

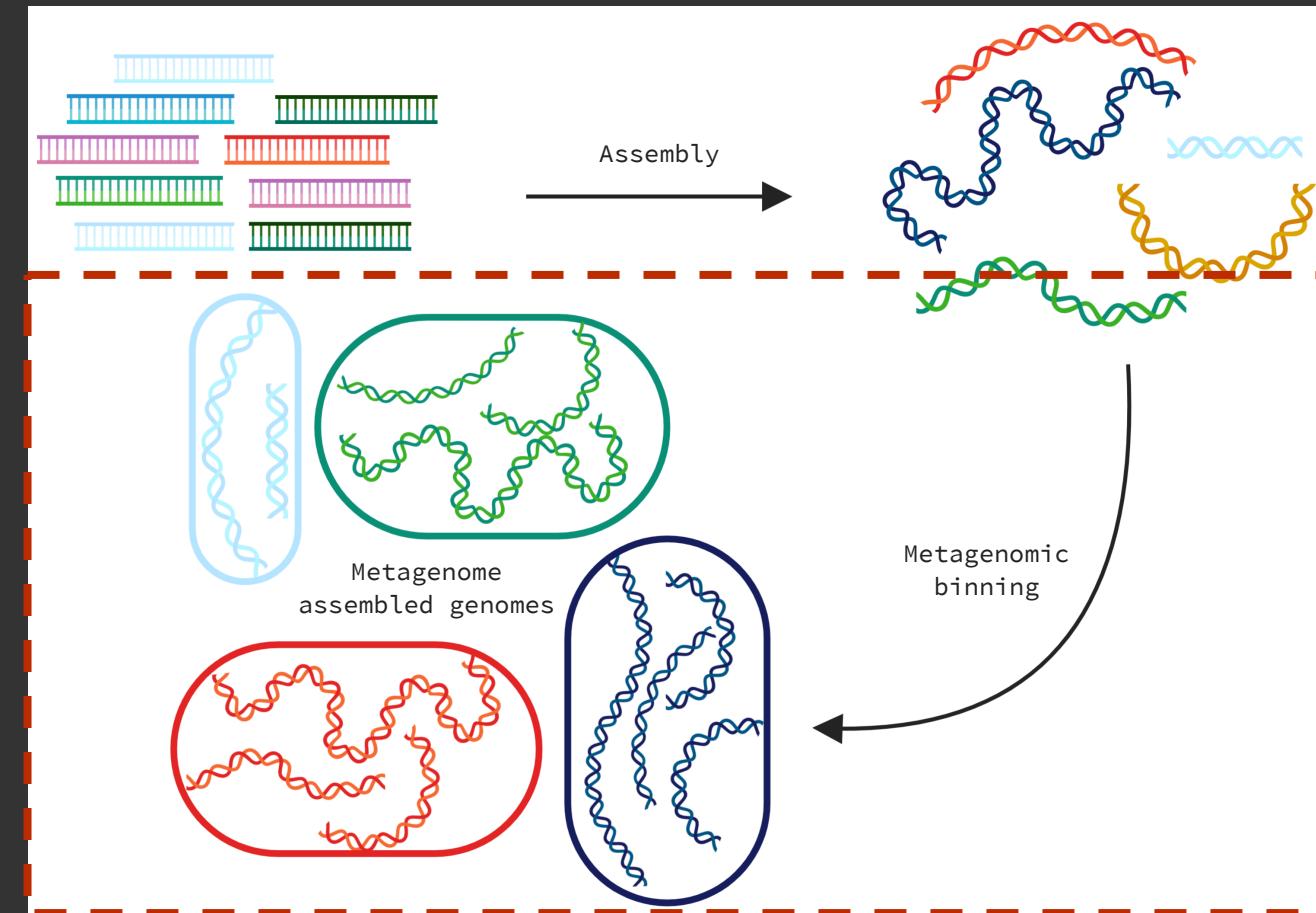


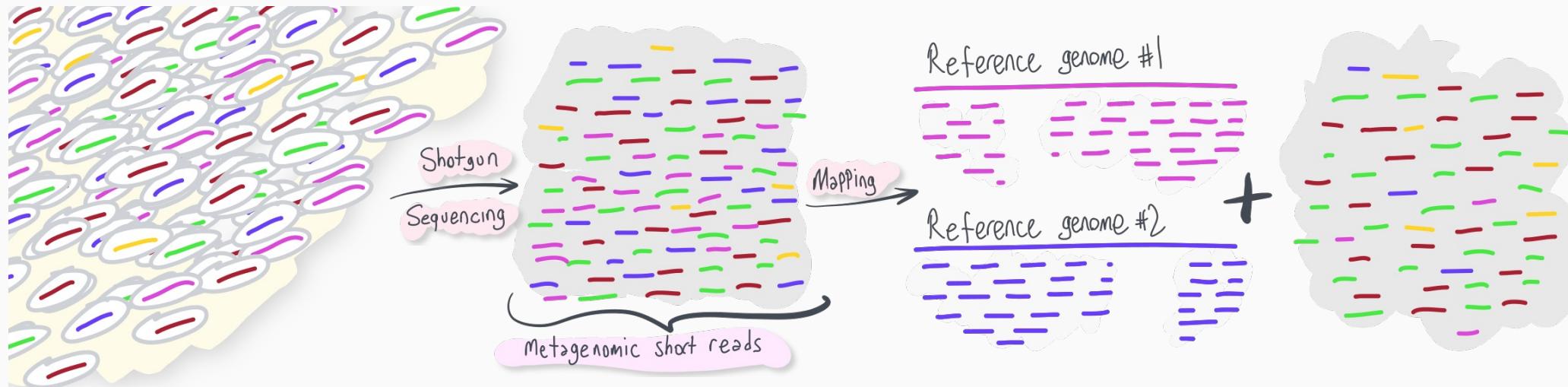
Introdução à metagenômica: curso prático

Metagenômica a nível de genomas

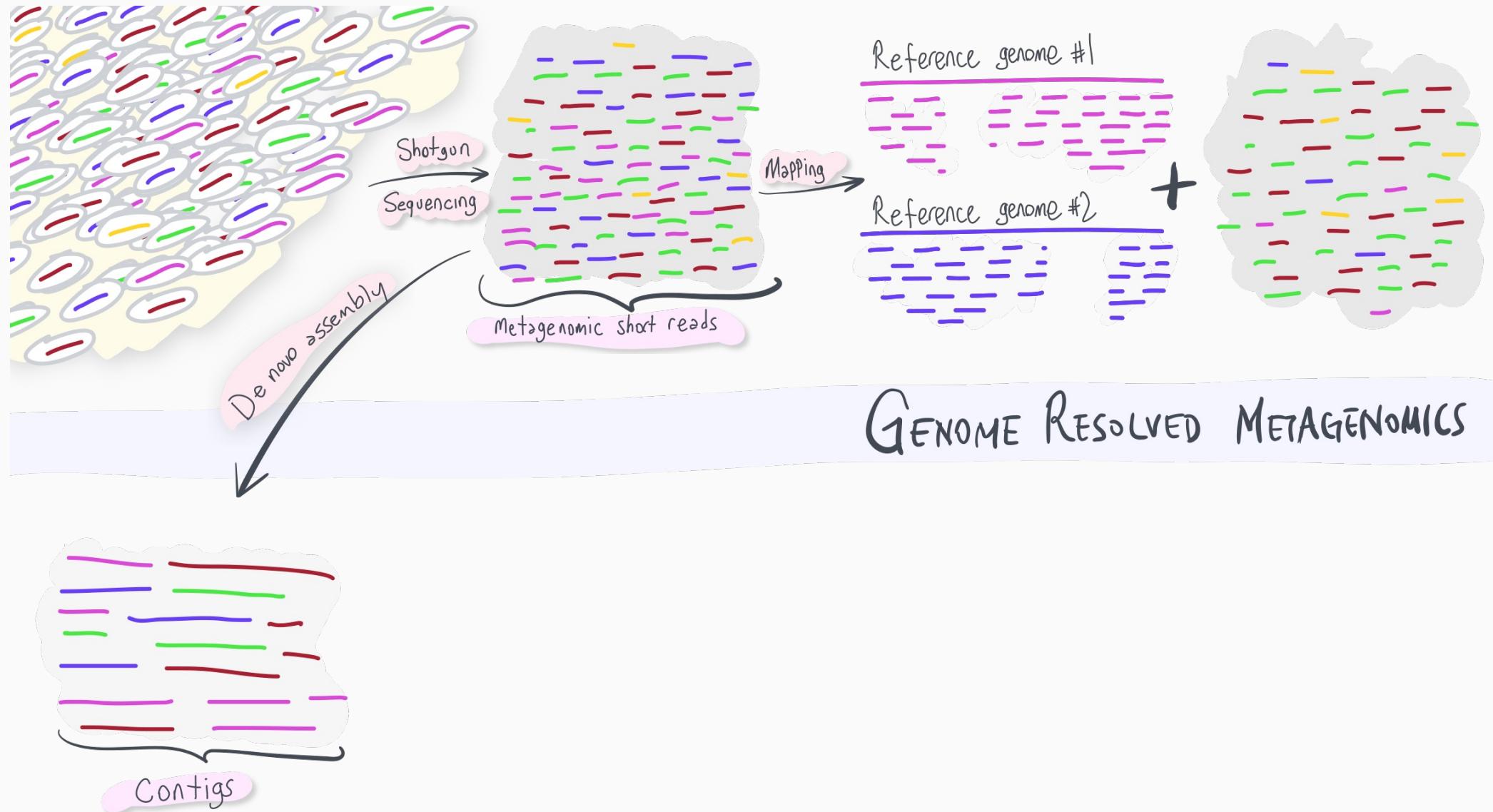
O que é metagenômica a nível de genomas (*genome-resolved metagenomics*)

Agrupamento de contigs que originam de um mesmo genoma (população)

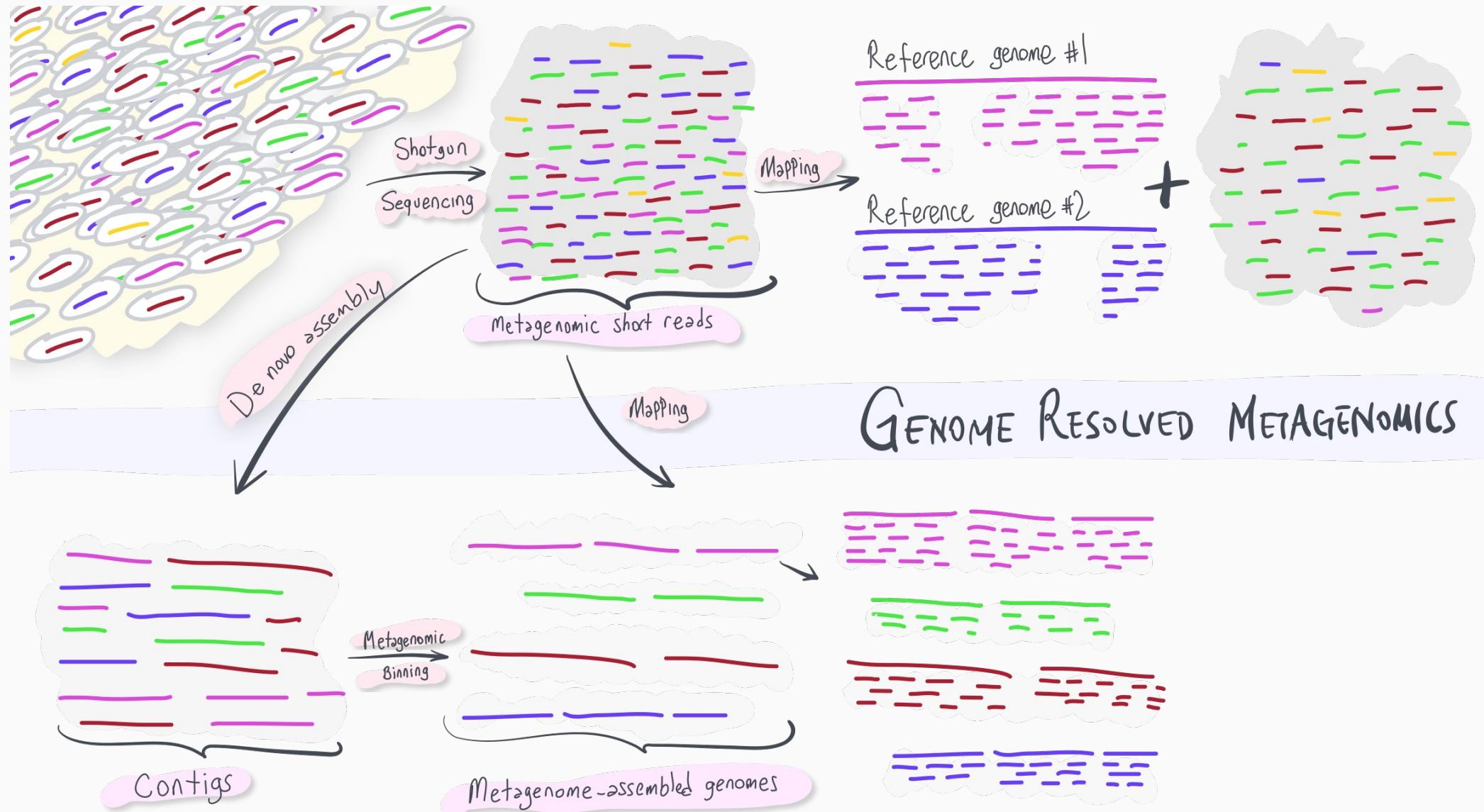




GENOME RESOLVED METAGENOMICS

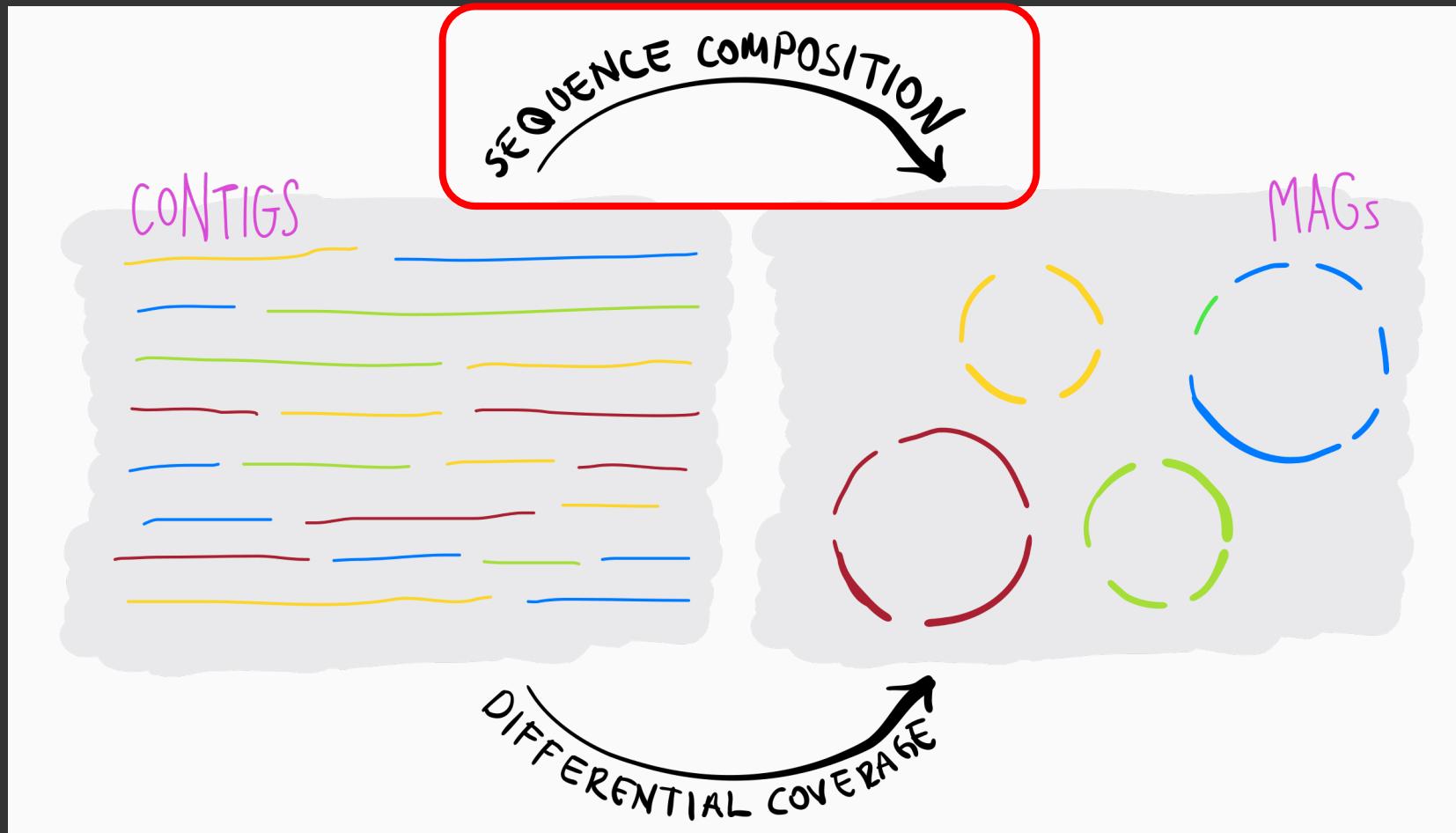


merenlab.org/momics



merenlab.org/momics

Agrupamento de contigs



GTTTGCGCATGATTAAGGGAGTTCTTTGTGCTTC

AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

k=2

merenlab.org/momics

GT	TTTGGCATGATTAAAGGGAGTTCTTTGTGCTTC
AA	AA
AC	AC
AG	AG
AT	AT
CA	CA
CC	CC
CG	CG
CT	CT
GA	GA
GC	GC
GG	GG
GT	GT
TA	TA
TC	TC
TG	TG
TT	TT

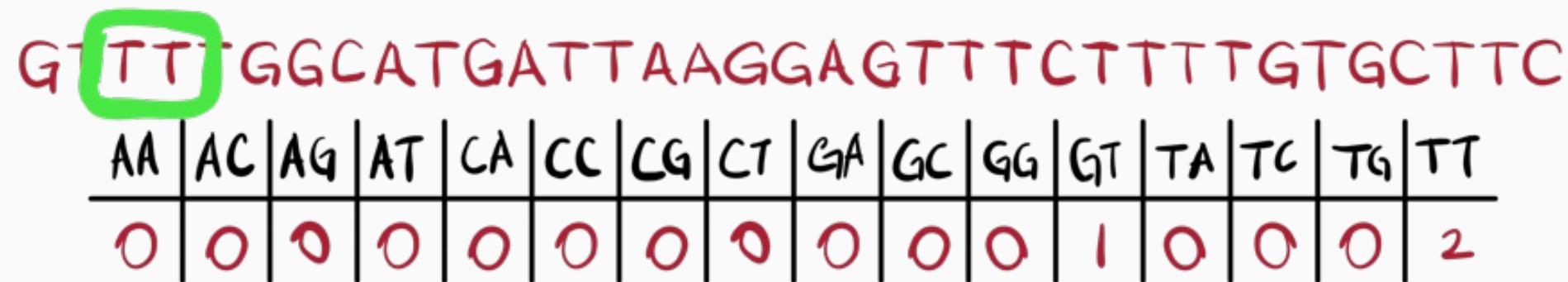
k=2

merenlab.org/momics

CTT	TGGCATGATTAAAGGGAGTTCTTTGTGCTTC														
AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1

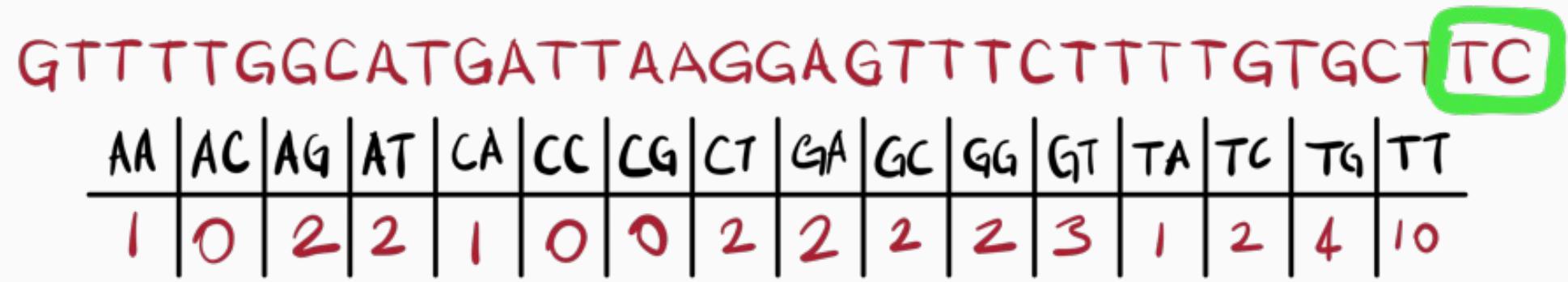
k=2

merenlab.org/momics



k=2

merenlab.org/momics



k=2

merenlab.org/momics

GTTTGCGATGATTAAAGGAGTTCTTTGTGCTTC

AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
1	0	2	2	1	0	0	2	2	2	2	3	1	2	4	10

9

GAAGCACAAAAGAAACTCCTTAATCATGCCAAAAAC

AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
10	3	2	2	4	2	0	2	2	2	6	0	1	2	1	1

k=2

merenlab.org/momics

GTTTGCGATGATTAAAGGAGTTCTTTGTGCTTC

AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
1	0	2	2	1	0	0	2	2	2	2	3	1	2	4	10



GAAGCACAAAAGAAACTCCTTAATCATGCCAAAAAC

AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
10	3	2	2	4	2	0	2	2	2	6	0	1	2	1	1

GTTTGCGATGATTAAAGGAGTTCTTTGTGCTTC
GAAGCACAAAAGAAACTCCTTAATCATGCCAAAAAC

AA	AC	AG	GA	CA	CC	CG	GC	AT	TA
11	3	4	4	5	2	0	2	2	1

k=2

GTTTGCGATGATTAAAGGGAGTTCTTTGTGCTTC

	AA	AC	AG	GA	CA	CC	CG	GC	AT	TA
X	11	3	4	4	5	2	0	2	2	1
Y										
Z										
L										
K										
M										

k=2

ACTTCCGCAGTCGGGCATTACGCGTTGTGGAATGA

	AA	AC	AG	GA	CA	CC	CG	GC	AT	TA
X	11	3	4	4	5	2	0	2	2	1
Y	4	5	2	4	5	4	4	3	2	1
Z										
L										
K										
M										

k=2

merenlab.org/momics

ACTTGCGCAGTCGCGCATTACGCGTAGTGGAAATAA

	AA	AC	AG	GA	CA	CC	CG	GC	AT	TA
X	11	3	4	4	5	2	0	2	2	1
Y	4	5	2	4	5	4	4	3	2	1
Z	4	5	3	2	4	1	5	5	2	3
L										
K										
M										

k=2

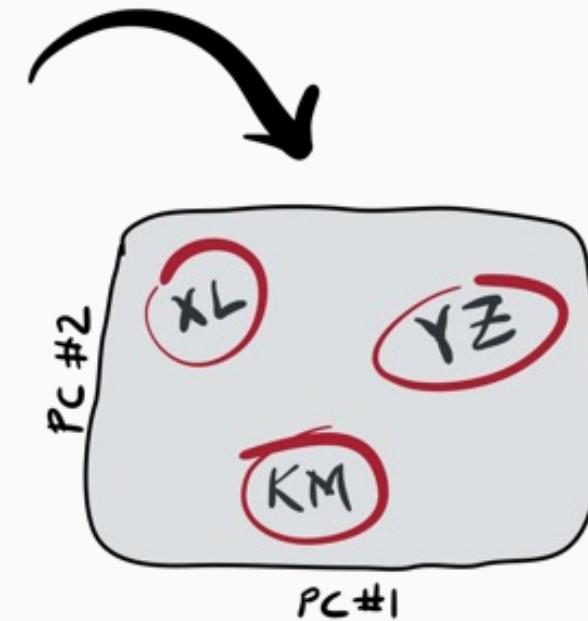
merenlab.org/momics

	AA	AC	AG	GA	CA	CC	CG	GC	AT	TA
X	11	3	4	4	5	2	0	2	2	1
Y	4	5	2	4	5	4	4	3	2	1
Z	4	5	3	2	4	1	5	5	2	3
L	11	6	3	2	2	3	2	1	1	4
K	1	1	2	2	1	8	9	10	0	0
M	0	4	4	3	4	10	4	5	0	0

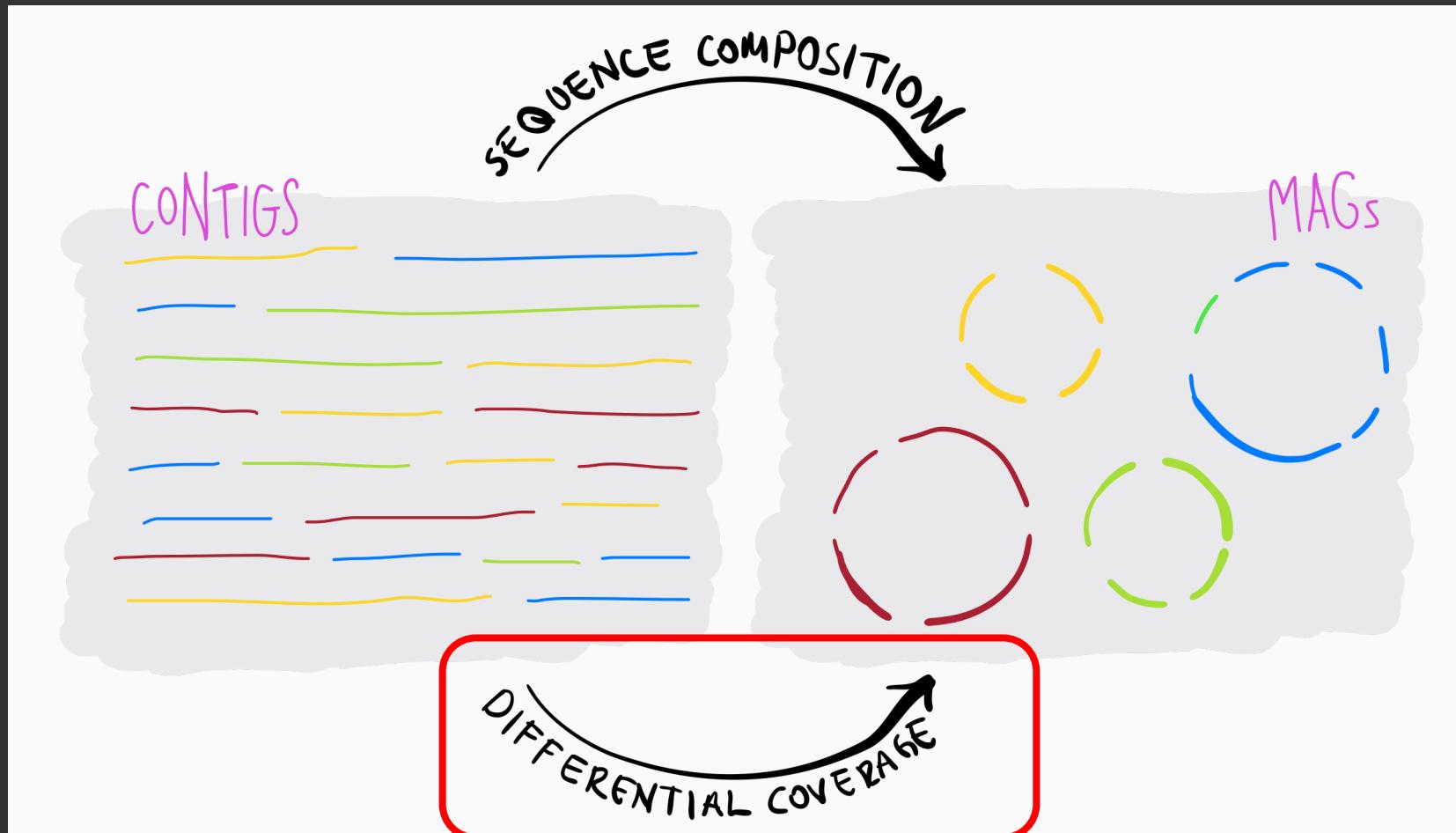
k=2

	AA	AC	AG	GA	CA	CC	CG	GC	AT	TA
X	11	3	4	4	5	2	0	2	2	1
Y	4	5	2	4	5	4	4	3	2	1
Z	4	5	3	2	4	1	5	5	2	3
L	11	6	3	2	2	3	2	1	1	4
K	1	1	2	2	1	8	9	10	0	0
M	0	4	4	3	4	10	4	5	0	0

k=2

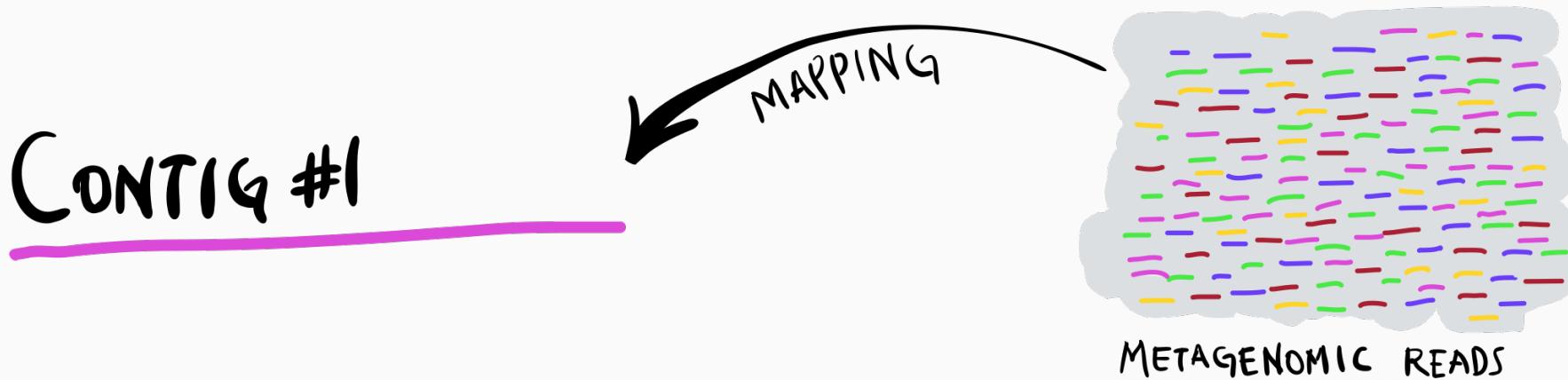


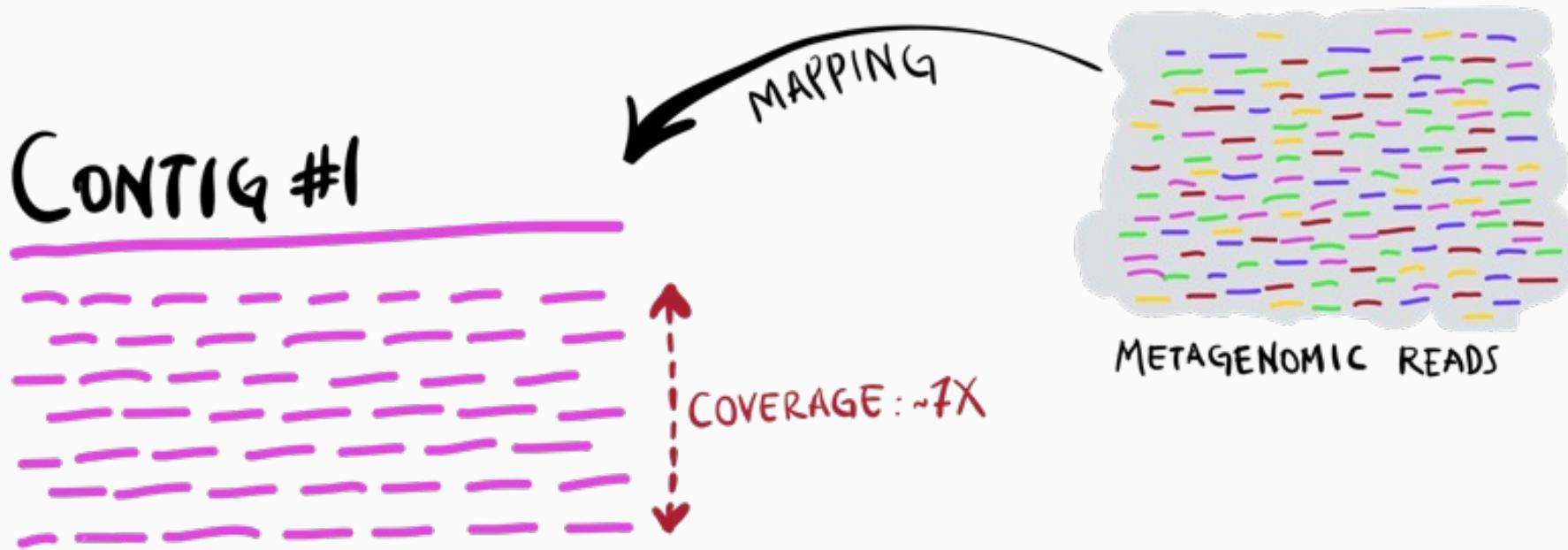
Agrupamento de contigs

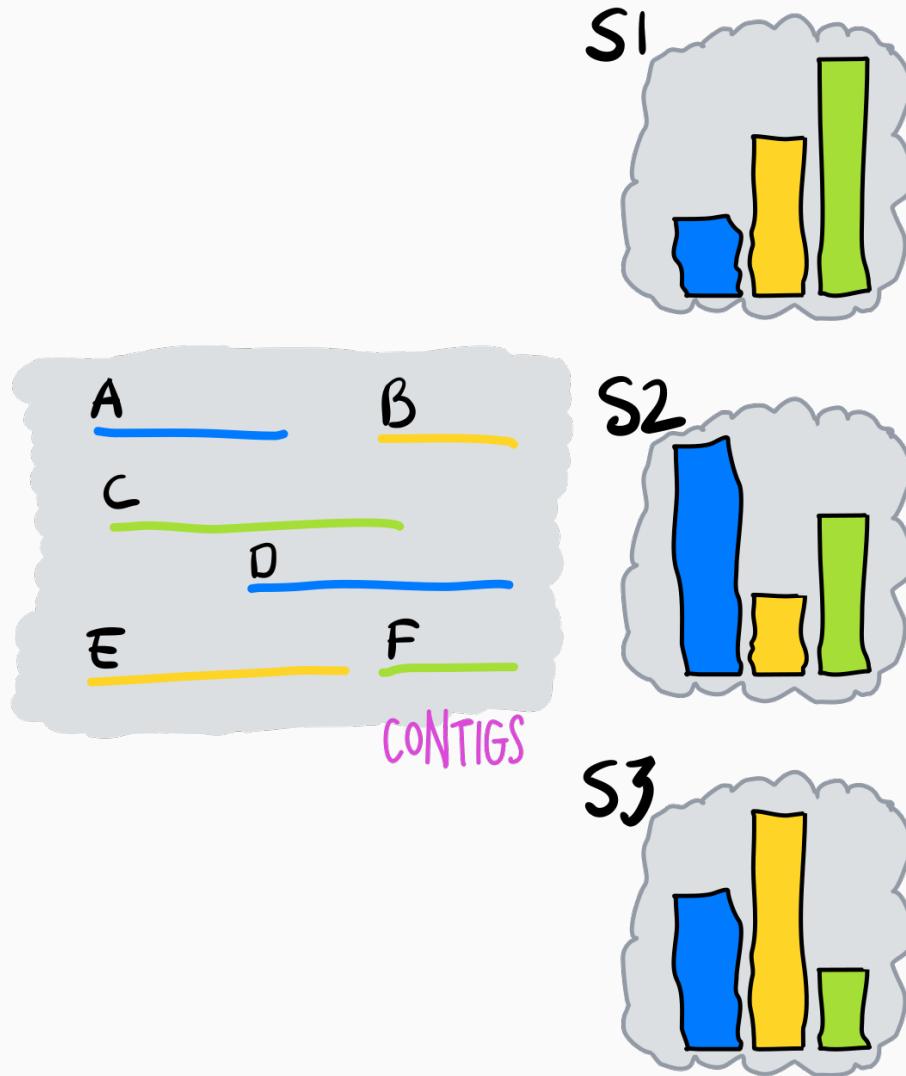


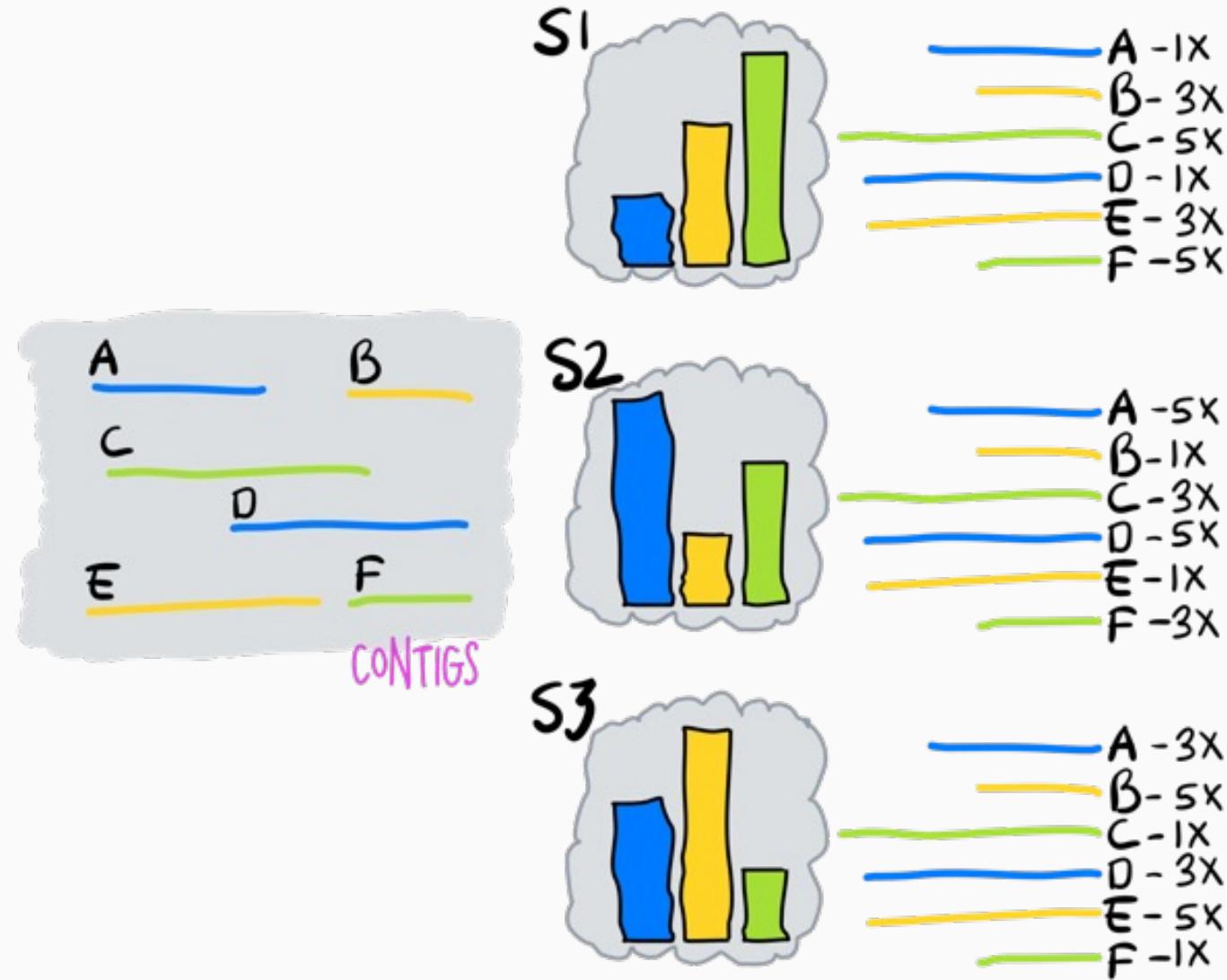
CONTIG #1

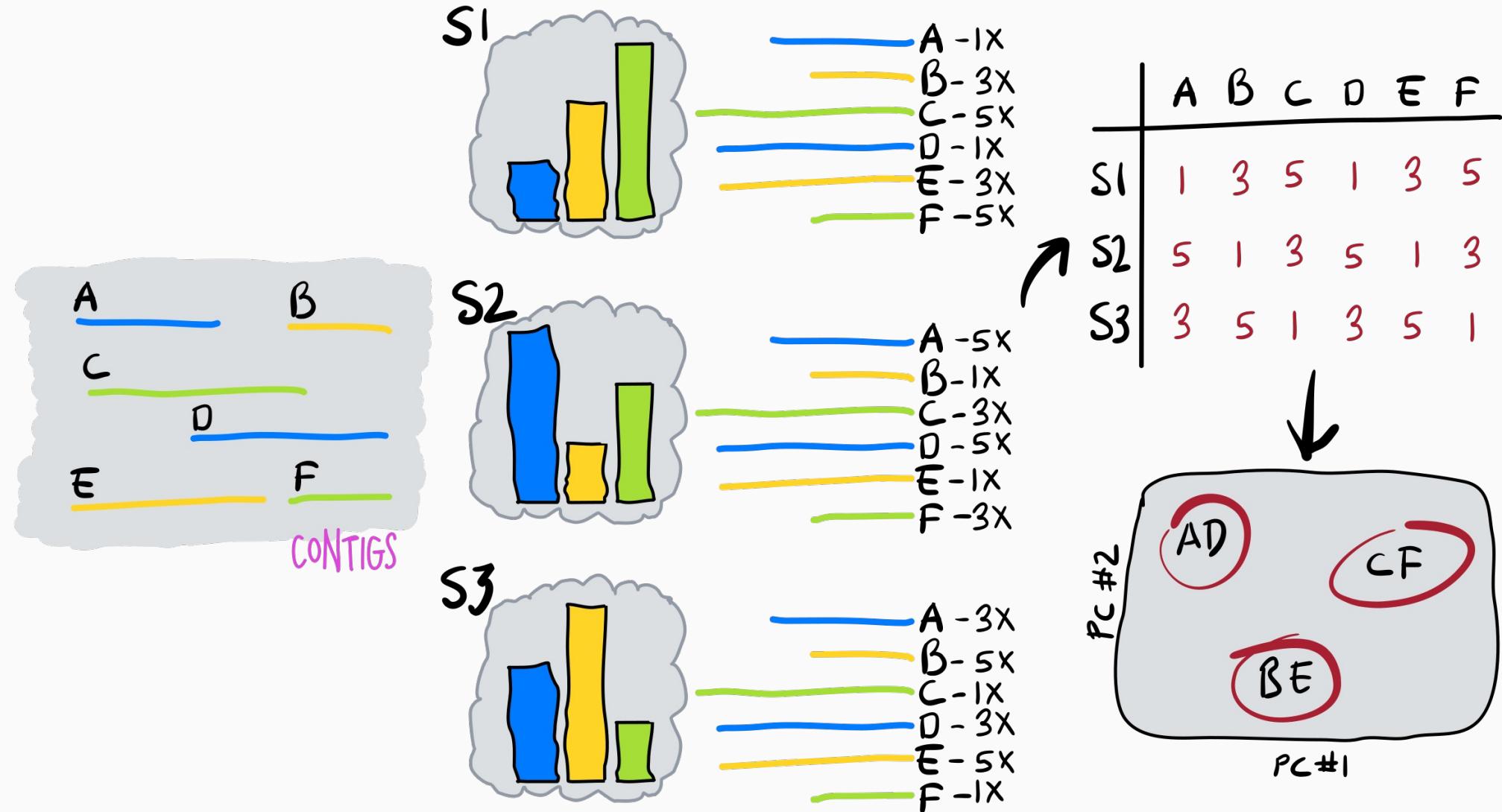
CONTIG #2









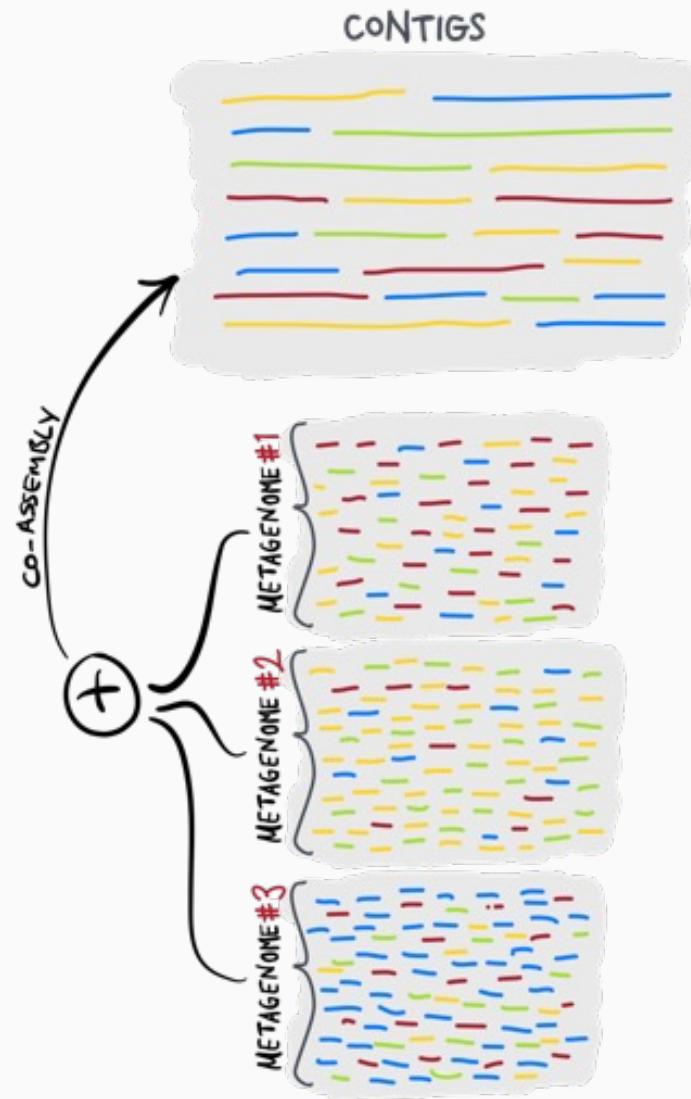


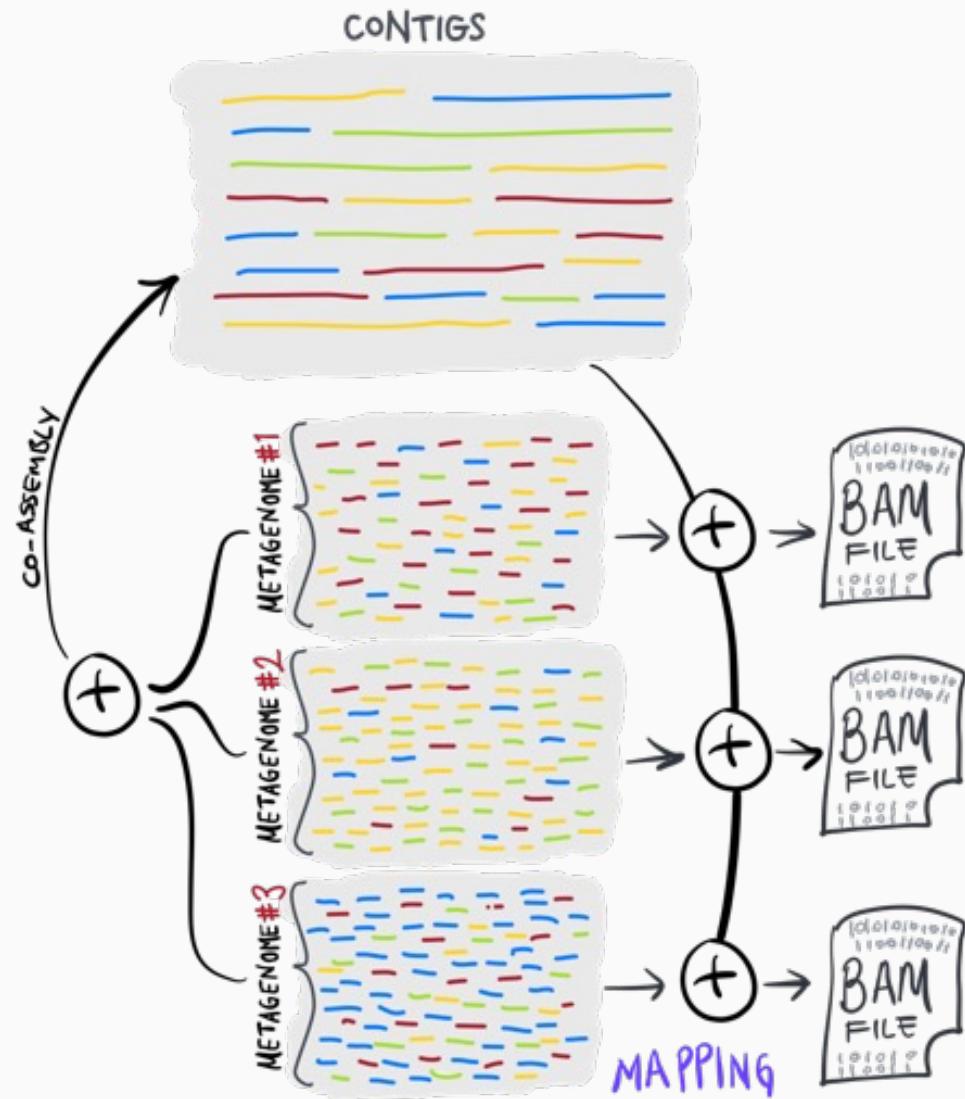
Na prática

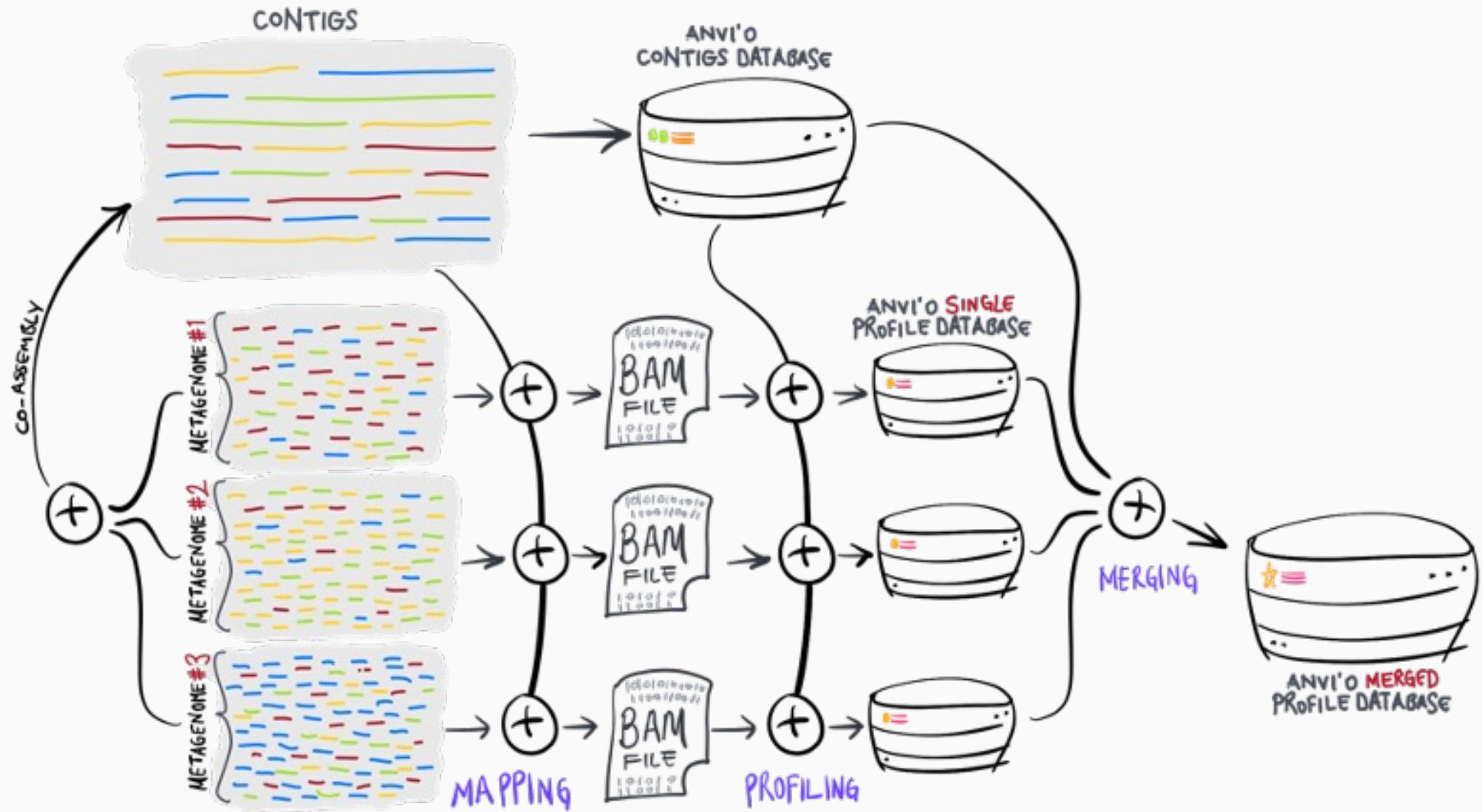
```
# Vários programas para o agrupamento automático de contigs
# CONCOCT
# MetaBat
# MaxBin
# BinSanity
# AutoMeta
# DAS Tool

# Agrupamento manual
# Anvi'o
```

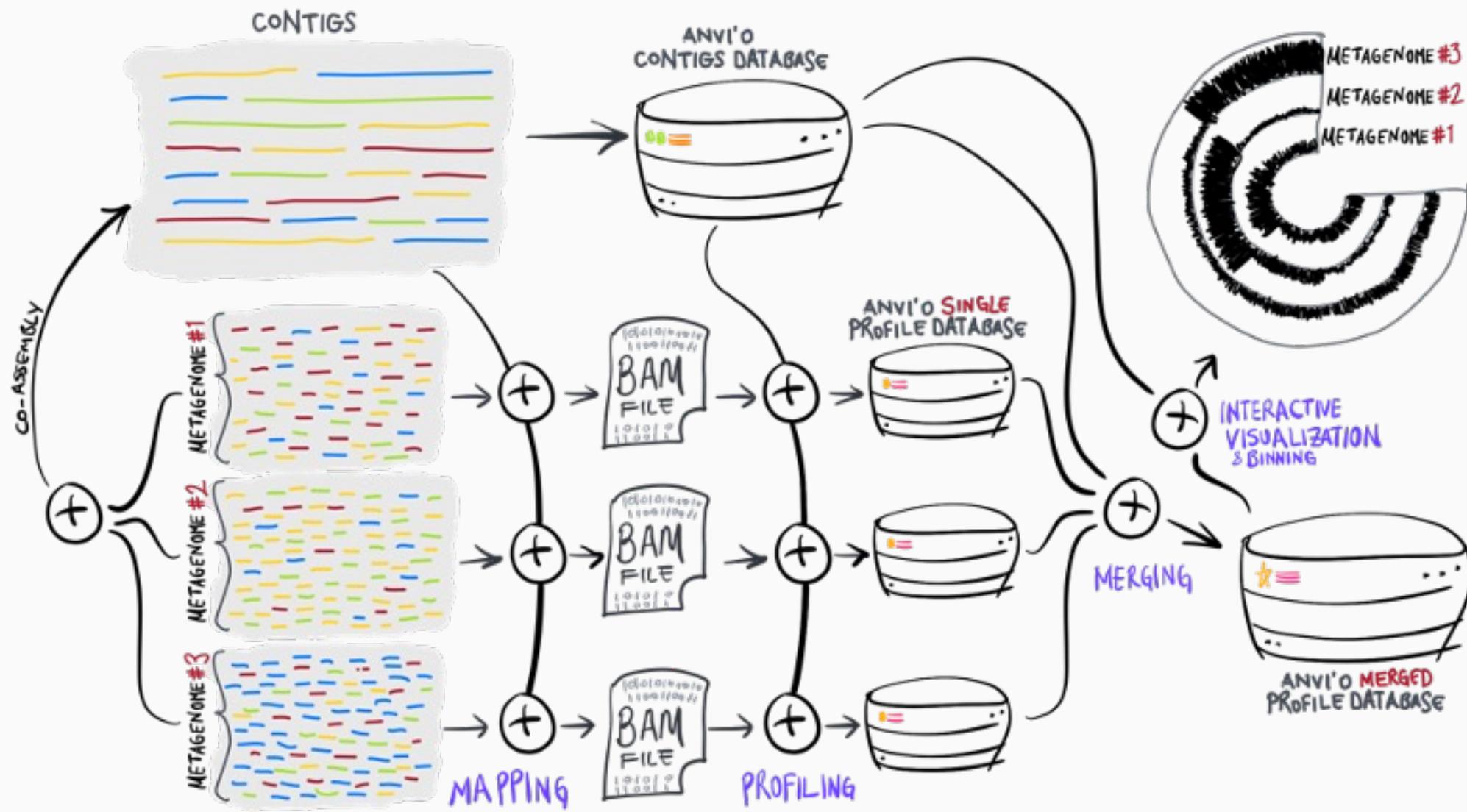


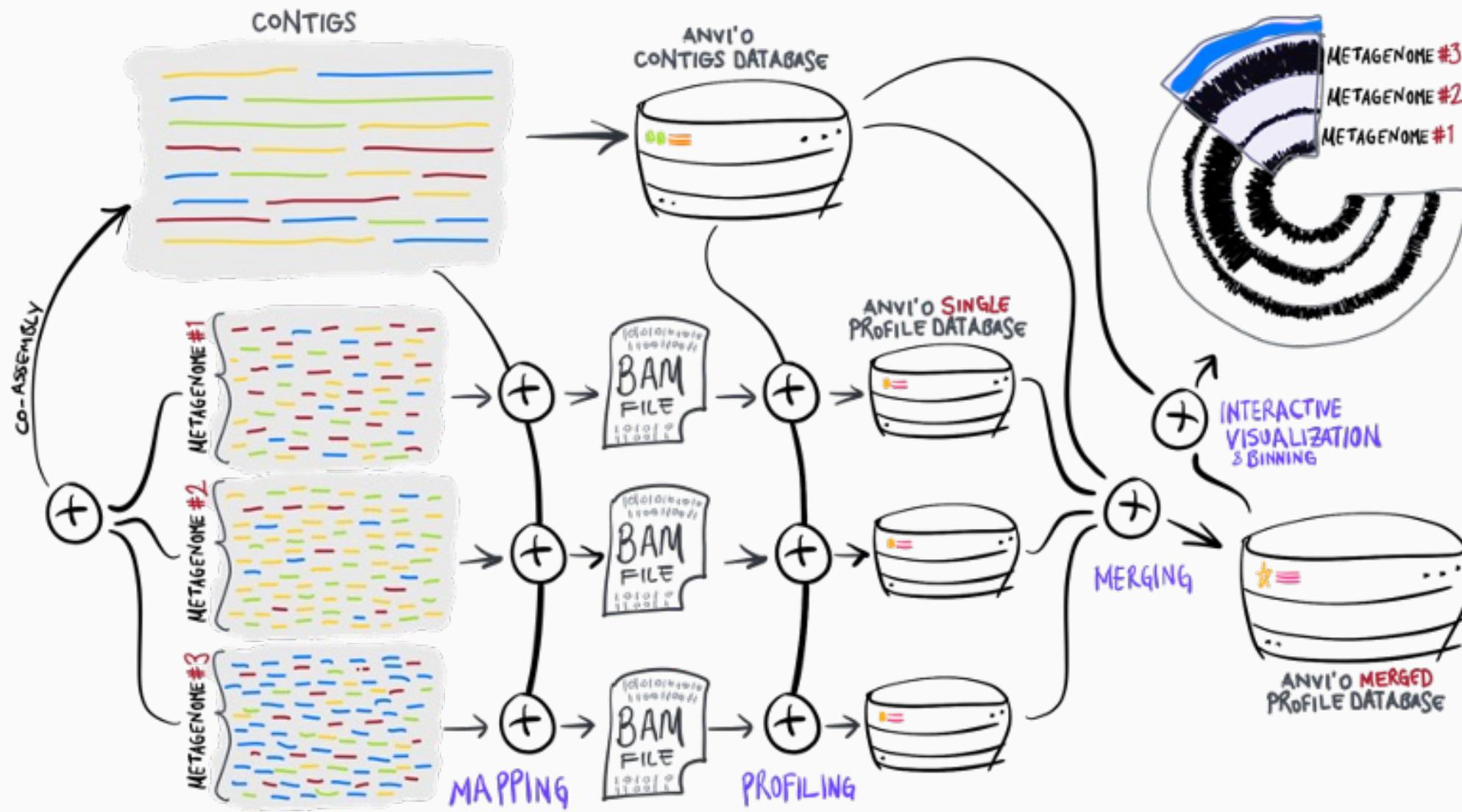


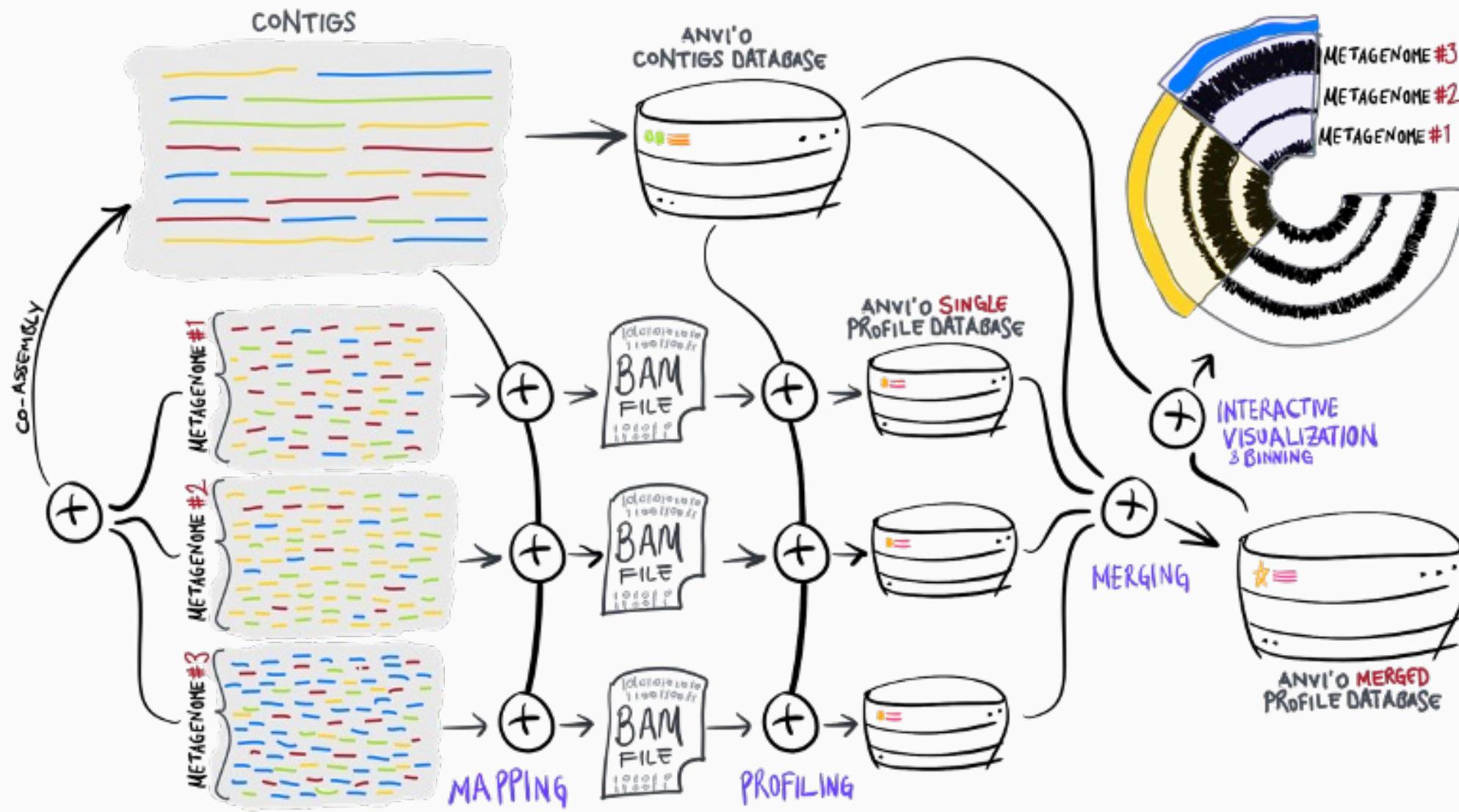




merenlab.org/momics

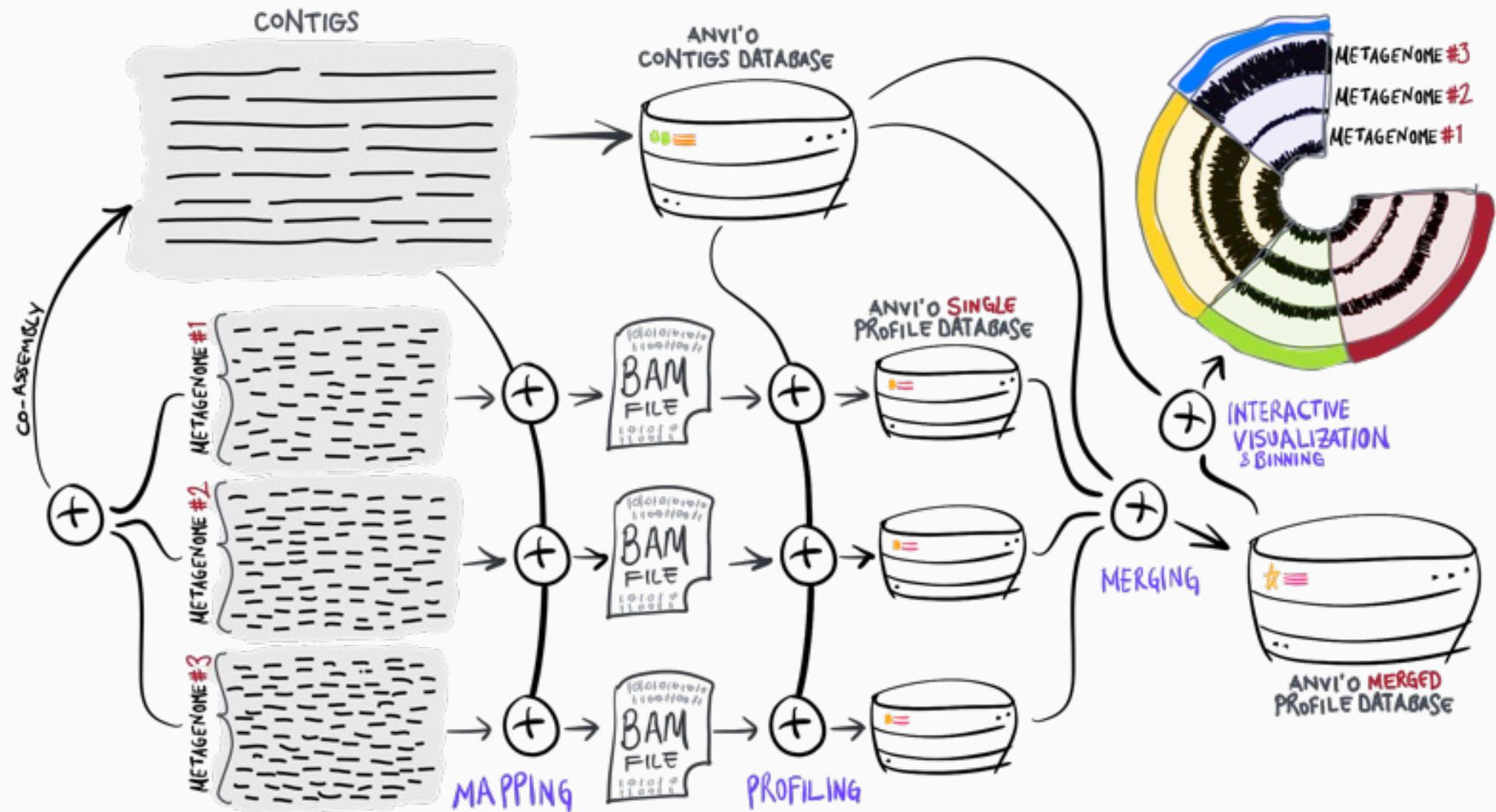






merenlab.org/momics

[igor_pessi@UniversityOfHelsinki]\$



merenlab.org/momics

[igor_pessi@UniversityOfHelsinki]\$ _

Para aprender mais

merenlab.org/2020/06/27/seminar-series-on-microbial-omics

anvio.org

anvio.org/#learn

anvio.org/help/main



discord.gg/C6He6mSNY4