

Fasta file



IMG_T annotation output

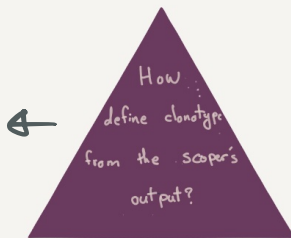
Summary and gapped nt files (n° 1 and 2)



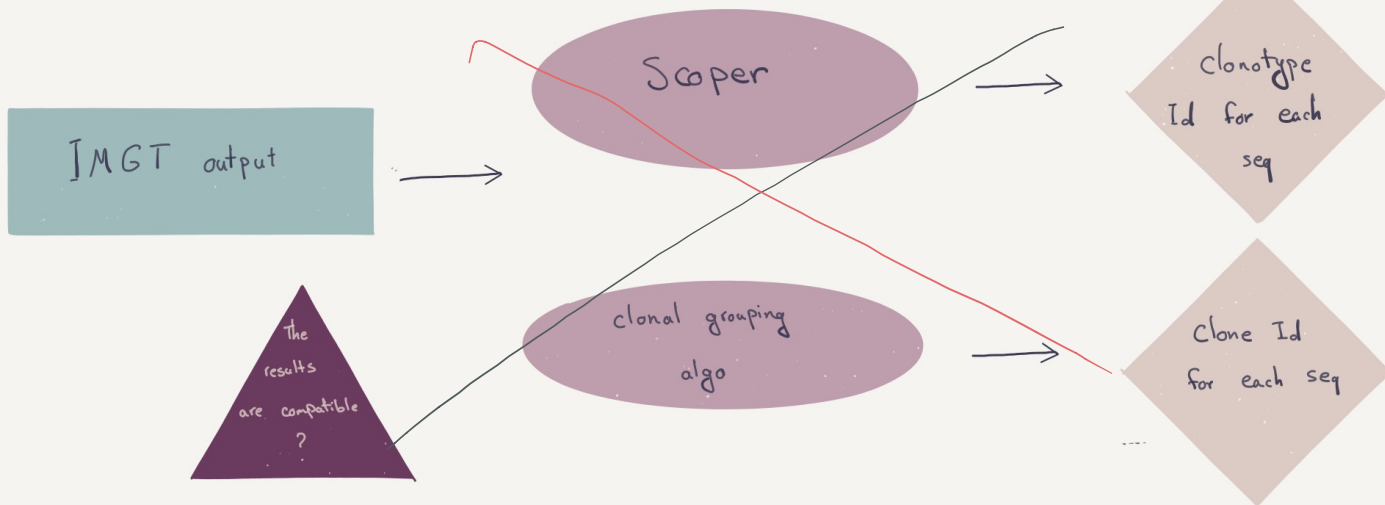
① scoper

② output scoper
for each clone

↳ find clonotyp
(IMGT)



or



Time needed

?

Informations to provide

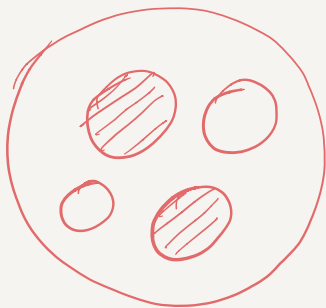
The abundance of each clone ^① → Analysing all the clones

The abundance of clonotypes → Analysing x most abundant clones / abundance threshold

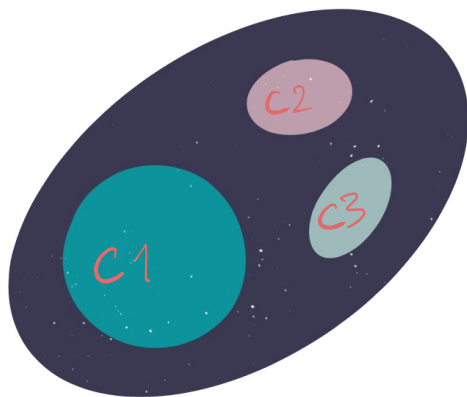
internal
param

^② → "User choice based on gene / CDR3 → if accept this option, we should modify the first page and add

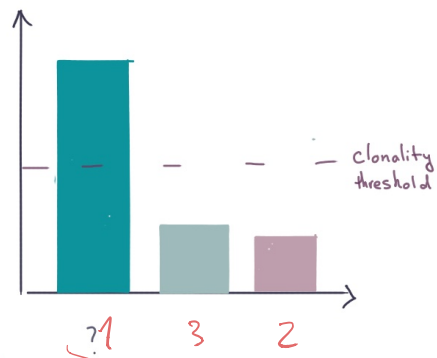
?

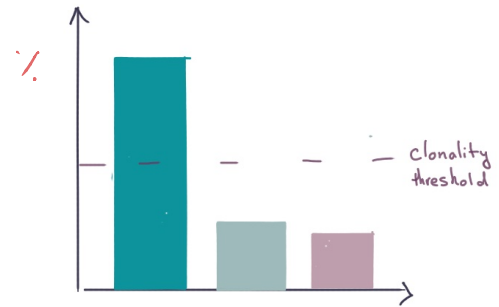
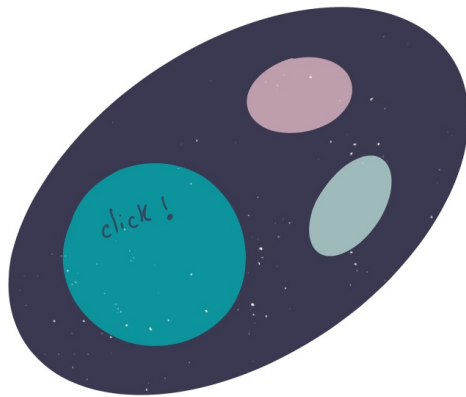


C1	v4_34	J5	CD3 1
C4	v4_34	J1	CD3 2



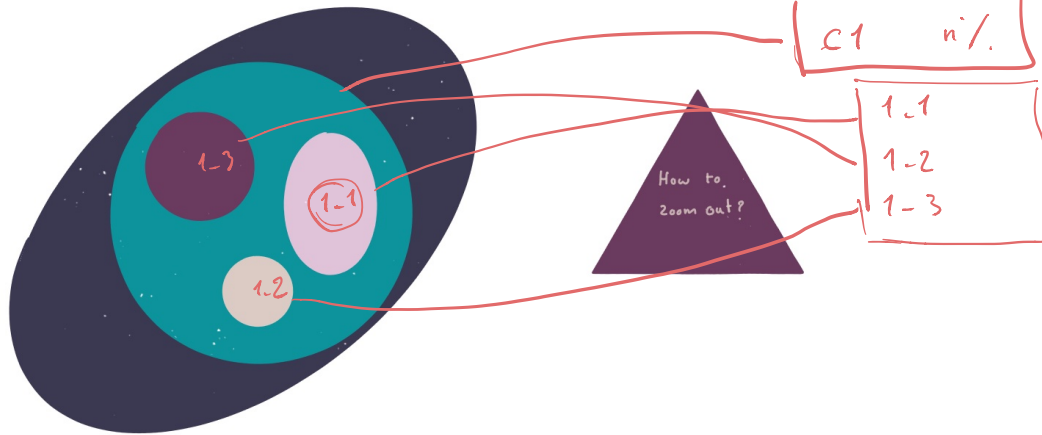
↙
number

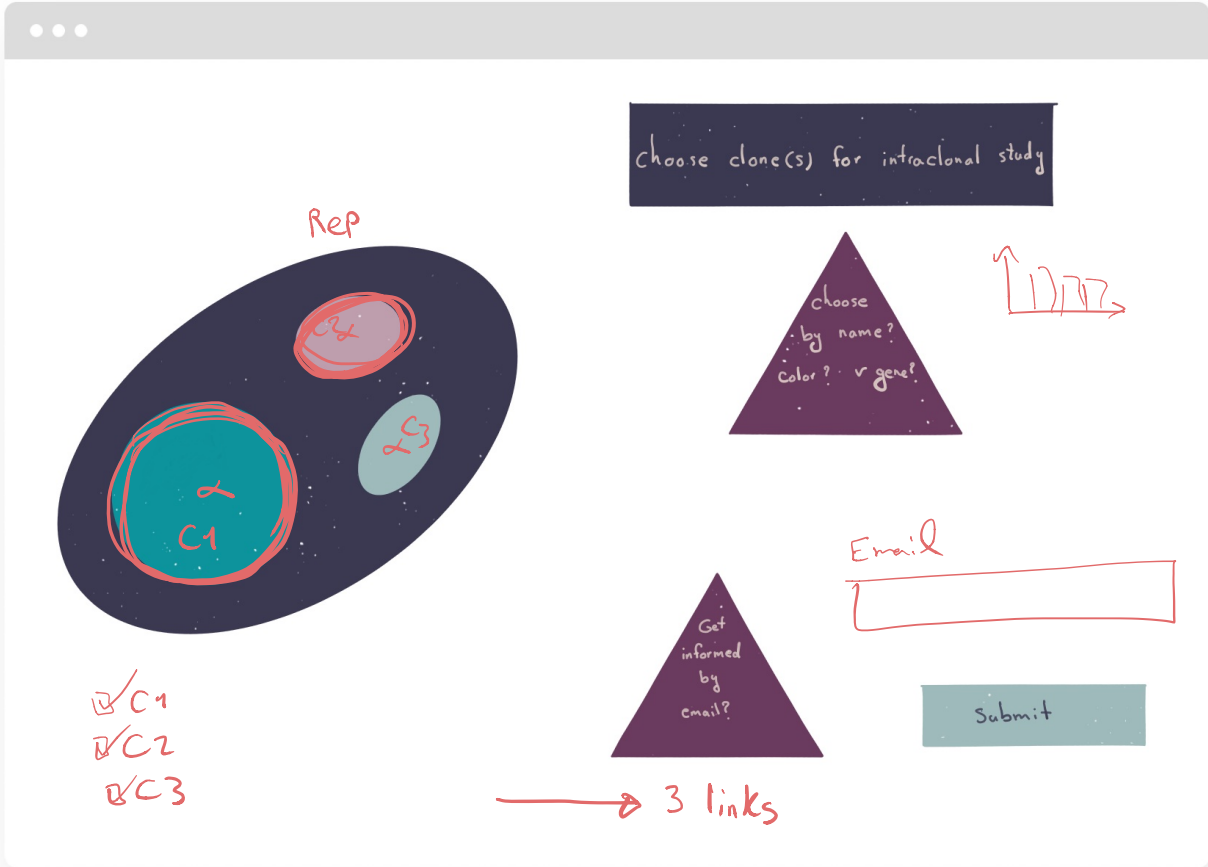




Zoom on clone

↳ clonotype and their abundance are visible





clone and its clonotypes

for each clonotype

creat
the consensus
seq

for the most
abundant clonotype

IMGT gapped seq

reverse

SHM

create
the germline seq
of the clone

Run GTree (or other
algo)

Tree
and
distances

- Date limite
- ordre de passage

base de
donner

creer
une
ligne

attendre
et
creer job

h
D
8

based on
IMGT
annotation

Aligned

