

Supplementary Text and Figures

Supplementary Notes

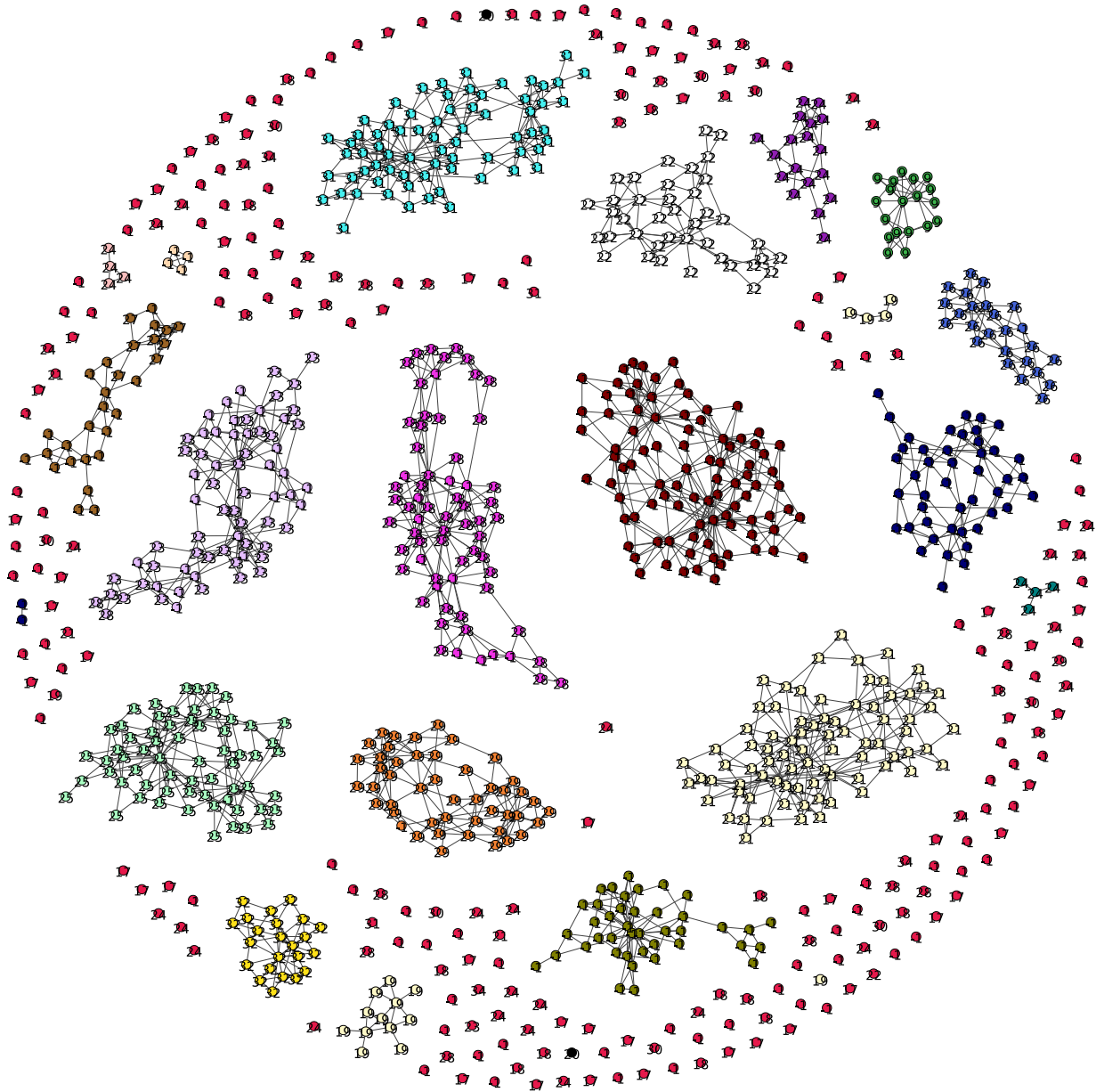
Supplementary Note 1. Computational time and memory usage

We evaluated the computational performance of different binning tools using the CAMI Low dataset (**Methods**). We excluded the preprocessing time to generate bam files for all binning tools (except for MaxBin, whose preprocessing is internal to the binning program). DeepMetaBin needed longer real time and larger maximum resident set size (RSS) than VAMB, MetaDecoder, and MetaBAT2, but its real time and memory usage were less than that of MetaCoAG and SolidBin (**Table 1.1**). This indicates that the binning tools using graph information may in general need higher running time and memory, but that DeepMetaBin is at least more efficient than the existing programs using the graph information.

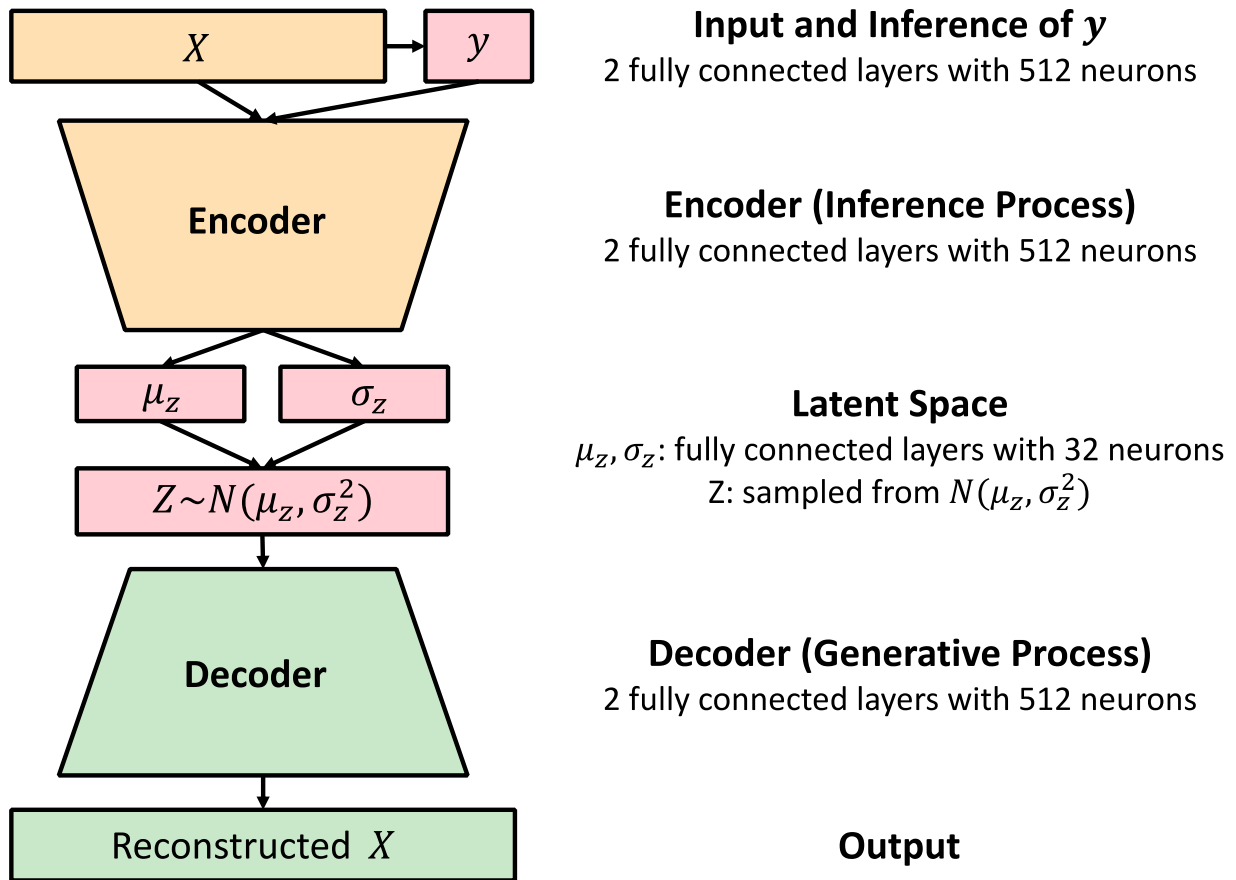
Binning Tool	CPU time (s)	Real time (s)	RSS (MB)
VAMB	1,167	444	320.16
MetaDecoder	163	12	339.36
MetaCoAG	1,128	1,830	2677.92
MetaBAT2	1,090	8	123.79
MaxBin	13,052	14,947	591.36
SolidBin	926	920	4005.64
DeepMetaBin	96,182	640	2074.72

Table 1.1. The CPU time, real time, and maximum resident set size (RSS) during the execution of seven different contig binning tools on the CAMI Low dataset.

Supplementary Figures



Supplementary Figure 1. The k-NN graph constructed using the read depths and TNFs of the contigs from the CAMI Low dataset. The colors (except for red) are the labels of preliminary clustering on the k-NN after DBSCAN and label propagation. The red color denotes noise nodes whose neighbors had different clustering labels and we removed all the noise edges in the k-NN graph to guarantee all neighbors of a contig have the same clustering labels with it. The numbers on the nodes are the true genome labels of the contigs by aligning the contigs to the reference genomes of the CAMI Low mock community.



Supplementary Figure 2. The network parameters of GMVAE.