4,
                    organism = 'euk',
                    run_mode = 'starter') %>%
  tmhmm(TM = 0) %>%
  targetp(network = 'N', run_mode = 'piper') %>%
  check_khdel(run_mode = 'piper')
```

# Future

- abstract wrapper function for integration of new methods
- “log-file” backbone system
- faster parallelization

Find out more

- [SecretSanta repository](#)
- [Documentation and use case scenarios](#)
- [Functions reference list](#)
- Anna Gogleva [anna.gogleva@slcu.cam.ac.uk](mailto:anna.gogleva@slcu.cam.ac.uk)  
[github.com/gogleva/SecretSanta](https://github.com/gogleva/SecretSanta)