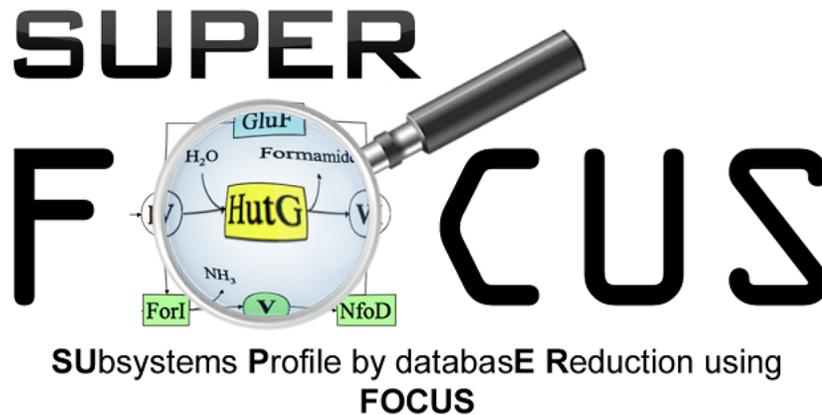


Annotating the function in the bins with SUPER-FOCUS



Subsystems Profile by database reduction using FOCUS (SUPER-FOCUS) combines the taxonomic profiling using FOCUS, which is rapid, and the functional profiling using *k*-mers or faster searches than blast using alternate algorithms including diamond or RAPsearch.

SUPER-FOCUS input is the same as FOCUS — you just need a folder with all the sequences from your metagenome. You can have one or more sequences in the folder, and they can be reads, or metagenome assembled genomes.

First download the database by running

```
superfocus__downloadDB -a diamond
```

to download the database for the diamond search algorithm (which is the fastest, but also requires the most memory).

Then to run superfocus, you use the command (e.g. for Algae_MetaBatBins)

```
superfocus.py -q Algae_MetaBatBins -m 1 -db DB_90 -dir Algae_MetaBatBins_Superfocus_results
```

The SUPER-FOCUS results for all the bins are saved in a folder called SUPER-FOCUS and are self explanatory!