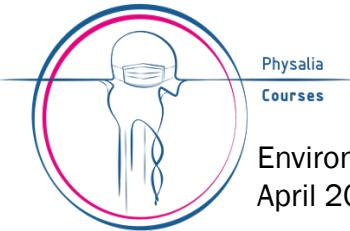


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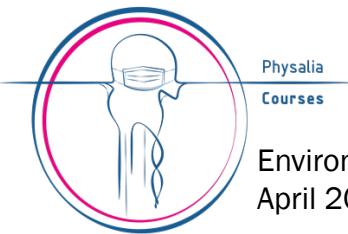
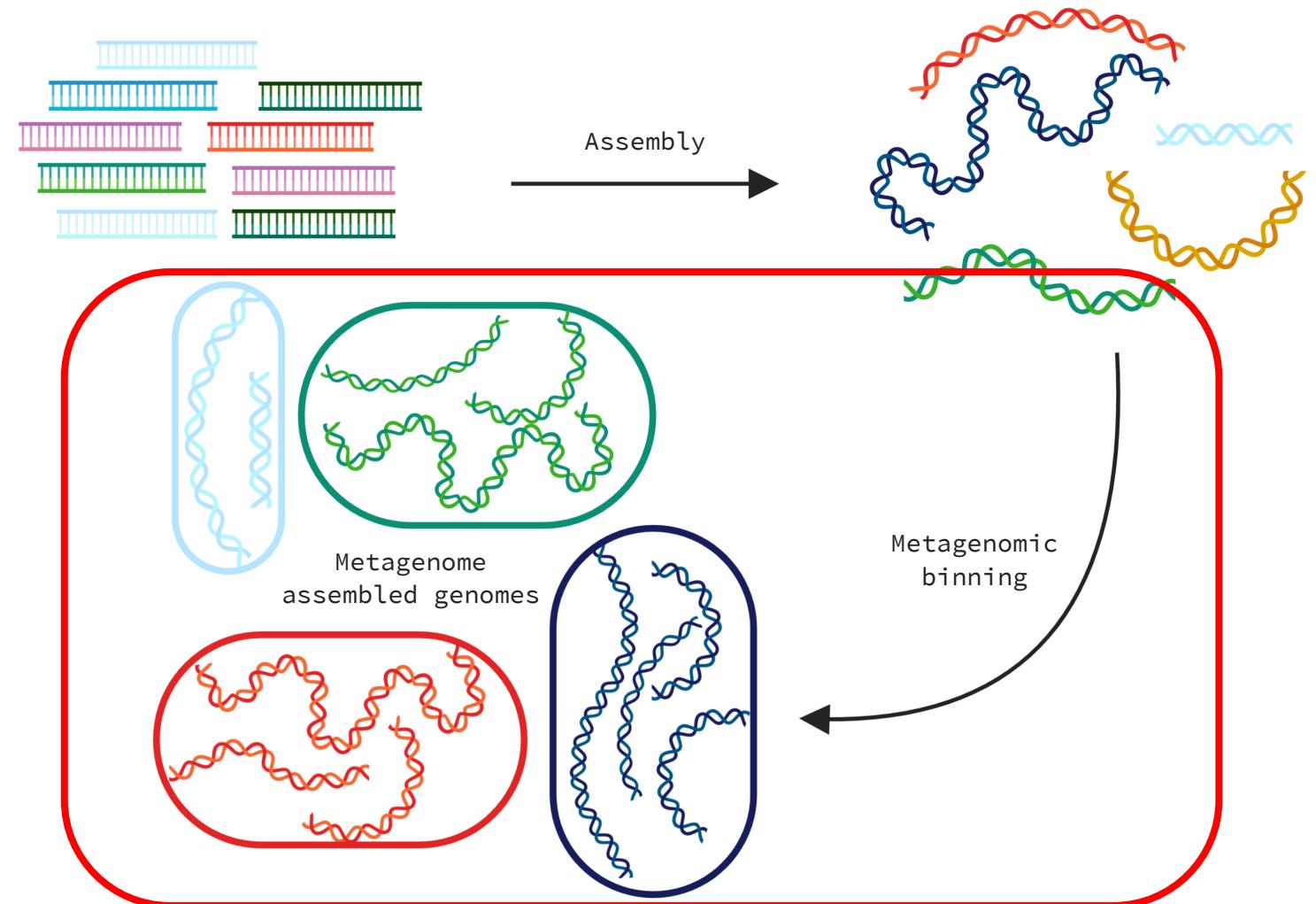
Genome-resolved metagenomics



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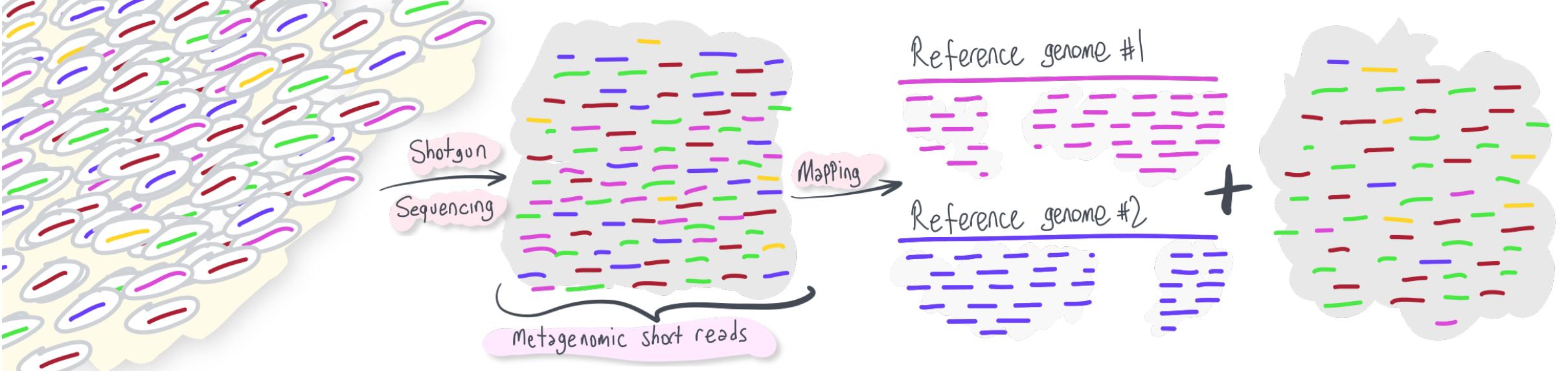
What is genome-resolved metagenomics?



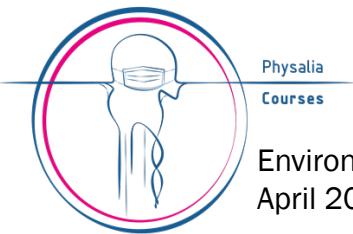
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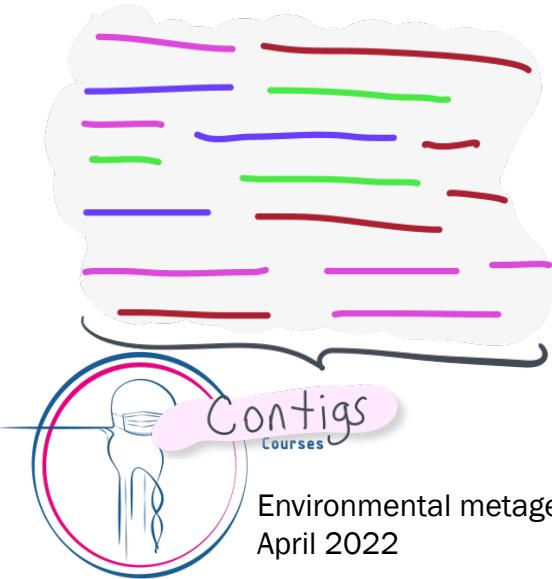
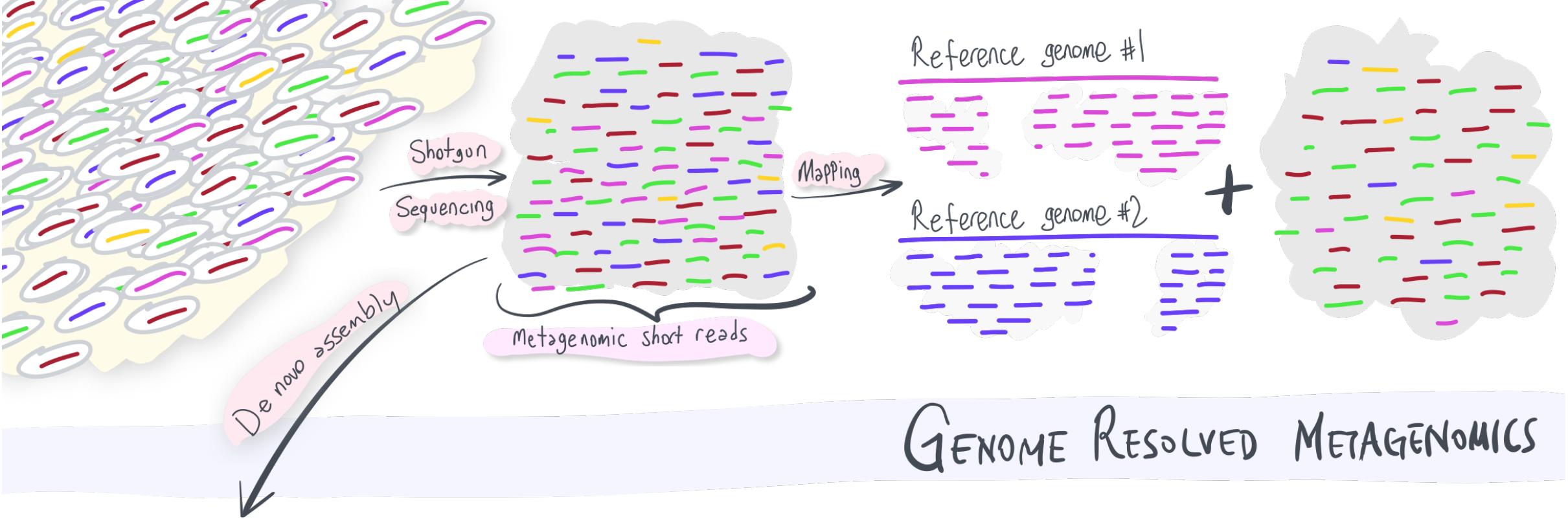
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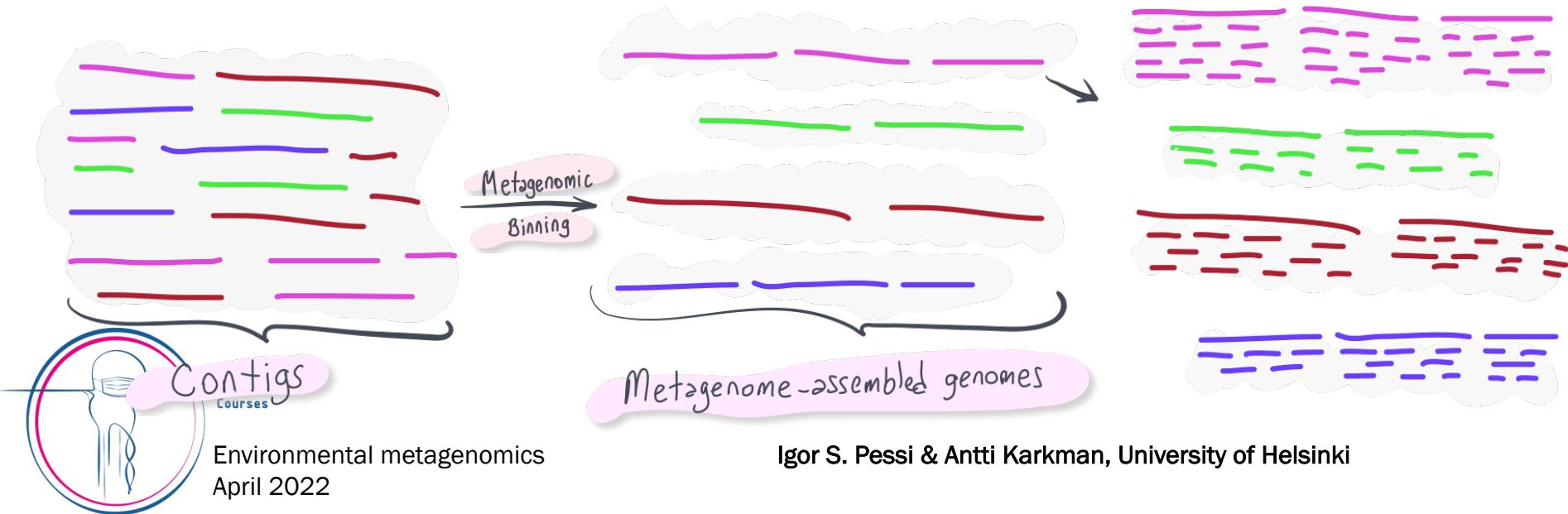
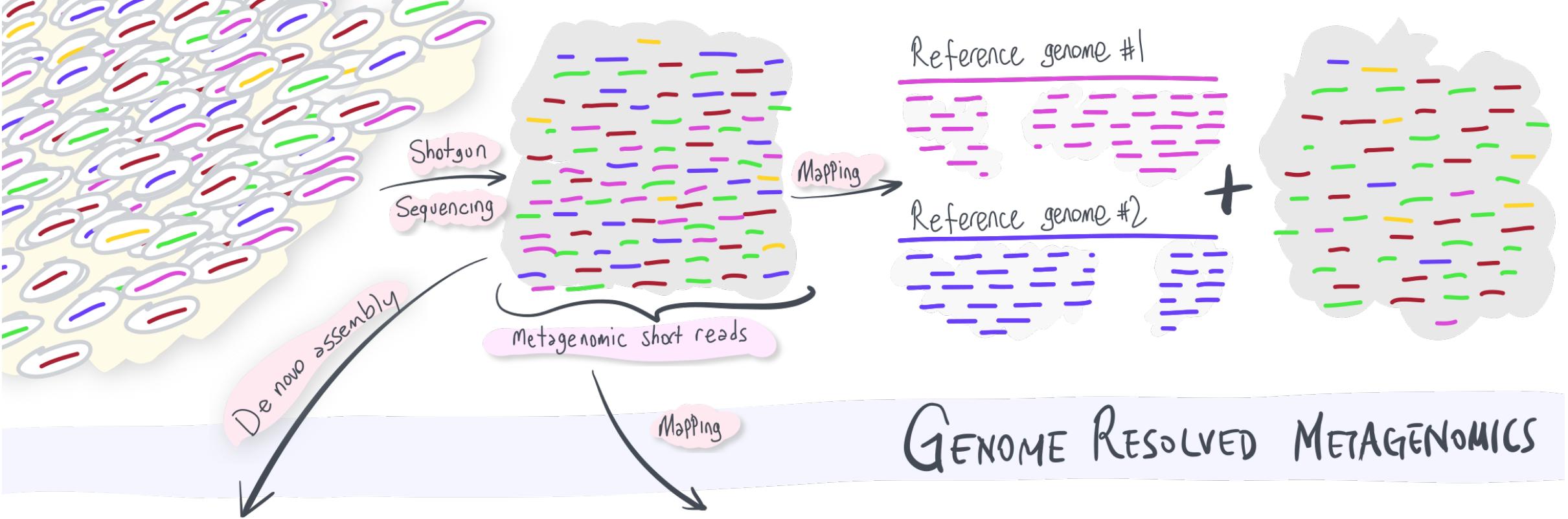
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GENOME RESOLVED METAGENOMICS

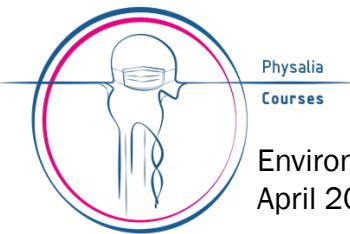
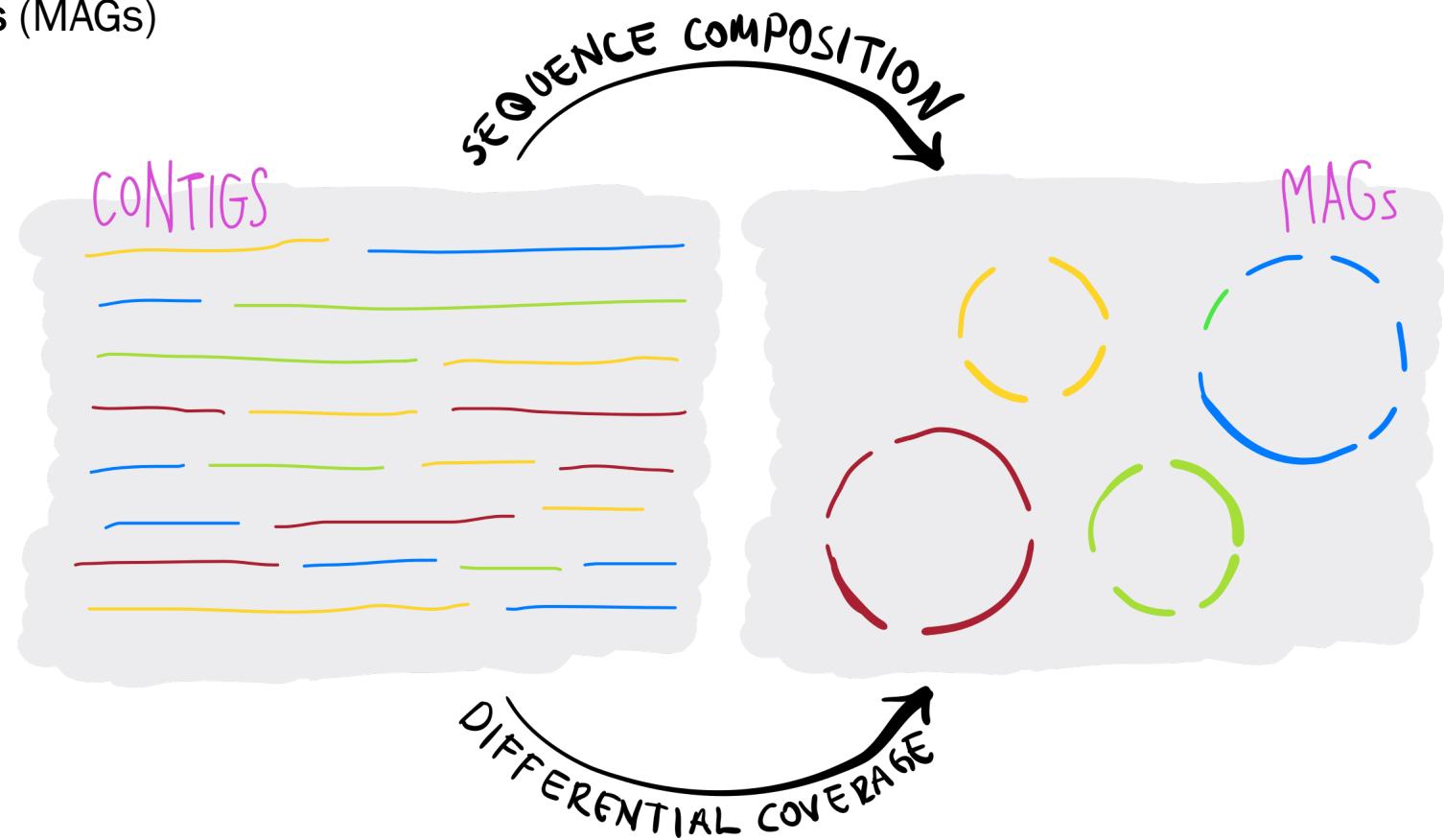




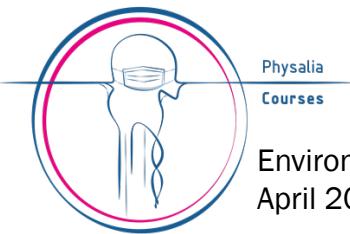
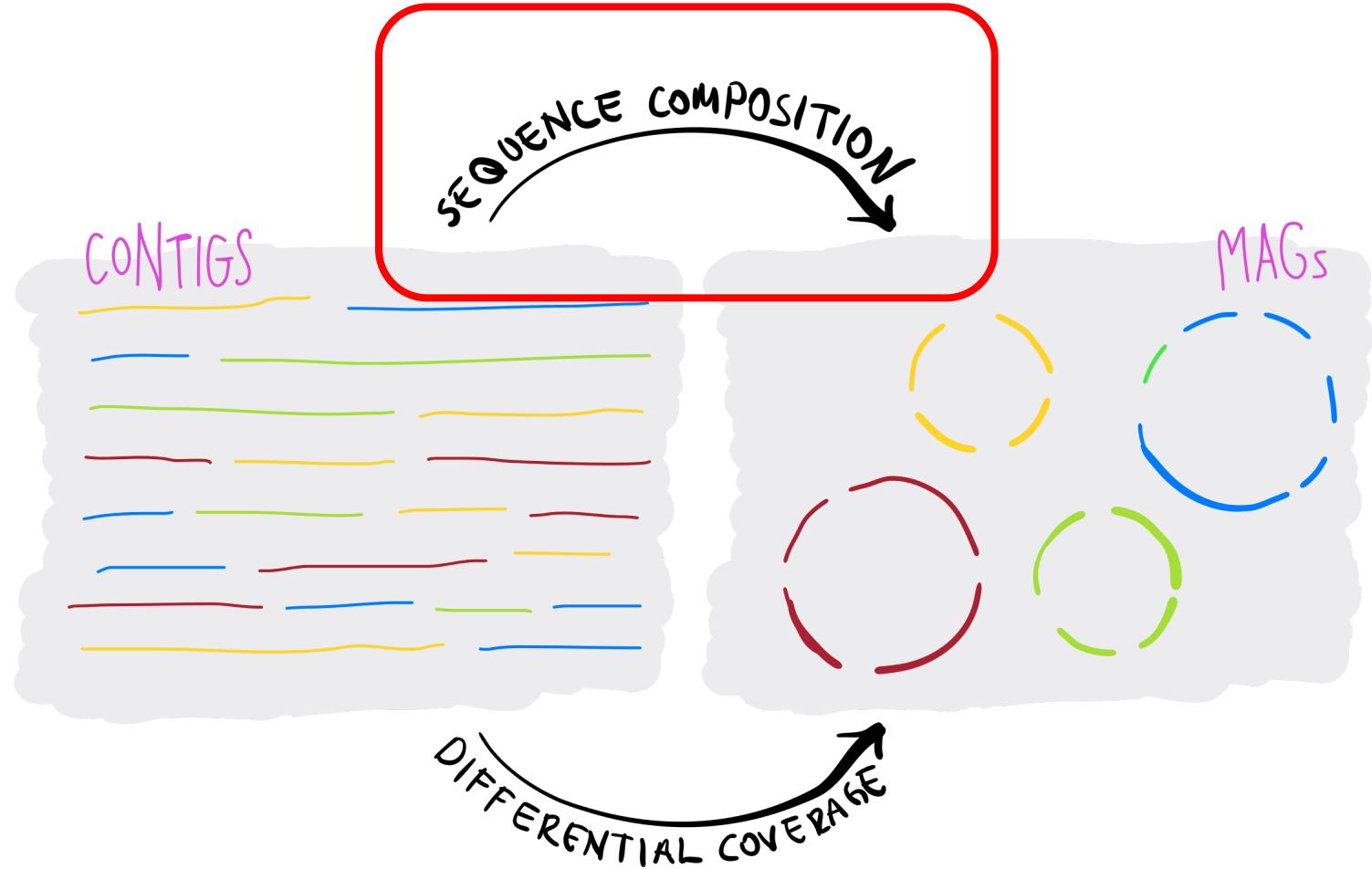


Metagenomic binning

From contigs to
metagenome assembled genomes (MAGs)



Sequence composition – kmers



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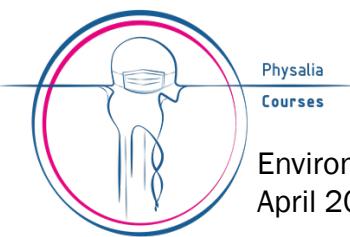
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<http://merenlab.org/momics>

GTTTGCGATGATTAAGGGAGTTCTTTGTGCTTC

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



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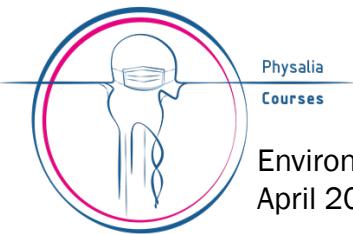
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TTGGCATGATTAAGGGAGTTCTTGTGCTTC

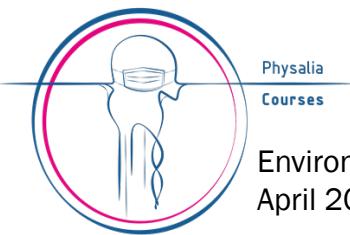
AA	AC	AG	AT	CA	CC	CG	CT	GA	GC	GG	GT	TA	TC	TG	TT
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k=2





k=2



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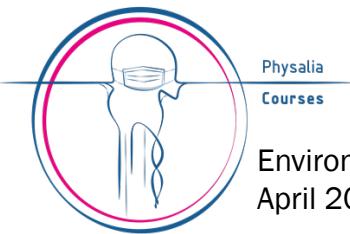
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k=2



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GTTTGCGATGATTAAGGGAGTTCTTGTGCTTC

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

k=2



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GTTTGCGCATGATTAAGGGAGTTCTTGTGCTTC

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	5	0	1	2	1	1

k=2



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13

GTTTGGCATGATTAAGGGAGTTCTTGTGCTTC

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

GAAGCACAAAAGAAAACCTCCTTAATCATGCCAAAAAC

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	5	0	1	2	1	1

GTTTGGCATGATTAAGGGAGTTCTTGTGCTTC
GAAGCACAAAAGAAAACCTCCTTAATCATGCCAAAAAC

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

k=2



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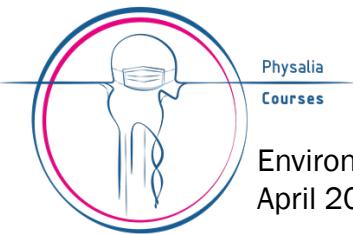
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14

GTTTGCGCATGATTAAGGGAGTTCTTTGTGCTTC

	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



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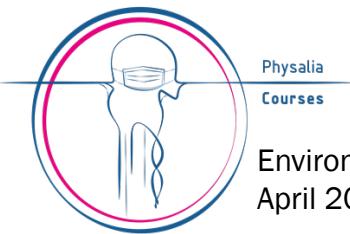
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15

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



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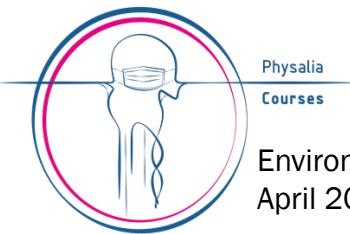
<http://merenlab.org/momics>

16

AC TTGCGCAGTCGCGCATTACGCGTAGTGGAAATAA

	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



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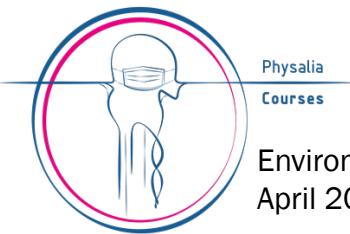
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	AA	AC	AG	GA	CA	CC	CG	GC	AT	TA
X	11	3	4	4	5	2	0	2	2	1
Y	4	5	2	4	5	4	4	3	2	1
Z	4	5	3	2	4	1	5	5	2	3
L	11	6	3	2	2	3	2	1	1	4
K	1	1	2	2	1	8	9	10	0	0
M	0	4	4	3	4	10	4	5	0	0

k=2



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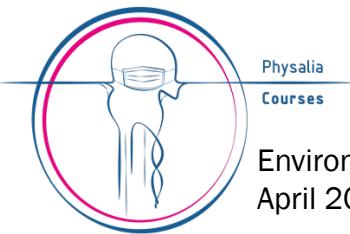
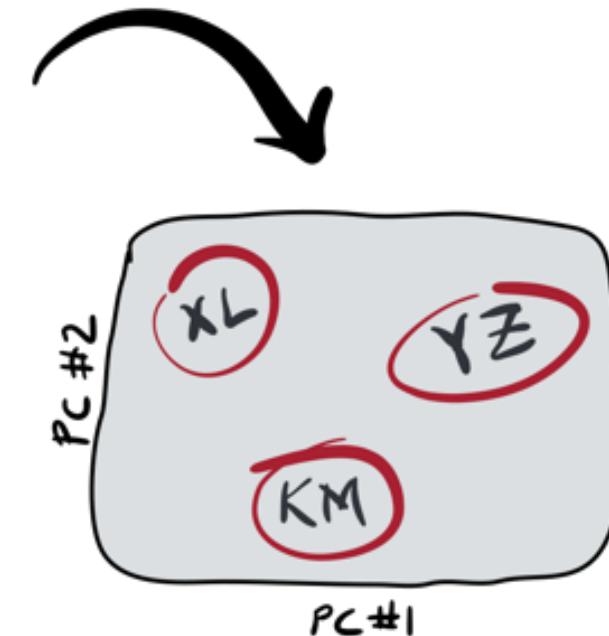
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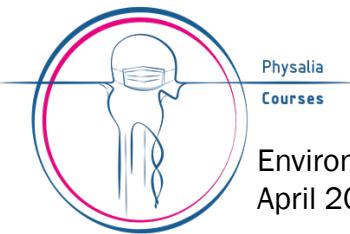
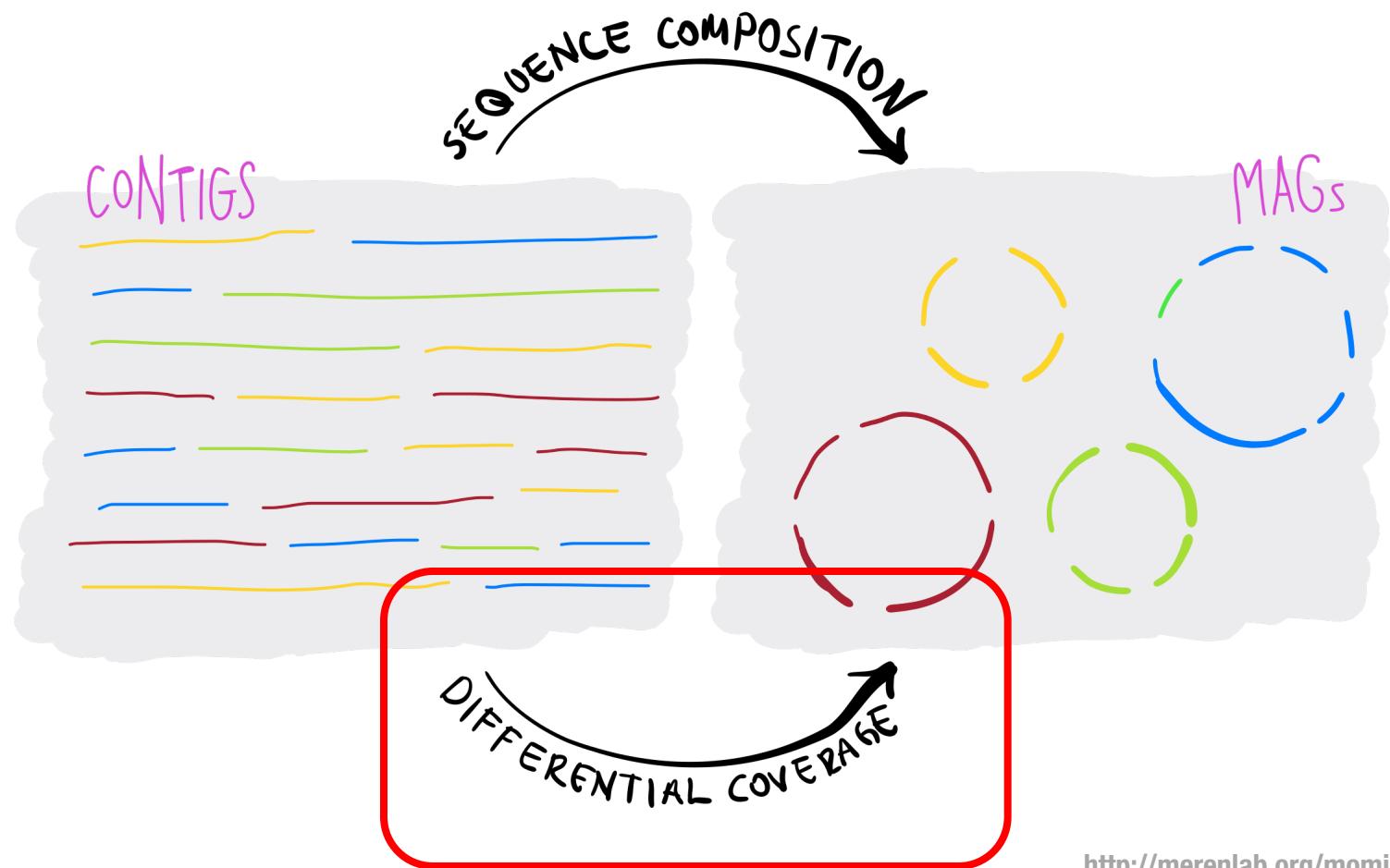
18

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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



Differential coverage



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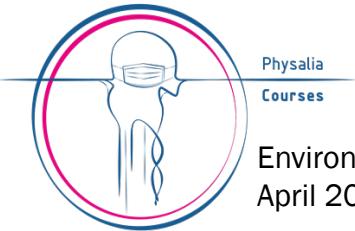
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CONTIG #1

CONTIG #2



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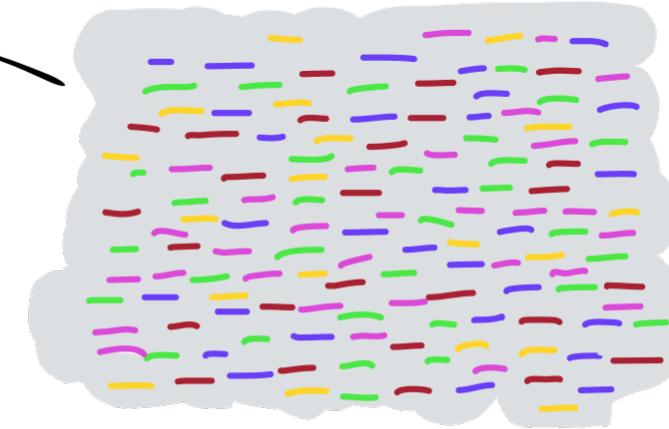
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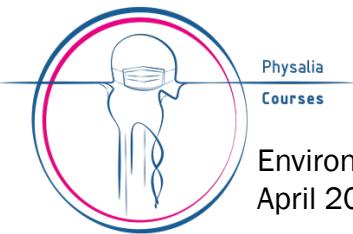
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CONTIG #1



METAGENOMIC READS

CONTIG #2



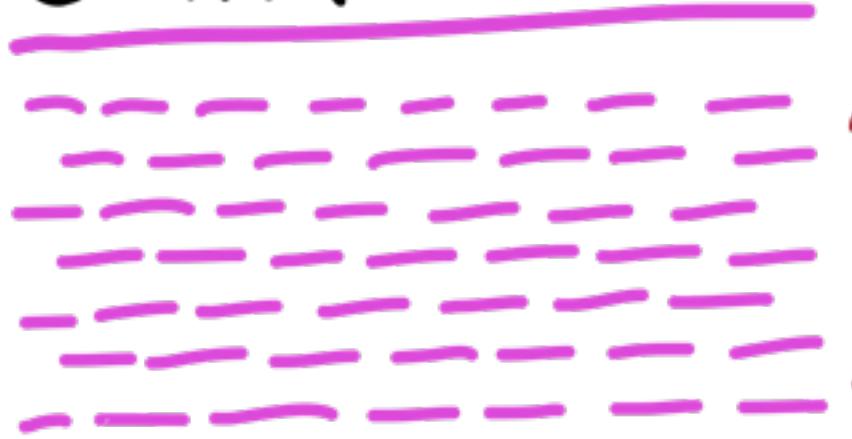
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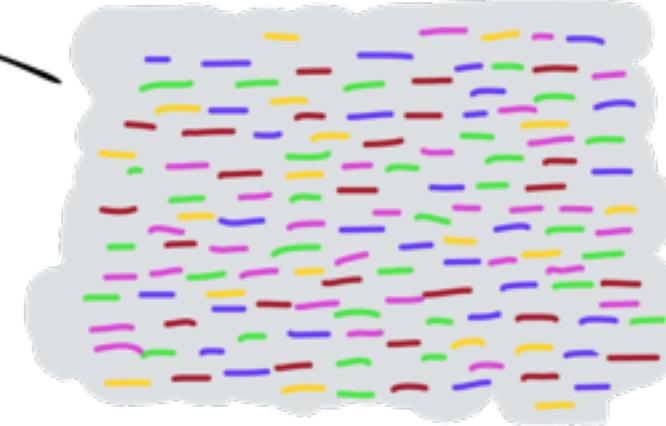
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<http://merenlab.org/momics>

CONTIG #1



MAPPING



METAGENOMIC READS

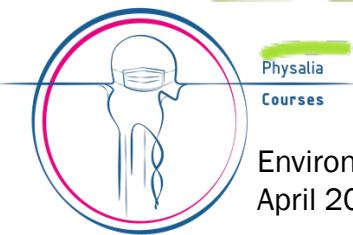
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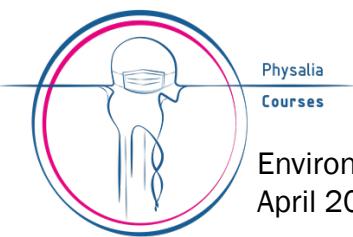
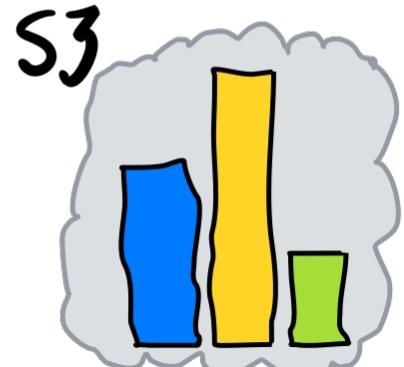
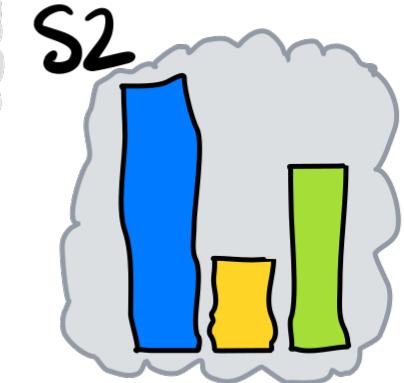
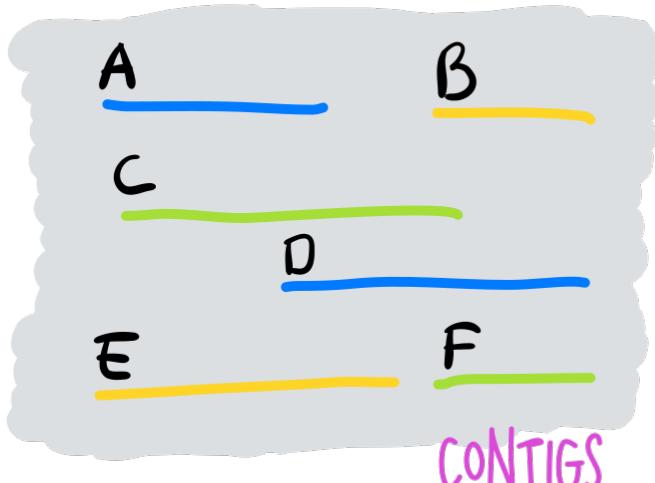
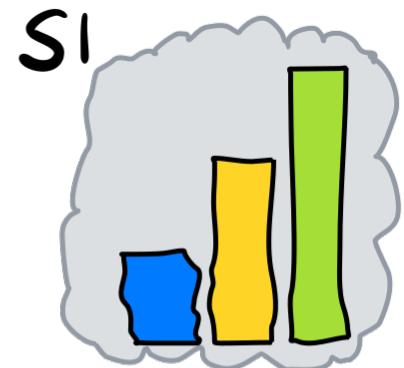


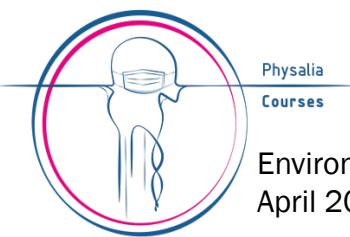
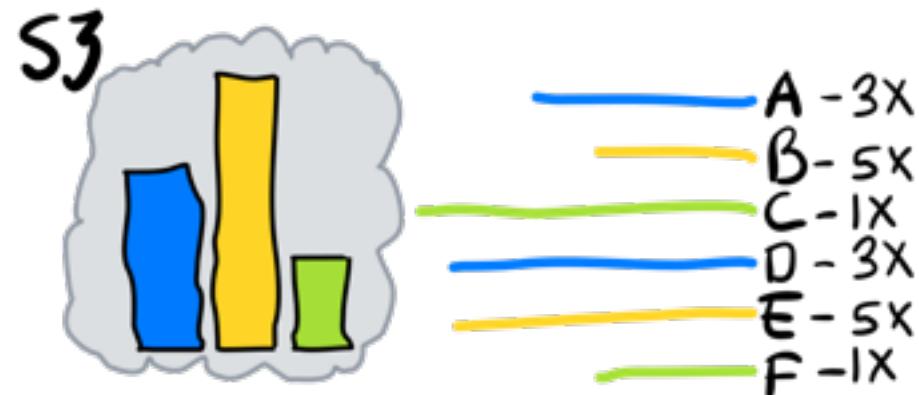
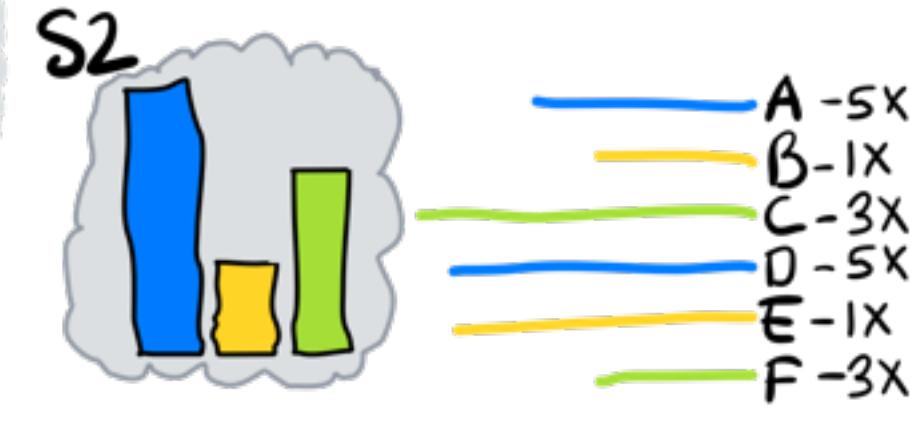
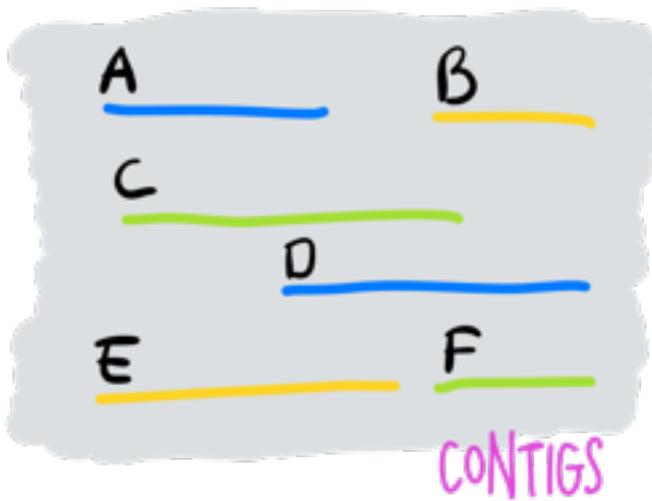
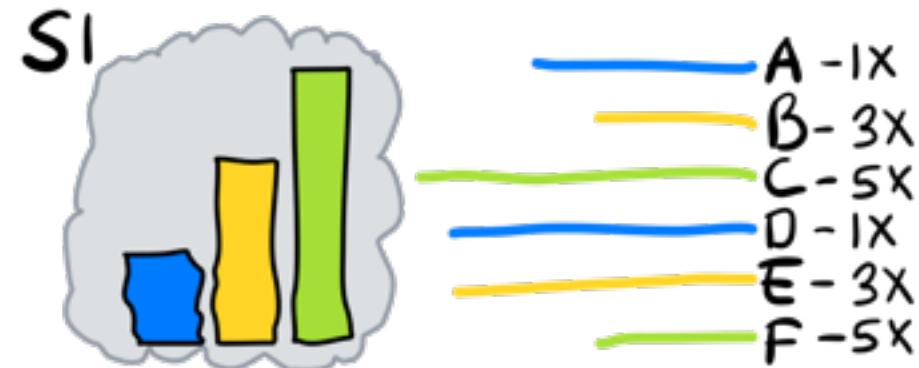
COVERAGE: ~7X

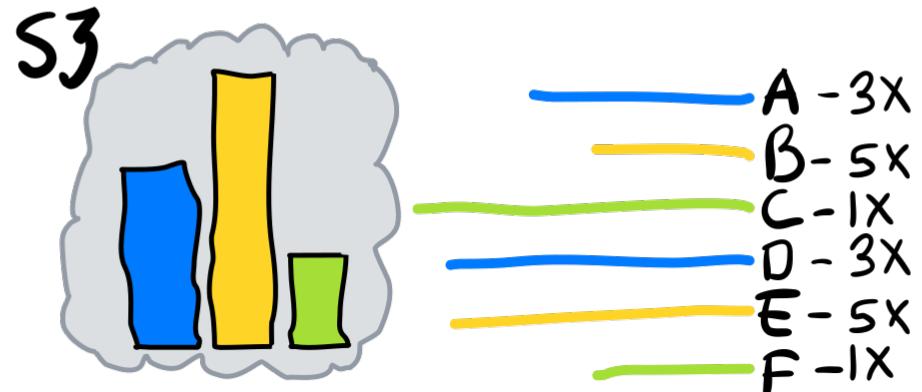
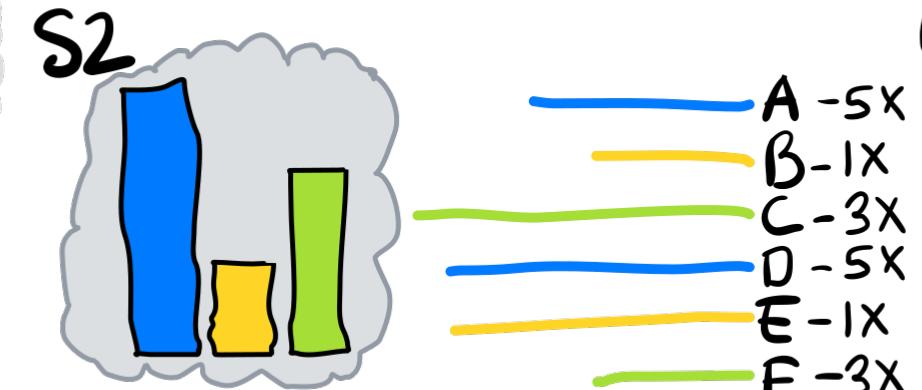
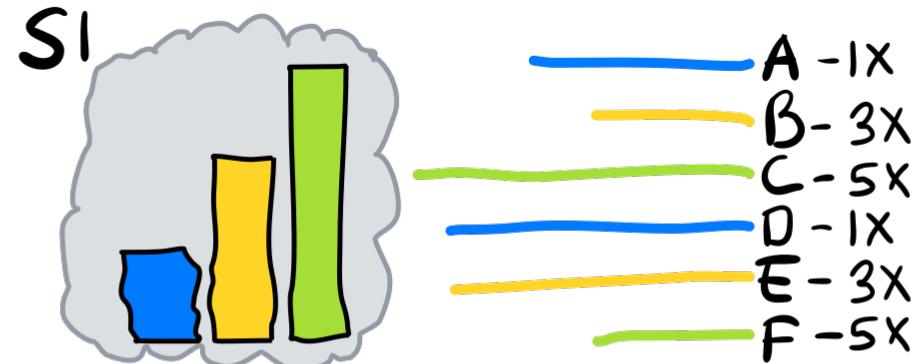
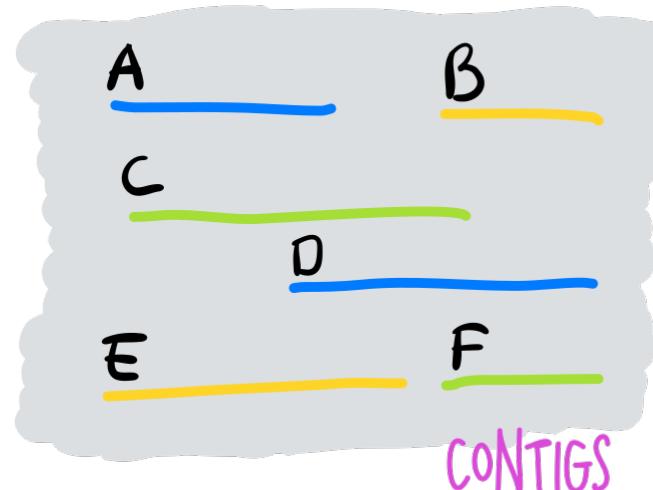
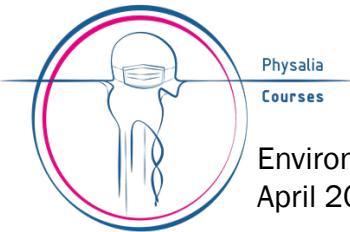


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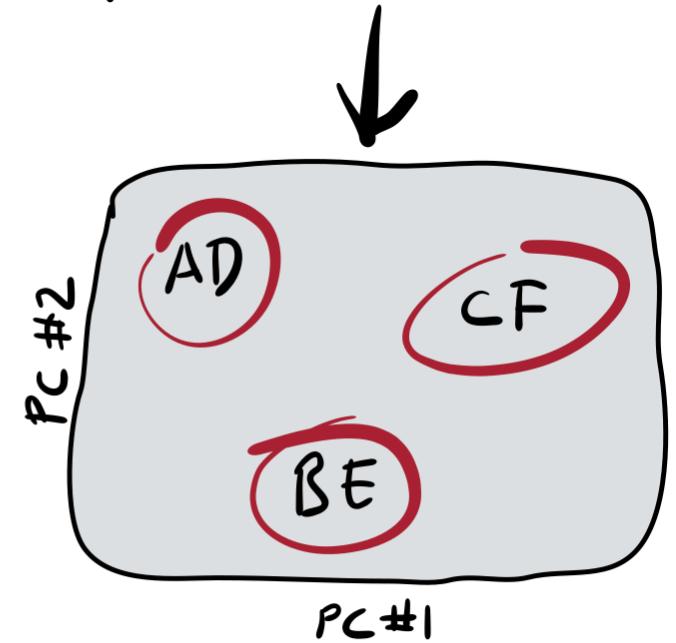




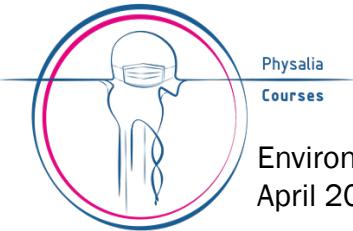




	A	B	C	D	E	F
S1	1	3	5	1	3	5
S2	5	1	3	5	1	3
S3	3	5	1	3	5	1



Genome-resolved metagenomics *in action*

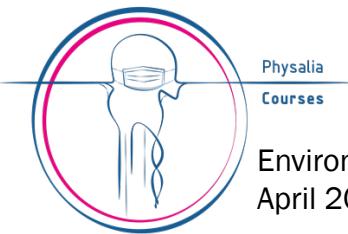


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Genome-resolved metagenomics *in action*

- Several automatic binning algorithms available
 - CONCOCT, MetaBat, MaxBin, BinSanity, Autometa, DAS Tool, ...
 - Various algorithms, but most rely on kmers and coverage
- Manual binning in anvi'o
 - Tetranucleotide frequency *and/or* differential coverage
 - Also, automatic binning results can be visualised

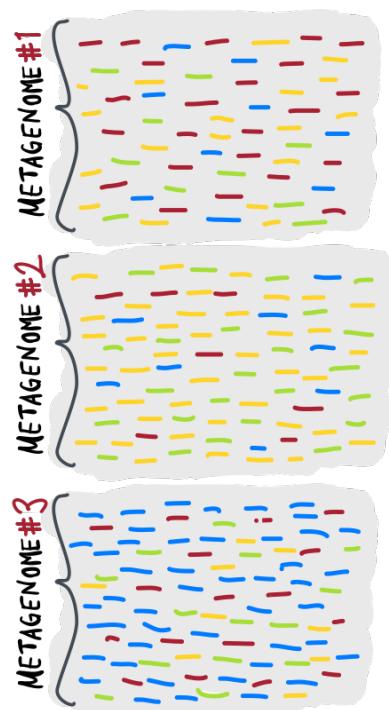
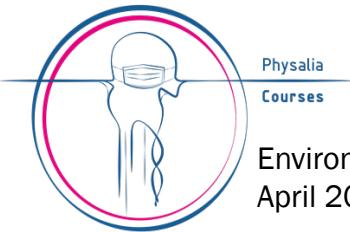


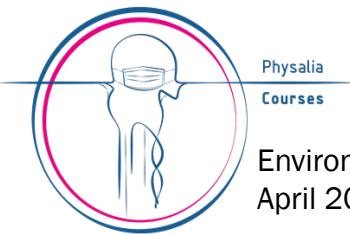
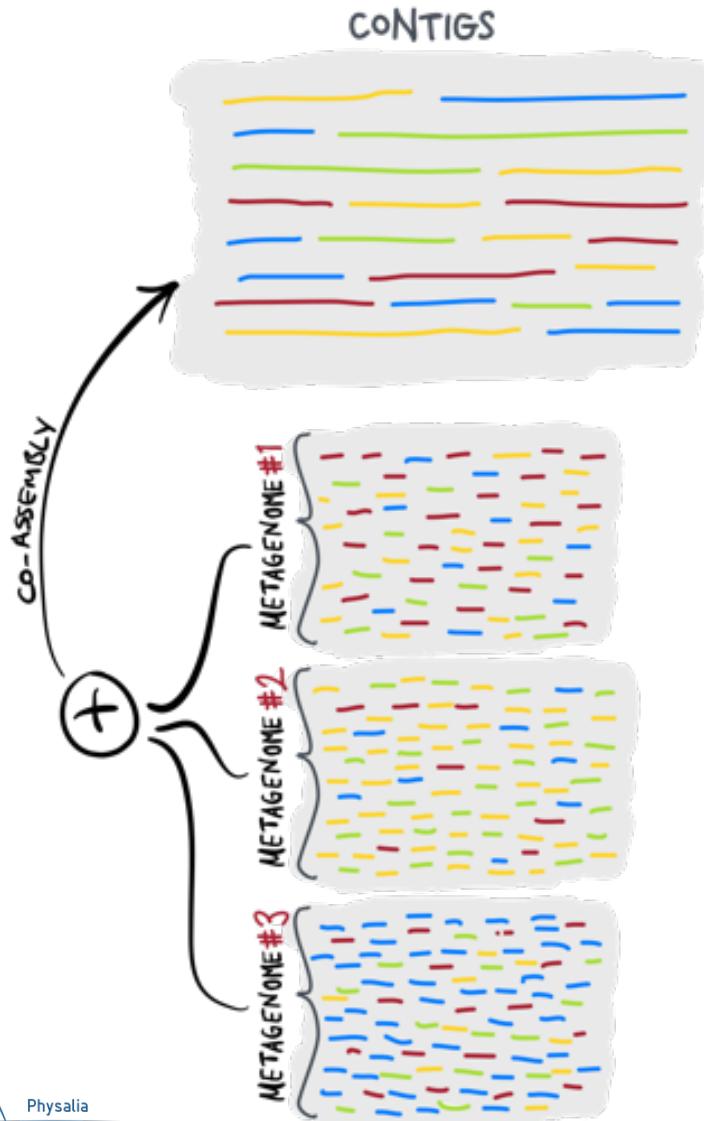
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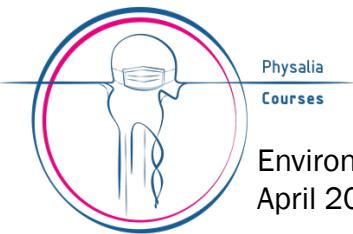
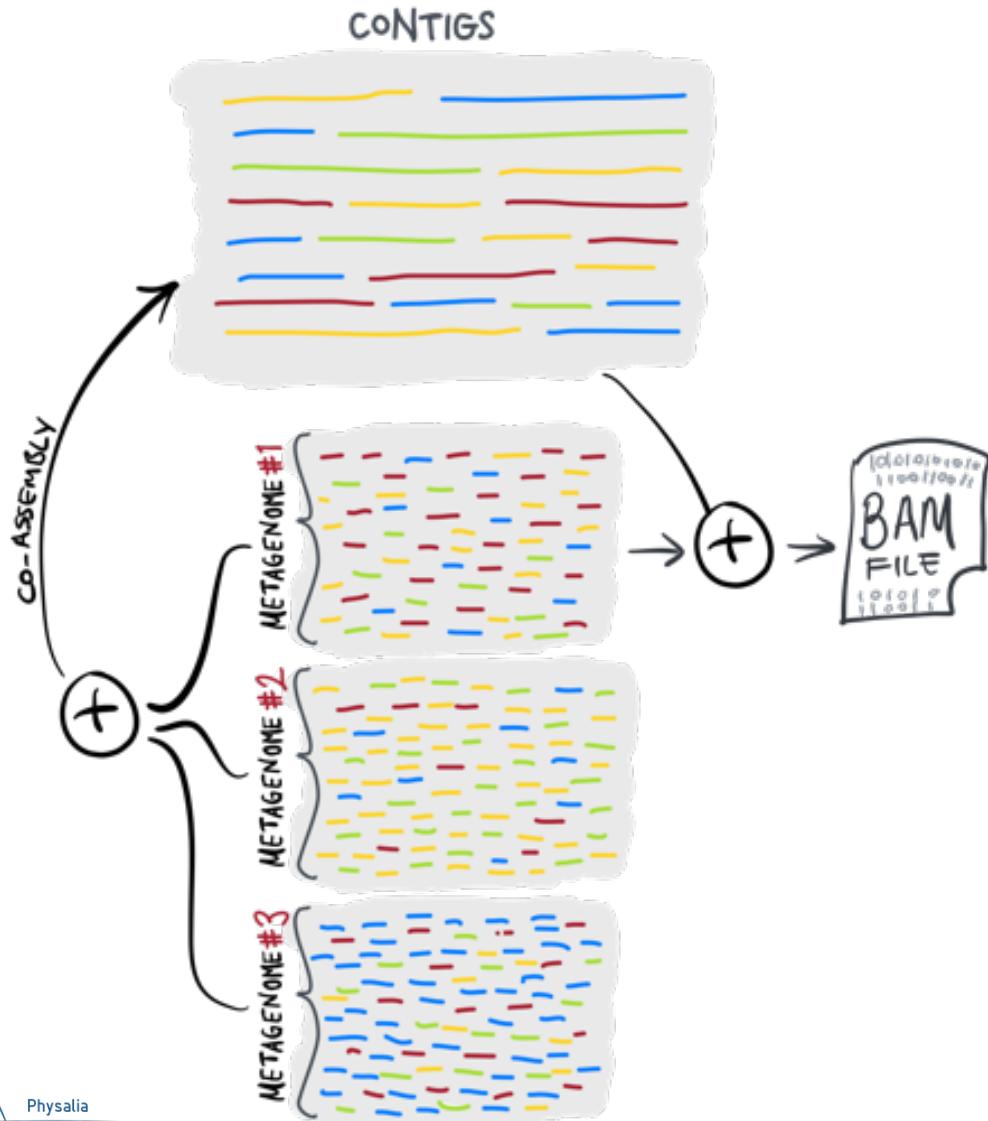
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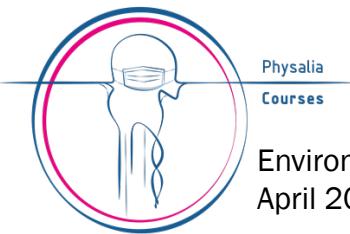
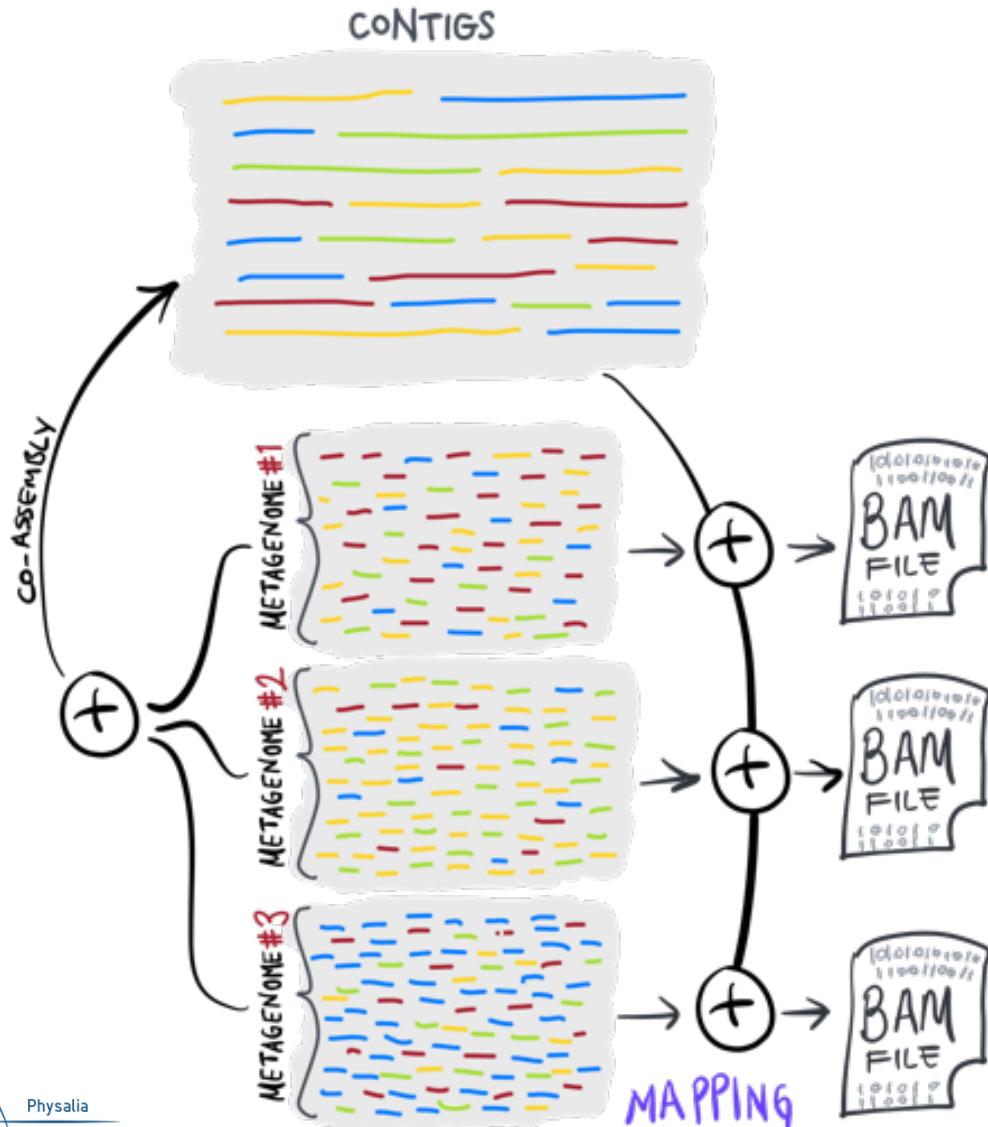
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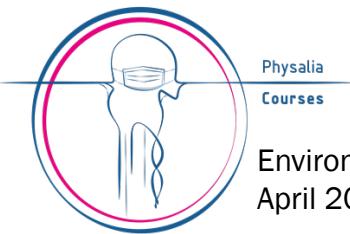
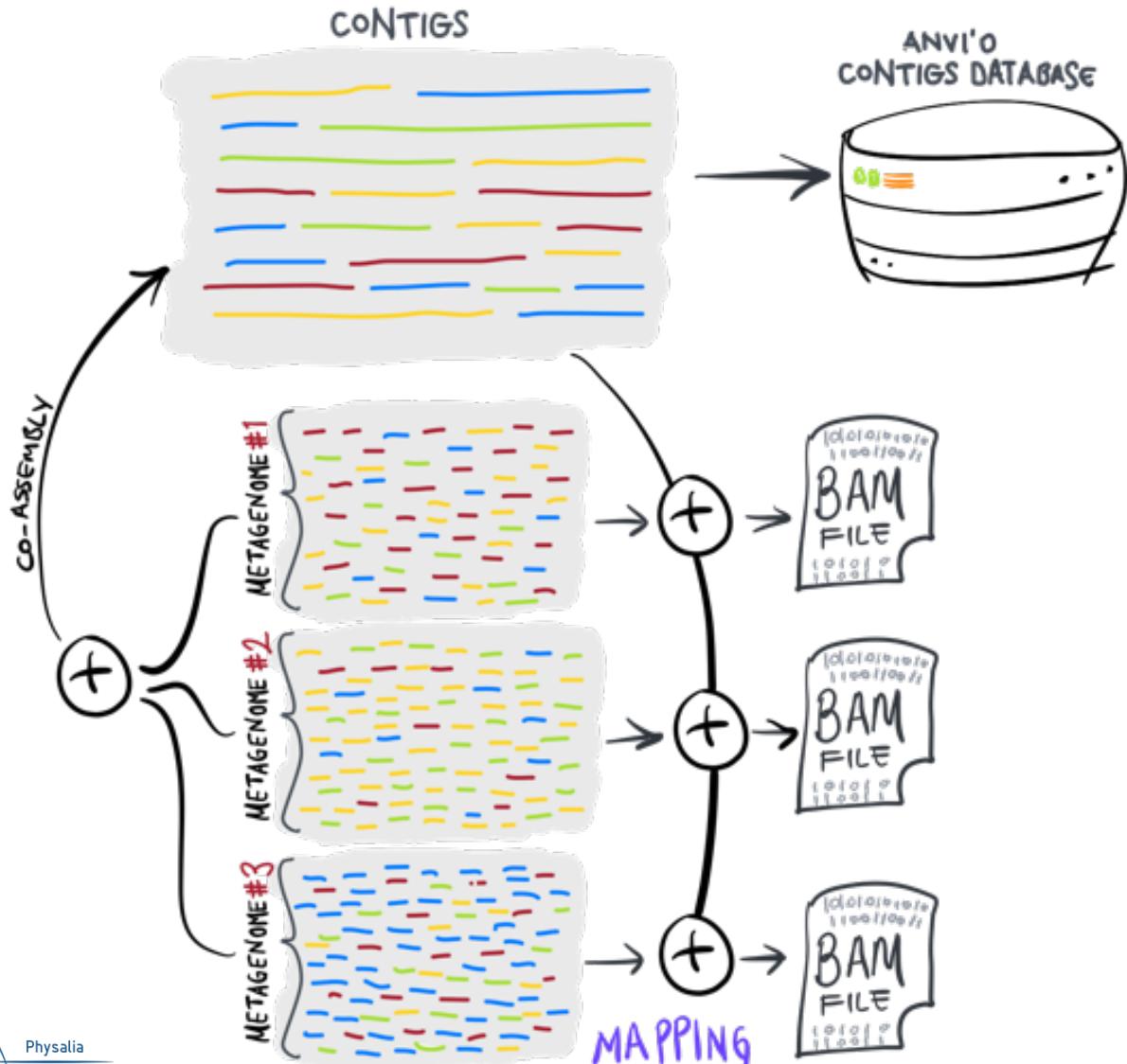
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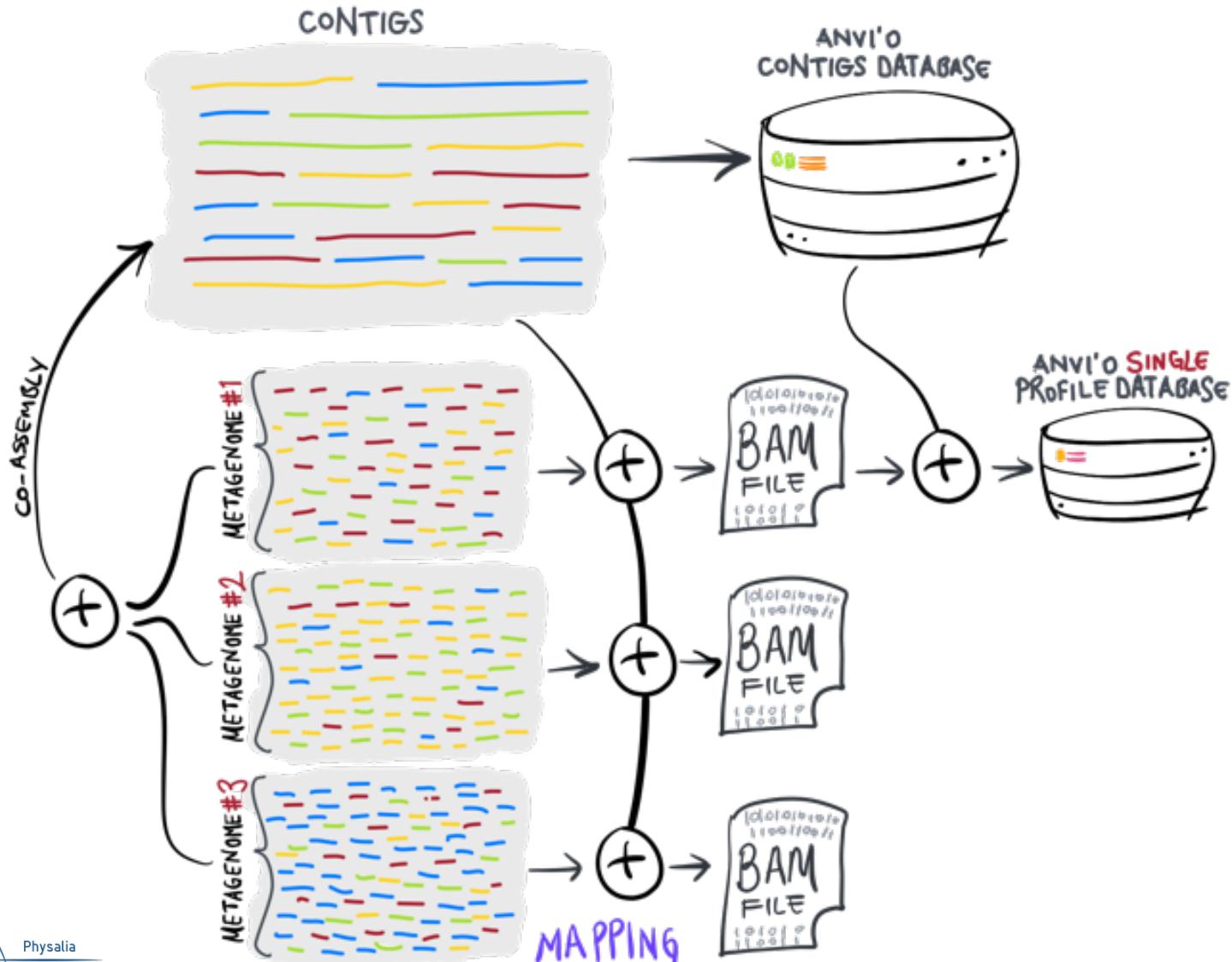


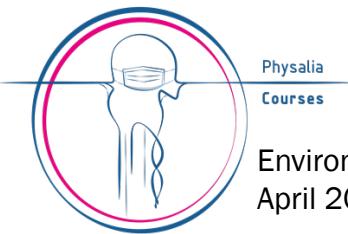
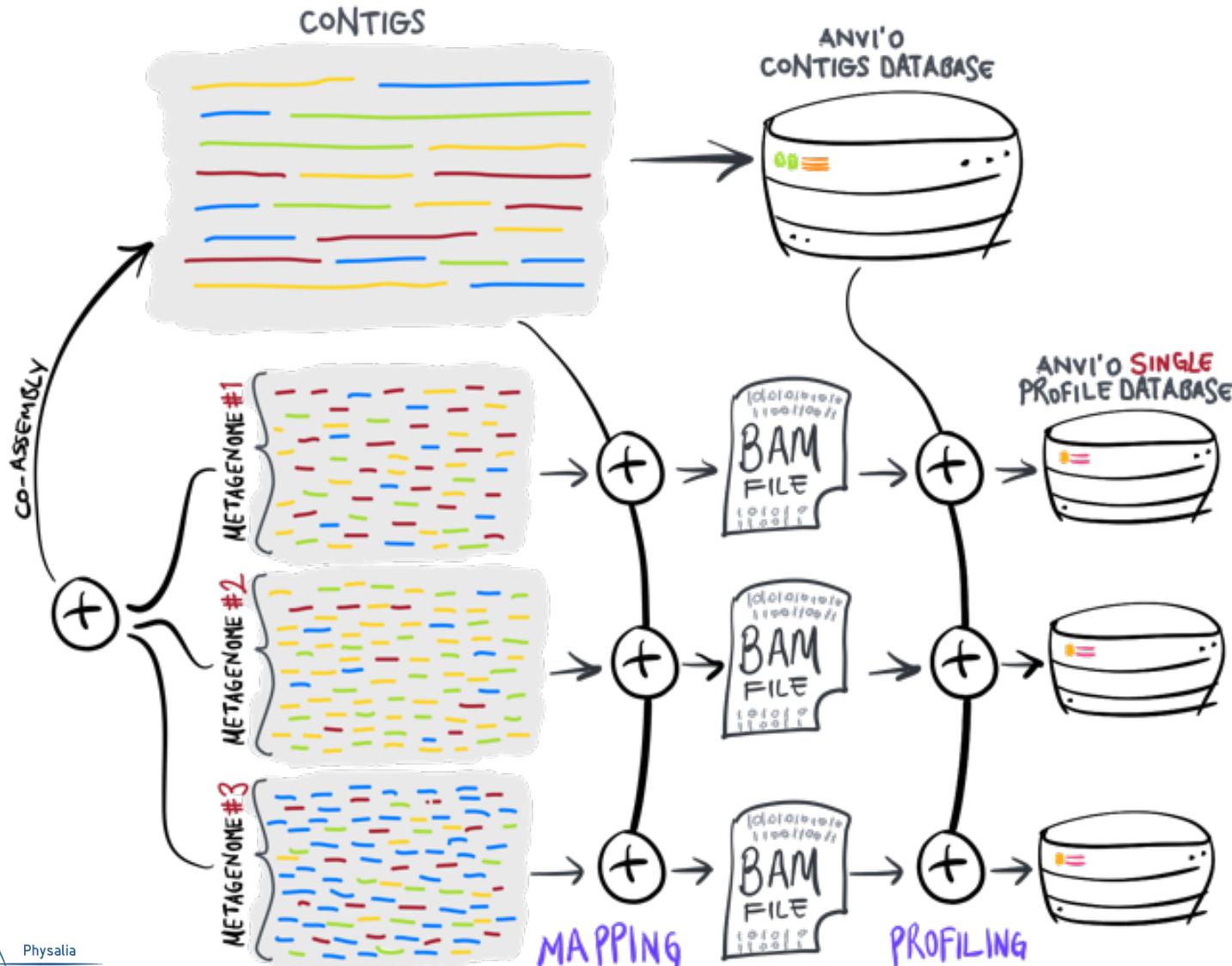


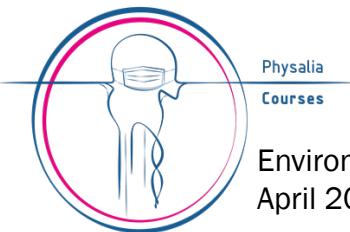
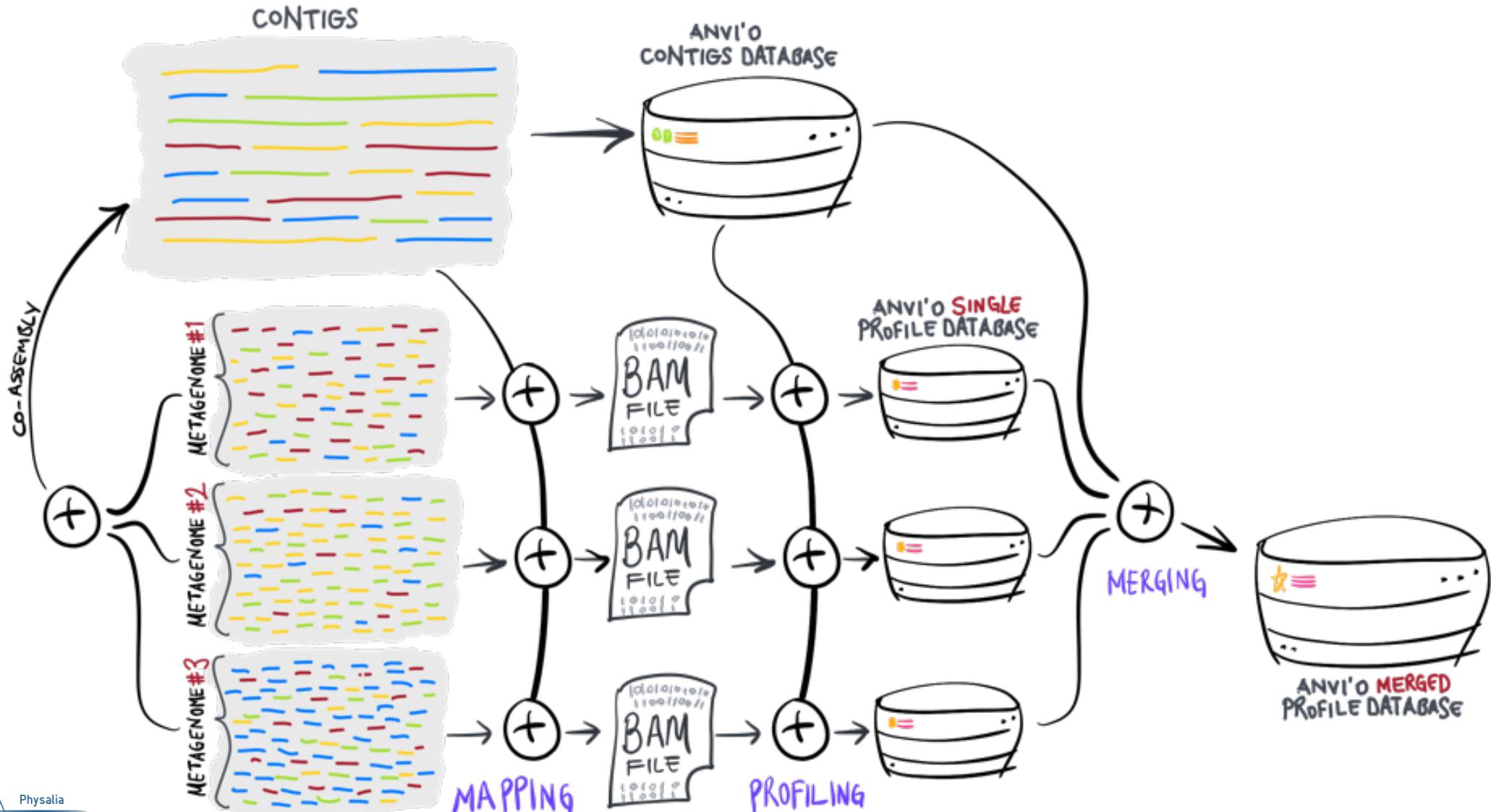


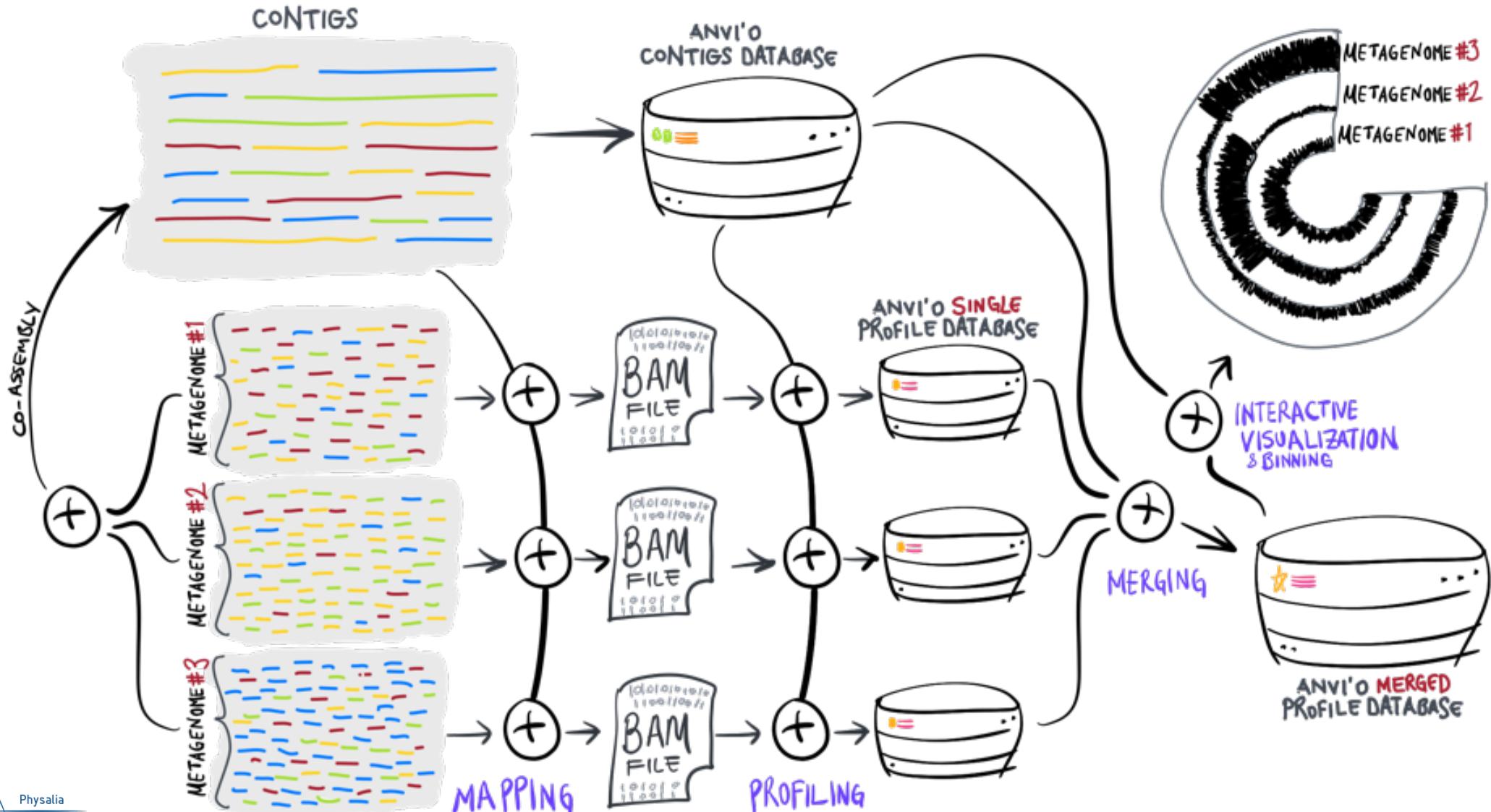


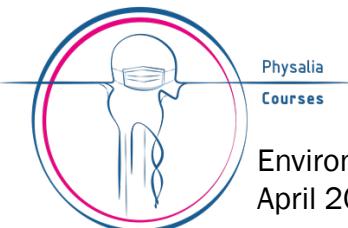
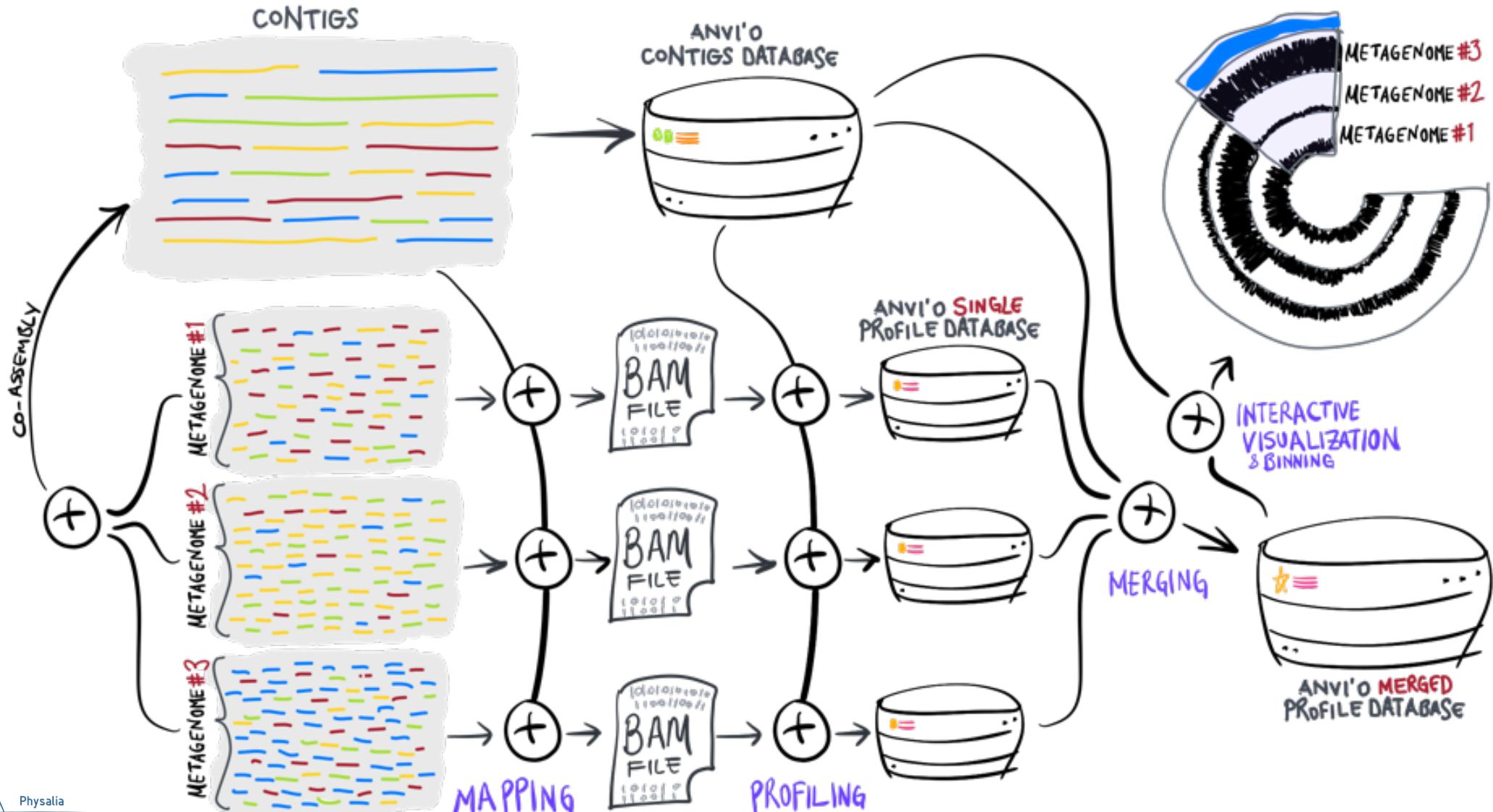


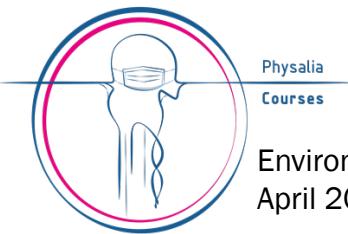
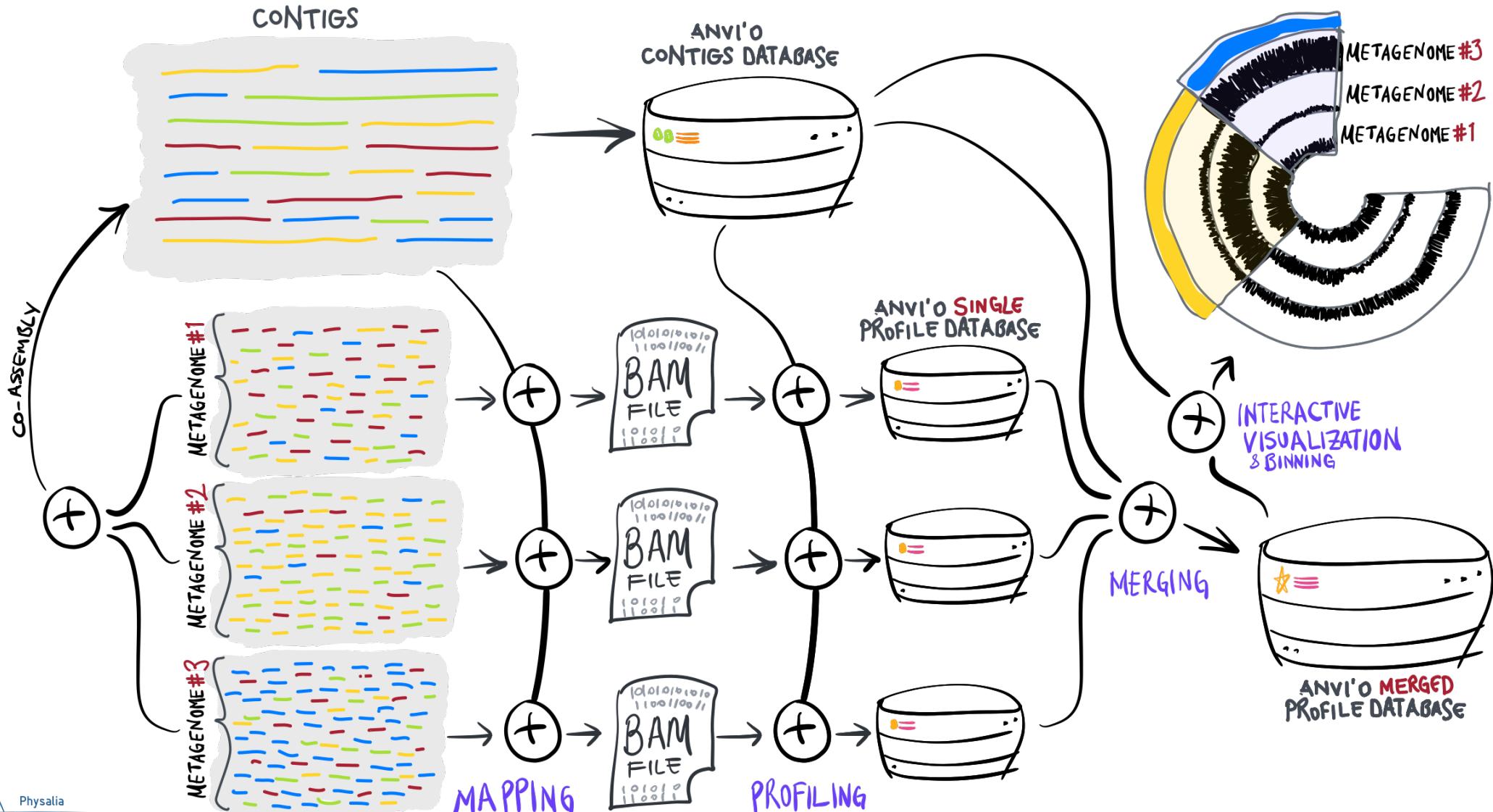


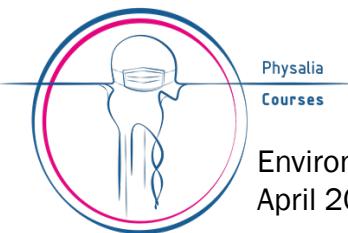
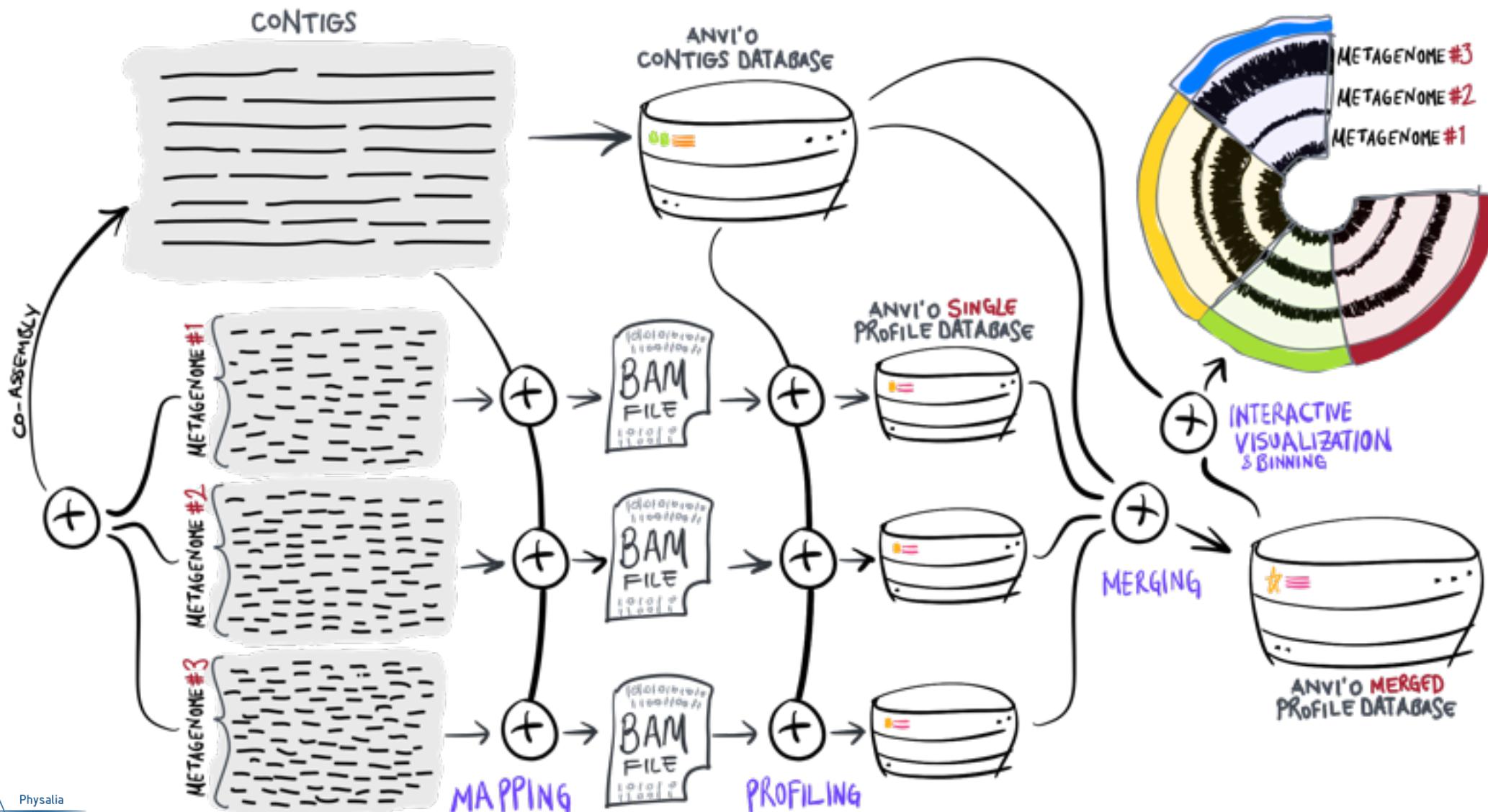




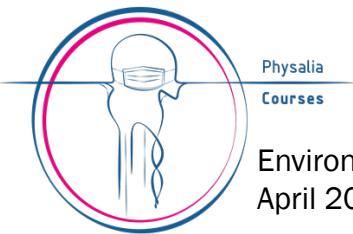
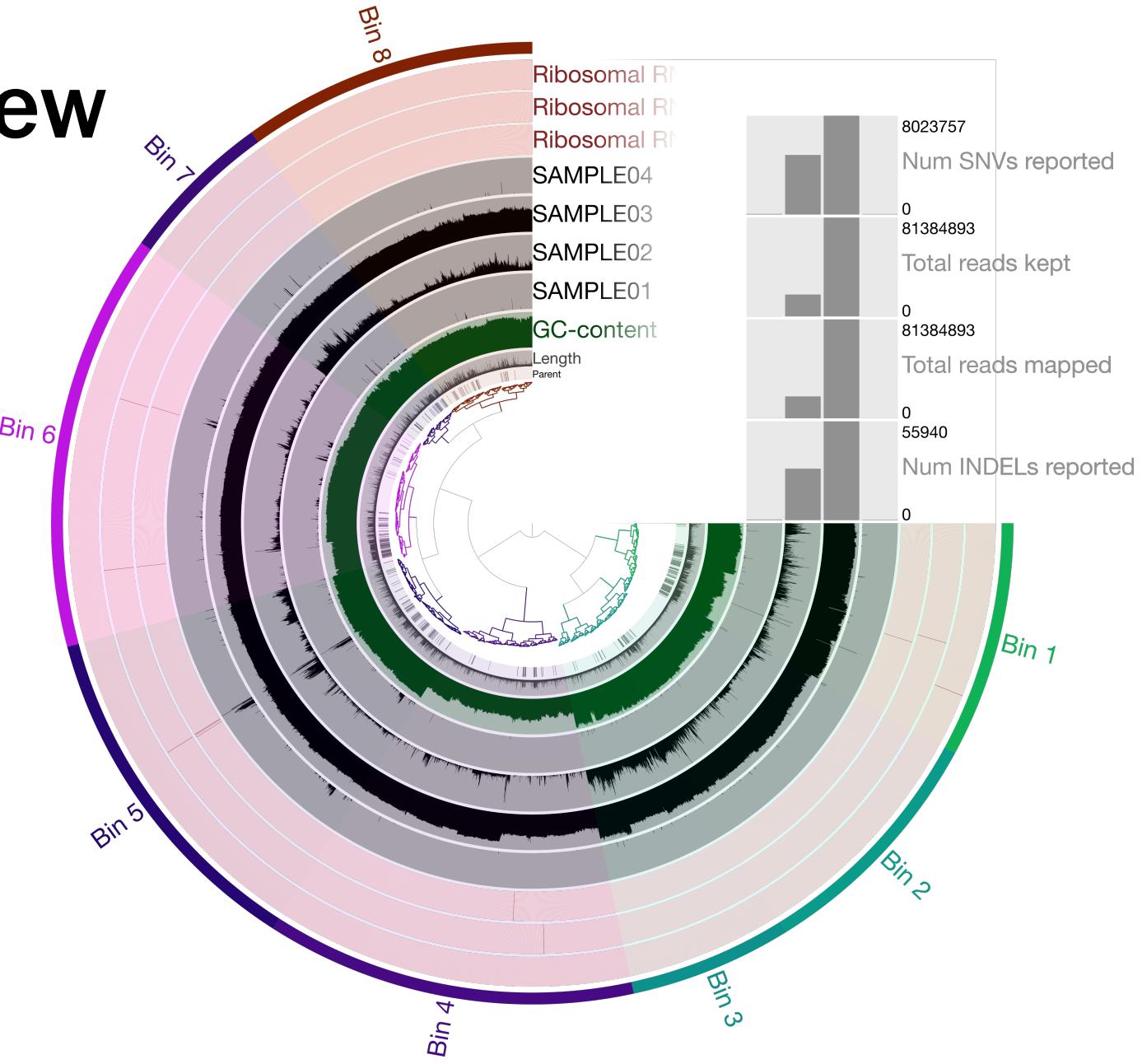








Anvi'o interactive view



Anvi'o interactive view

Four samples

Four assemblies

Four anvi'o projects

A lot of manual binning

