ENVIRONMENTAL METAGENOMICS

Physalia course, online, 11-15 November 2024

MAG binning

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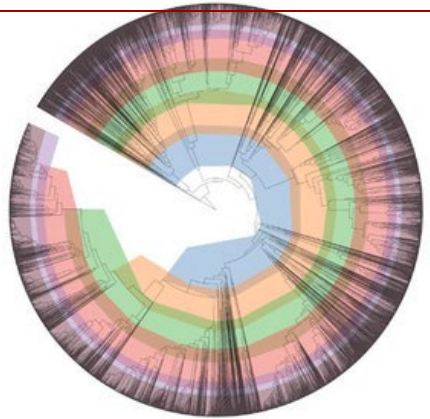

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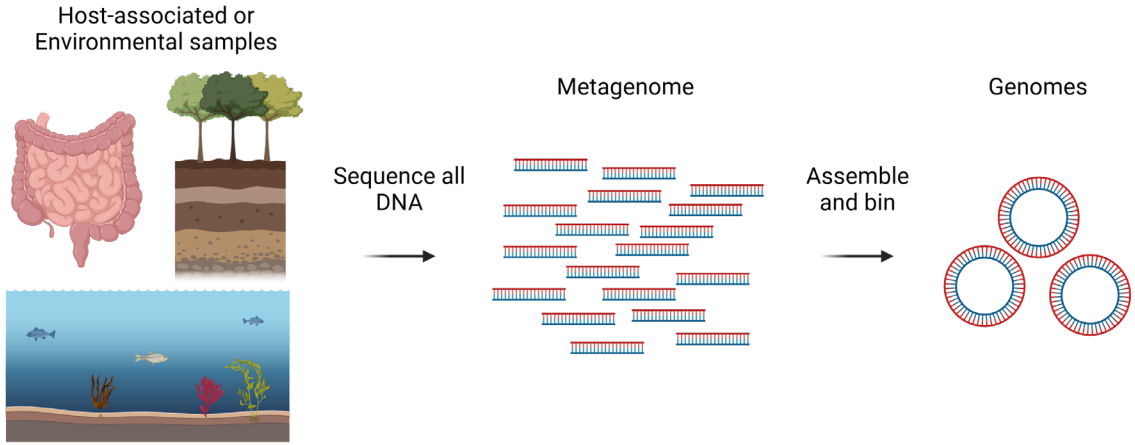
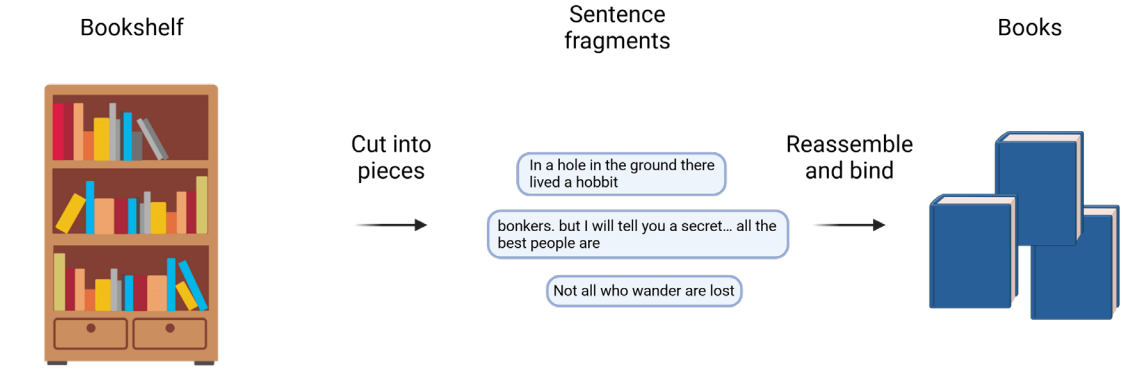
NB: original course material courtesy:
Dr. Antti Karkman, University of Helsinki
Dr. Igor Pessi, Finnish Environment Institute (SYKE)
As. Prof. Luis Pedro Coelho

Binning: collating contigs into collections





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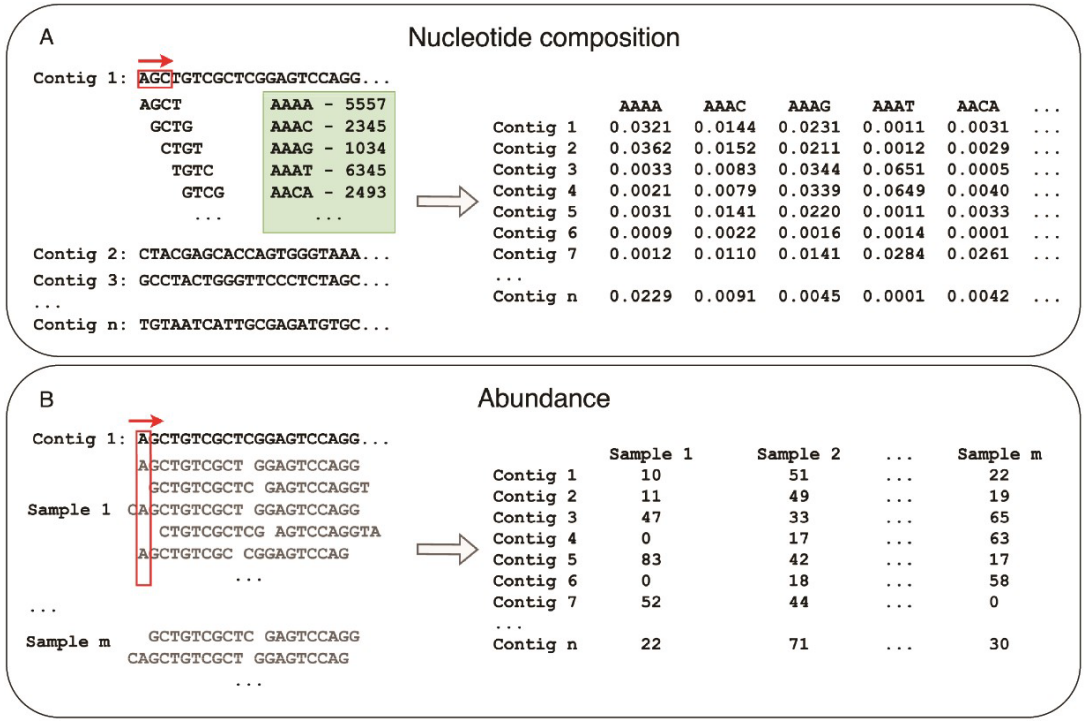
Standard binning strategies

- Nucleotide composition
  - Microbes tend to have similar %GC and codon choice across genome
- Abundance
  - The whole genome should be present at similar copy number



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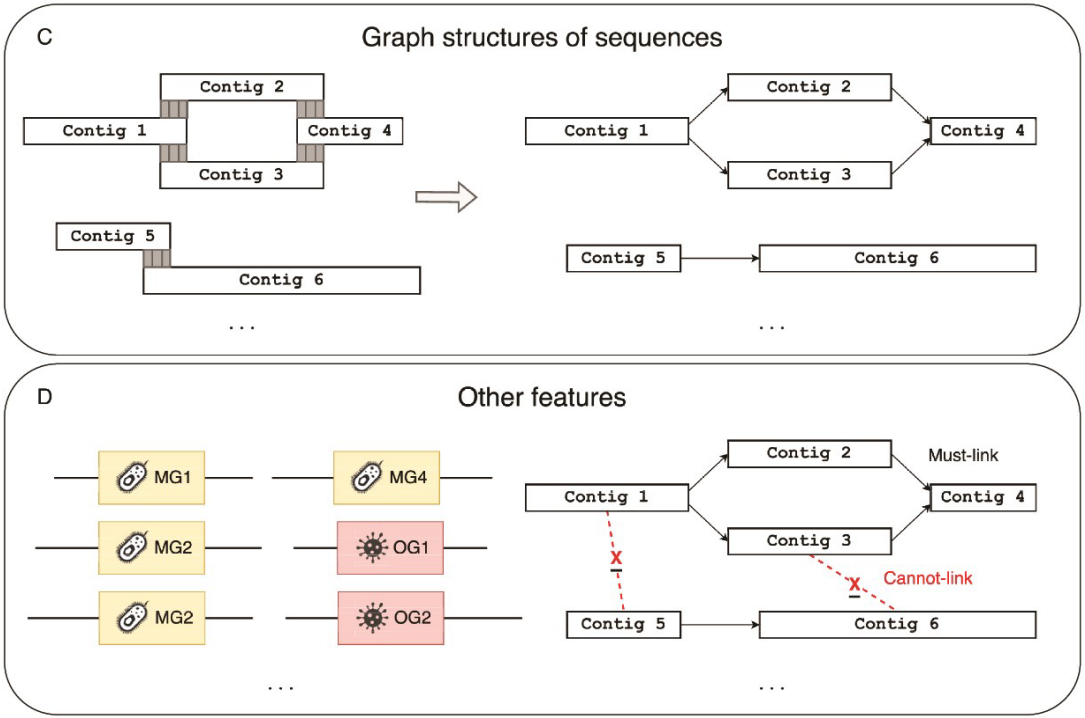
More binning strategies

- Graph structures
  - Assembly graph structures can be reused

- Other features
  - Methylation patterns
  - Single-copy marker genes
  - Machine learning inputs



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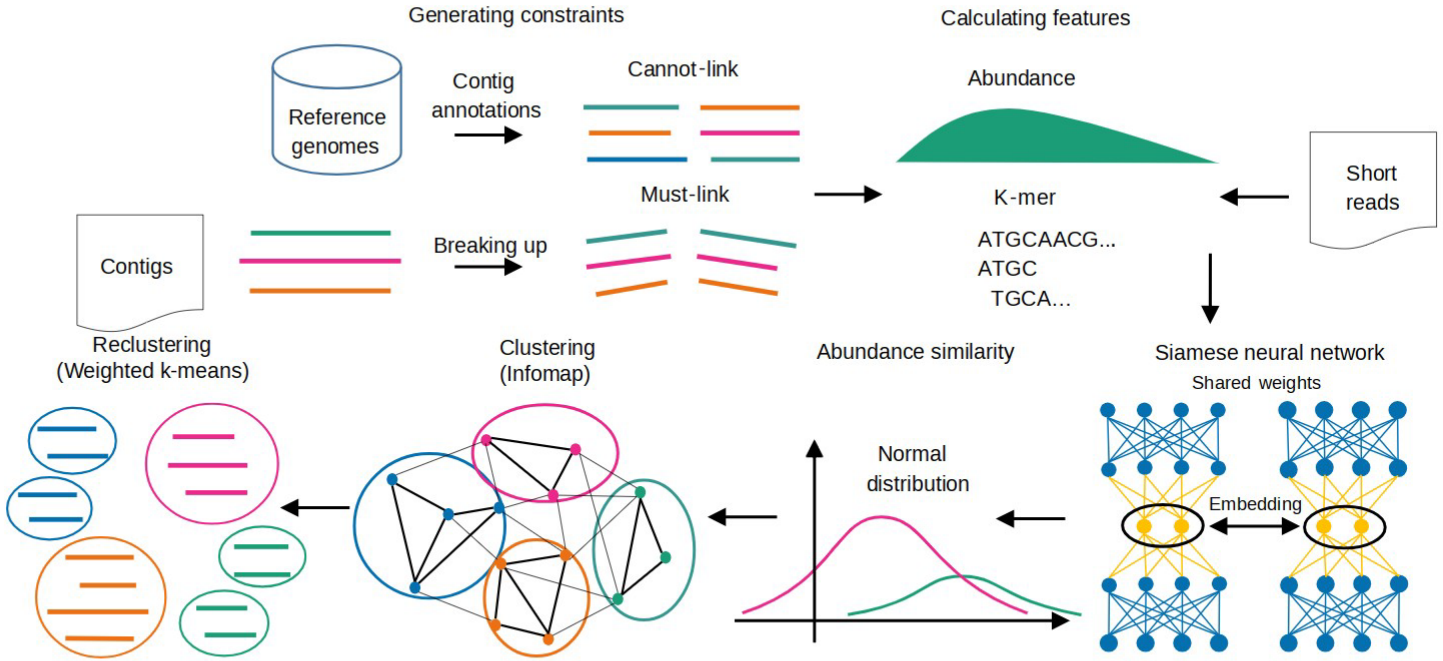
Semibin



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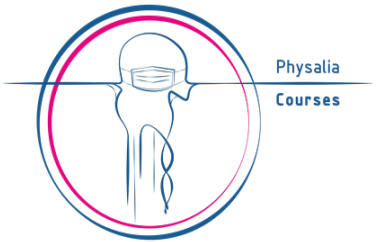
Learning a new model is resource intensive

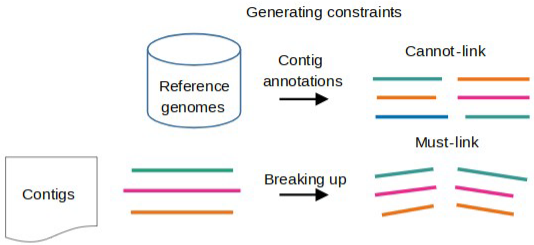
- SemiBin uses a learned model
- Generating the data for training is expensive (mmseqs2 is slow)
- Learning is slow (a GPU helps, but few people have a GPU cluster)

		Single-sample		
		Human gut	Dog gut	Ocean
Computing features	Time(min)	5	9	12
	Memory(MB)	923	736	1,675
Generating cannot-link	Time(min)	88	81	114
	Memory(MB)	39,070	37,904	46,091
Training(CPU)	Time(min)	181	209	222
	Memory(MB)	2,497	2,373	3,211
Training(GPU)	Time(min)	34	36	45
	Memory(MB)	4,487	4,355	5,222
Binning	Time(min)	2	2	3
	Memory(MB)	4,501	3,641	7,622



From Semi- to self-supervised learning

- In SemiBin1, must-links were self-supervised
- In SemiBin1, cannot-links were from a reference taxonomy



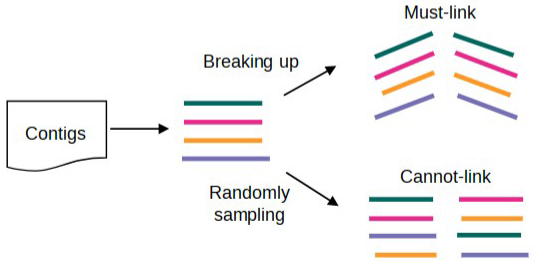
Use random sampling to generate cannot-links

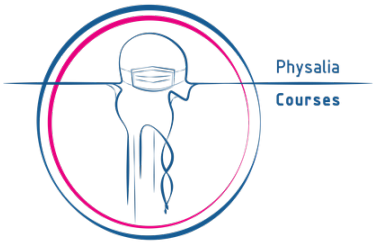
Random sampling advantages

1. Random sampling is faster than MMSeqs2
2. It has no database biases

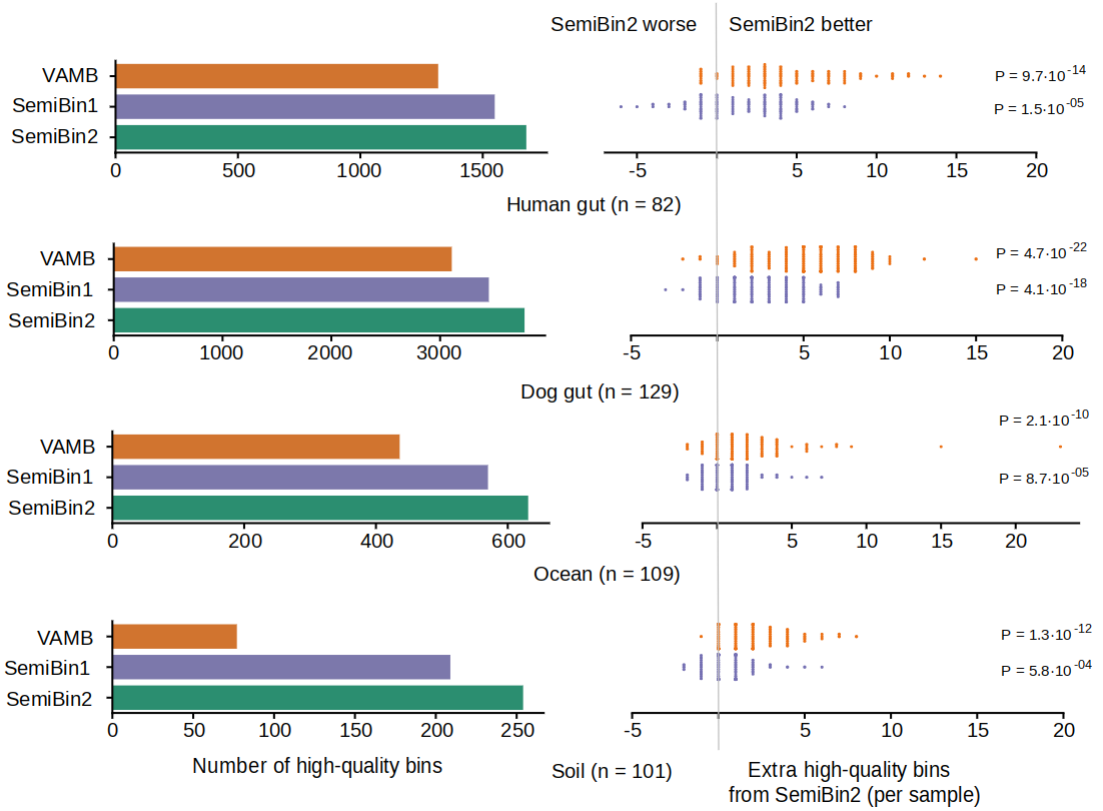
Random sampling disadvantages

1. Random sampling introduces errors (naturally)





Semibin vs Semibin2



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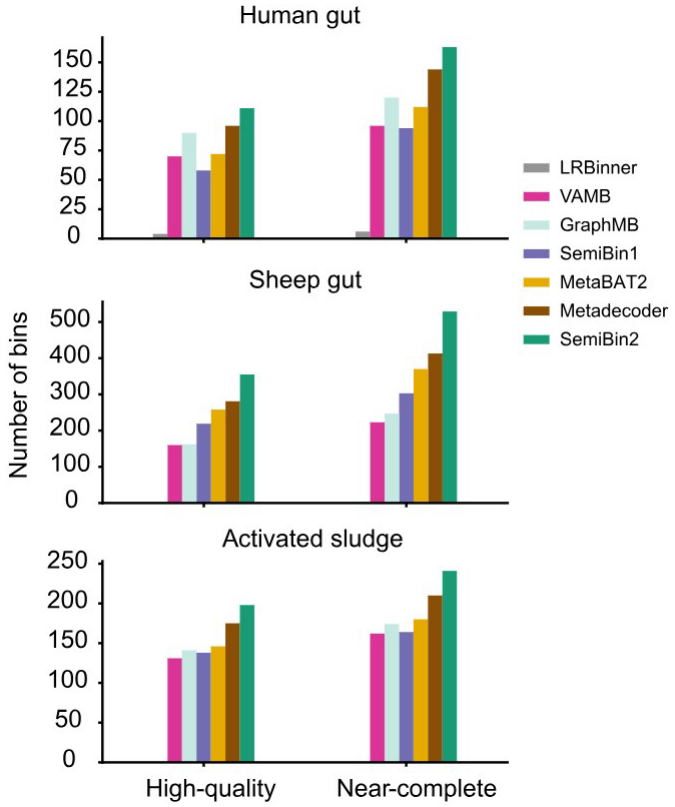
SemiBin2 surpasses alternatives for long-read binning

- Three datasets: human gut, sheep gut, and activated sludge
- Some of the alternatives (like SemiBin1) are not designed for long-reads
- We used CheckM2 & GUNC to evaluated the results
- SemiBin2 is also best using checkM1, but the two tools share some of the same marker genes (so evaluation is partly circular)



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All the binners

Binning metagenomic contigs by coverage and composition

Johannes Alneberg[1,8], Brynjar Smári Bjarnason[1,8], Ino de Bruijn[1,2], Melanie Schirmer[3], Joshua Quick[4,5], Umer Z Ijaz[3], Leo Lahti[6,7], Nicholas J Loman[4], Anders F Andersson[1,9] & Christopher Quince[3,9]

Effective binning of metagenomic contigs using contrastive multi-view representation learning

Received: 28 June 2023
Accepted: 7 December 2023

Ziye Wang[1], Ronghui You[1], Haitao Han[1], Wei Liu[1], Fengzhu Sun[2] & Shanfeng Zhu[1,3,4,5,6]

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met
biome
datasets across different environments

Shaojun Pan[1,2], Chengkai Zhu[1,2,3], Xing-Ming Zhao[1,2,4,5] & Luis Pedro Coelho[1,2]

MaxBin 2.0: an automated binning algorithm to recover genomes from multiple metagenomic datasets

Yu-Wei Wu[1,2,*], Blake A

Improved metagenome binning and assembly using deep variational autoencoders

Jakob Nybo Nissen[1,2], Joachim Johansen[2], Rosa Lundbye Allesøe[2], Casper Kaae Sønderby[3], Jose Juan Almagro Armenteros[1], Christopher Heje Grønbech[3,4], Lars Juhl Jensen[2], Henrik Bjørn Nielsen[5], Thomas Nordahl Petersen[6], Ole Winther[3,4,7] and Simon Rasmussen[2]

MetaBAT, an efficient tool for accurately reconstructing single genomes from
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[2] Ge
[3] Sch

MetaBAT 2: an adaptive binning algorithm for robust and efficient genome reconstruction from metagenome assemblies

Dongwan D. Kang[1], Feng Li[2], Edward Kirton[1], Ashleigh Thomas[1], Rob Egan[1], Hong An[2] and Zhong Wang[1,3,4]

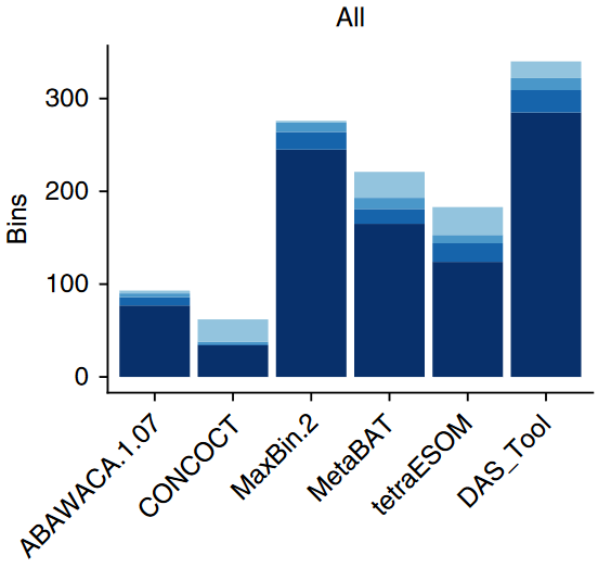
SemiBin2: self-supervised contrastive learning leads to better MAGs for short- and long-read sequencing

Shaojun Pan[1,2], Xing-Ming Zhao[1,2,3,4,*], Luis Pedro Coelho[1,2,*]

Ensemble binning

- Combining bins from multiple binners

  - DAS Tool
  - MetaWRAP
  - MetaBinner
  - BASALT



Sieber et al. *Nature Microbiology* 2018

Aviary: Our Assembly + Binning pipeline

- Snakemake pipeline (automatically submit jobs to a cluster)
- Assembly: metaSPAdes or MegaHit
  - Particularly good at hybrid short+long read
- Binning
  - MetaBAT1/2, VAMB, SemiBin1/2, CONCOCT, MaxBin2, Rosella
  - DAS Tool

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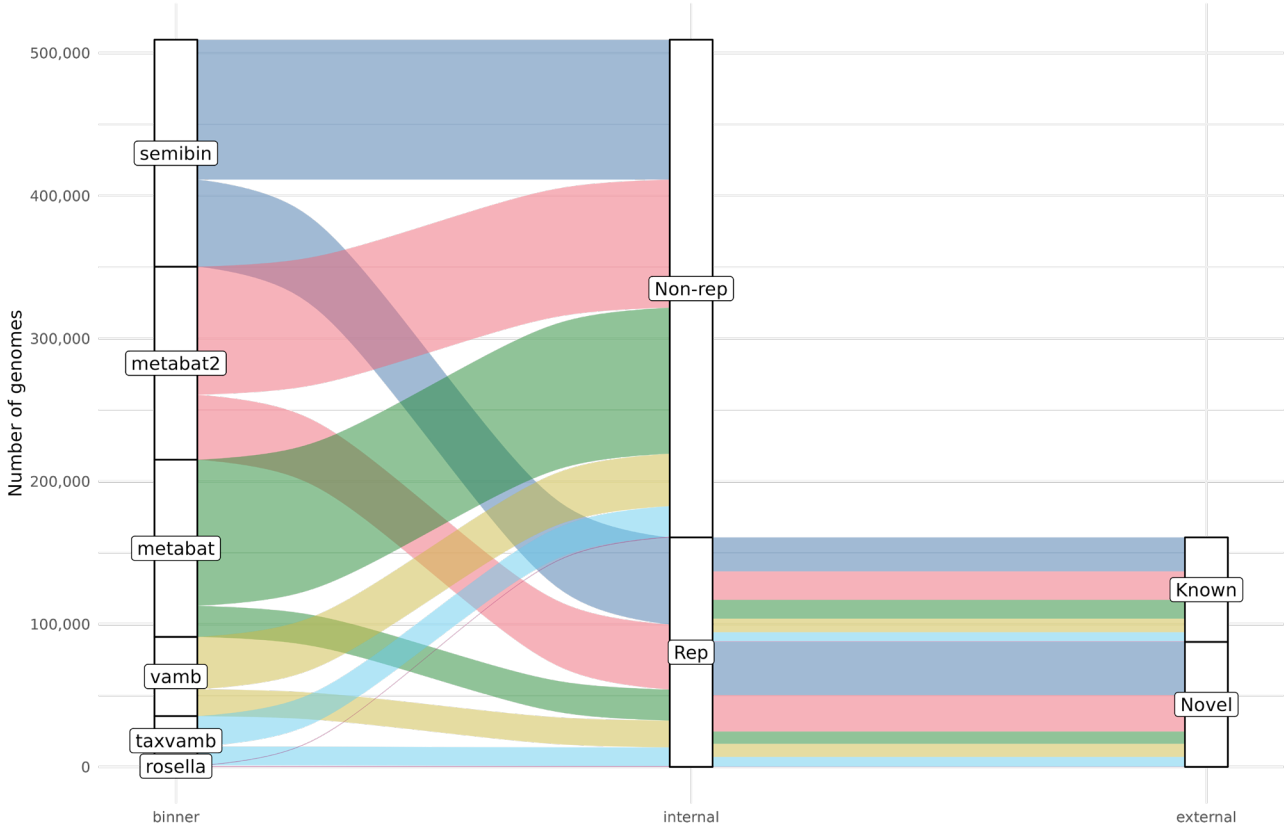
All the binners - comparison

semibin = Semibin2



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