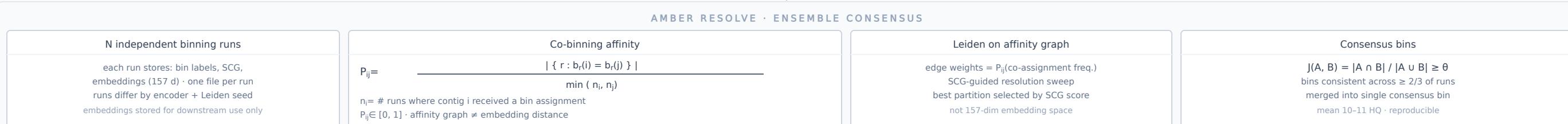
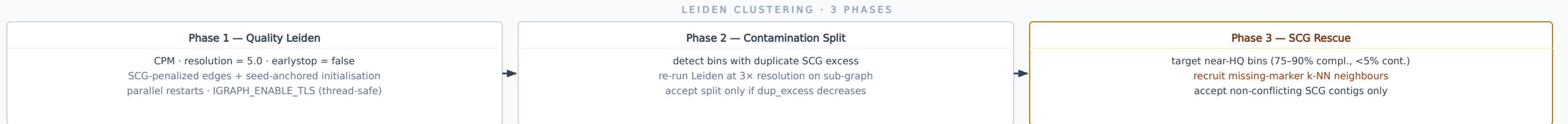
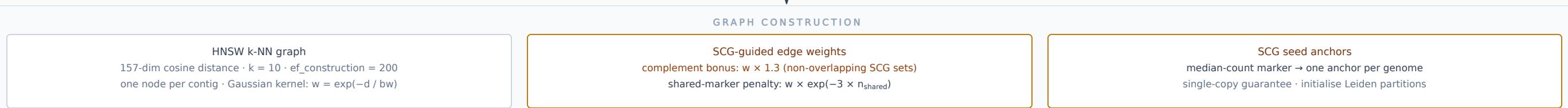
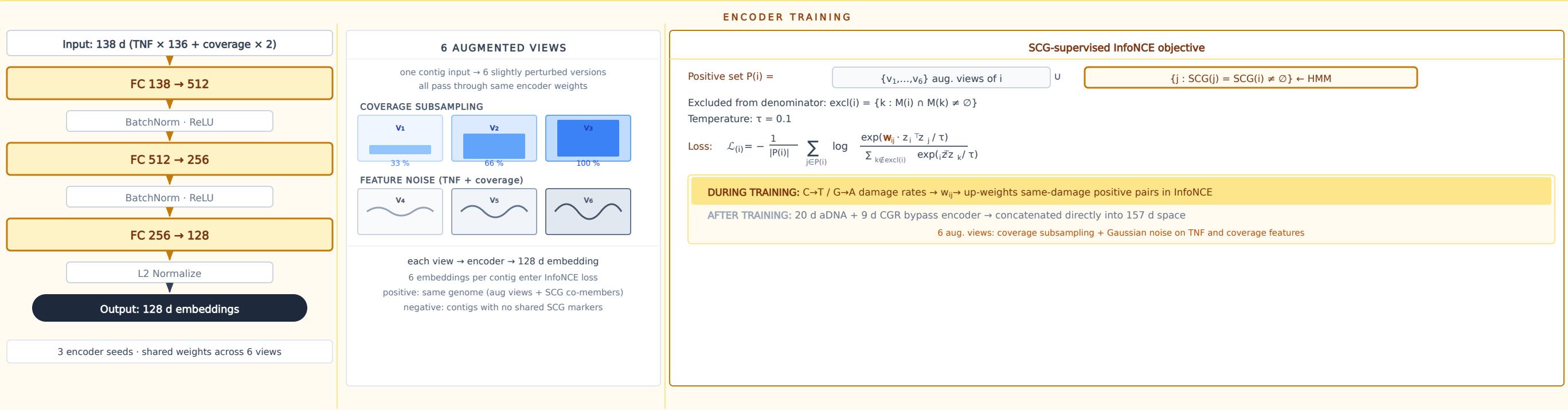
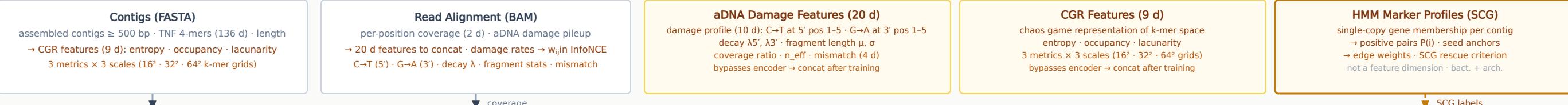


# AMBER

Ancient Metagenomic Binning with aDNA-aware Encoder and Refinement



Genomic bins (.fa) · HQ  $\geq 90\%$  completeness / <5% contamination · MQ  $\geq 50\%$  / <10%  
per-bin: SCG profile · aDNA damage rates · completeness · contamination · Jaccard · embeddings