CompositeSearch Tutorial

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STEP 1: SEQUENCE SIMILARITY

BLASTP parameters:

- -seg yes
- -soft_masking true
- -max_target_seqs 5000
- -outfmt "6 qseqid sseqid evalue pident bitscore qstart qend qlen sstart send slen"

STEP 2: CLEAN BLASTP OUTPUT

Your sequence name are:

1) integers:

./cleanBlastp -i blastp.out

2) not integers:

./cleanBlastp -i blastp.out -n 1

OUTPUT FILES:

- blastp.out.cleanNetwork
- blastp.out.cleanNetwork.genes
- blastp.out.cleanNetwork.dico (if you used -n 1)

STEP 3: CompositeSearch

Find help: ./compositefinder -help

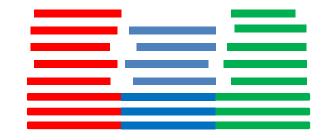
STEP 3: CompositeSearch

(algorithm: composites)

Example:

./compositeSearch -i blastp.out.cleanNetwork -n blastp.out.cleanNetwork.genes -m composites -e 1e-05 -p 30 -c 80 -l 20 -t 20

composites



(algorithms: composites)

CompositeSearch give 3 files for the gene families detection.

-File 1 : family.nodes

-File 2 : family.edges

-File 3 : family.info

(algorithm: composites)

- CompositeSearch give 3 files for the gene families detection:
 - family.nodes : gene families sequences ID (fasta format)

```
>F6
268103
201232
10
```

family.edges : gene families sequences similarity (fasta format)

```
>F6
201232 268103
10 201232
10 268103
```

family.info : family ID, Nb nodes, Nb edges and connectivity

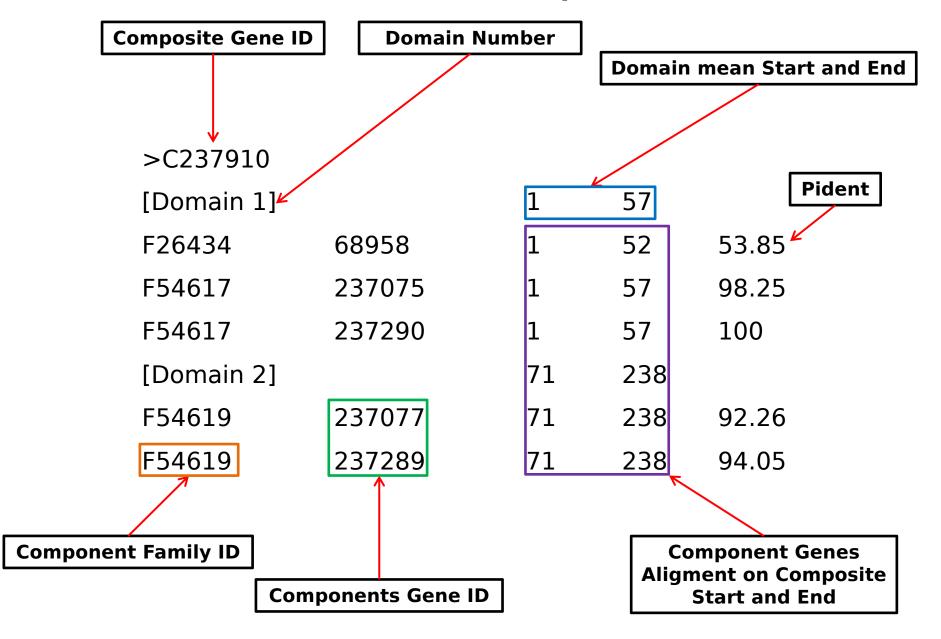
(algorithm: composites)

CompositeSearch give 2 files for the composite genes detection:

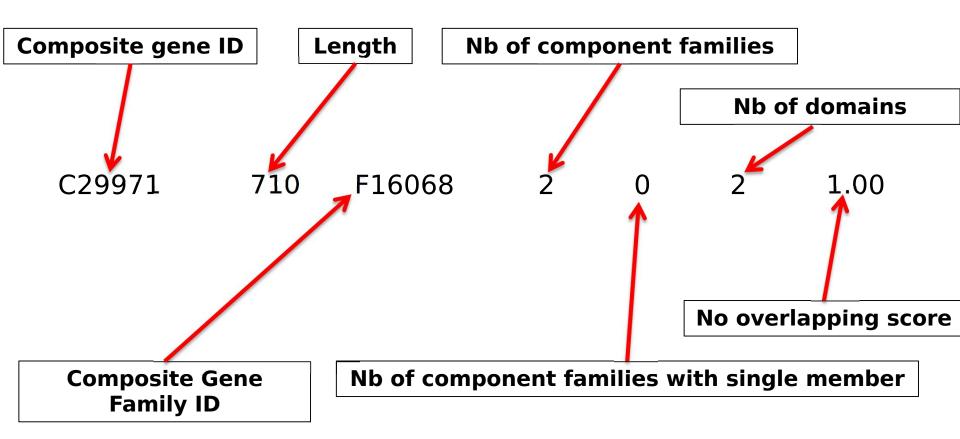
-File 1 : xxxxx.compoistes (detailed information)

-File 2 : xxxxx.compositesinfo (general information)

File 1 : xxxxx.composites



File 2: xxxxx.compositesinfo



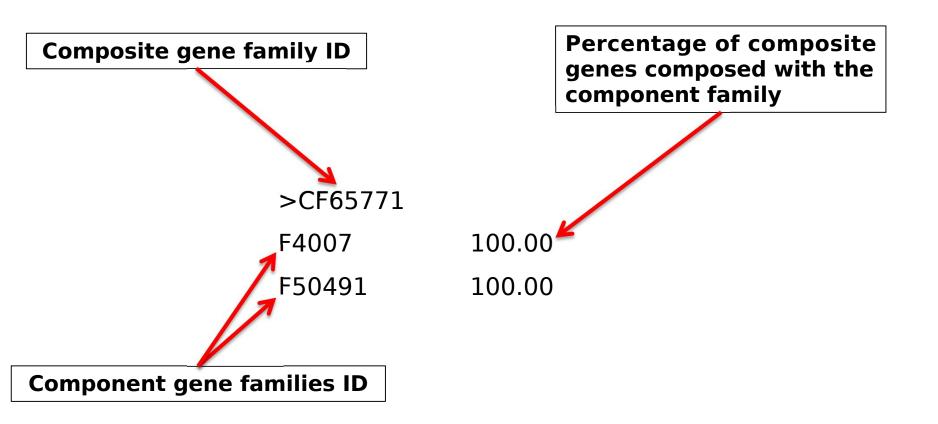
(algorithm: composites)

CompositeSearch give 2 files for the composite genes detection:

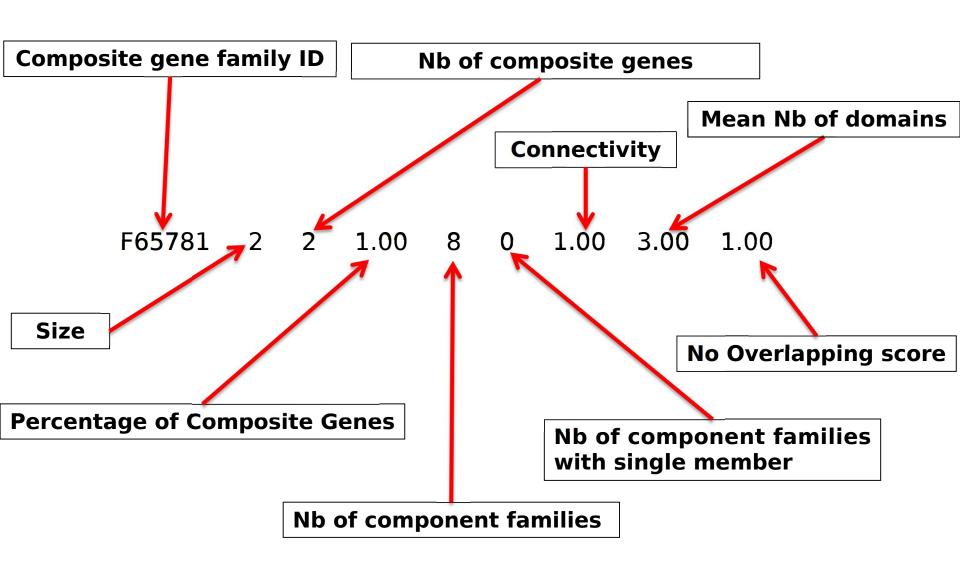
-File 1 : xxxxx.compoistefamilies (detailed information)

-File 2 : xxxxx.compositefamiliesinfo (general information)

File 1 : xxxxx.compositefamilies

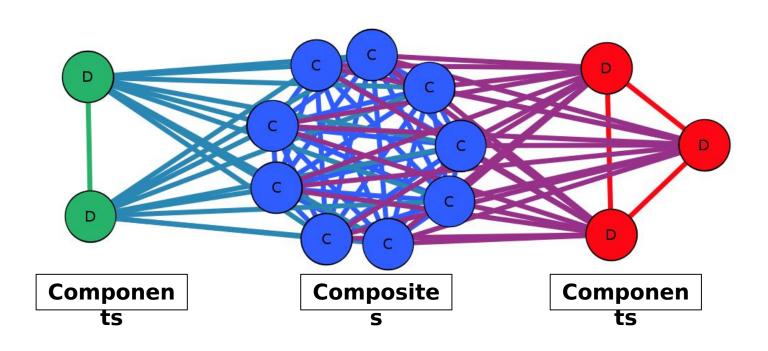


File 2: xxxxx.compositefamiliesinfo

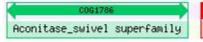


PLASMIDS

EXAMPLE N°1 (clique)



BLASTP



EXAMPLE N°2 (quasi clique)

