

iLund^{4U} hotspot annotation mode

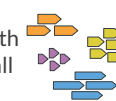
Proteomes
in GFF format
with sequences

Results:

- proteome network
- variable islands
- hotspots
- annotation tables
-

iLund^{4U}
Database

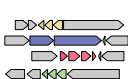
Defining groups of
protein homologues with
MMseqs clustering of all
proteins



Building network of
proteomes based on fraction
of shared homologues and
community detection



Annotation of variable
islands for each
proteome and their
core neighborhood



Annotation of variable
protein groups based on
presence in a community
of proteomes



Building network of islands based
on fraction of shared neighbours
and hotspot annotation by
community detection

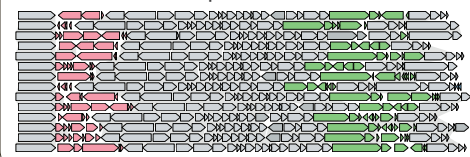


Additional functional
annotation variable
island and neighborhood
encoded proteins

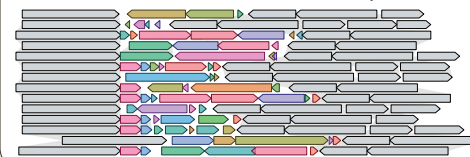
Virulence factors
Defence Systems
Anti-defence
AMR

LoVis^{4U} visualisation

Visualisation of proteome communities



Visualisation of individual hotspots



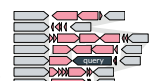
protein search mode

Single protein
sequence in
fasta format

MMseqs search versus
database to define
protein homology group



Retrieving hotspots
containing query
protein homologues



iLund^{4U}
Database
Precomputed

proteome annotation mode

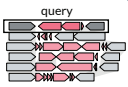
MMseqs search versus
database to define homology
groups for all proteins



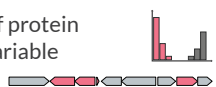
Defining proteome
community by searching
versus database network



Hotspot mapping and
additional functional
annotation of proteins



Annotation of protein
groups and variable
islands



Single proteome
in GFF format
with sequence

If homologous proteins are found:

Results:

- List of hotspots with proteins and their annotation (e.g. fraction of defence, AMR..)
- Publication quality visualisation

If community of related proteomes is found

Results:

- Updated database network of proteomes with query proteome
- Annotation of protein classes
- Annotation of hotspots
- Publication-quality visualisation