

All metagenomic reads from all fecal samples



Retain reads that align to reference genomes



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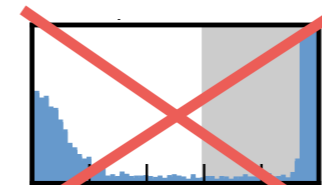
Retain species/sample combos with high coverage



Retain QP species/sample combos



Major allele freq

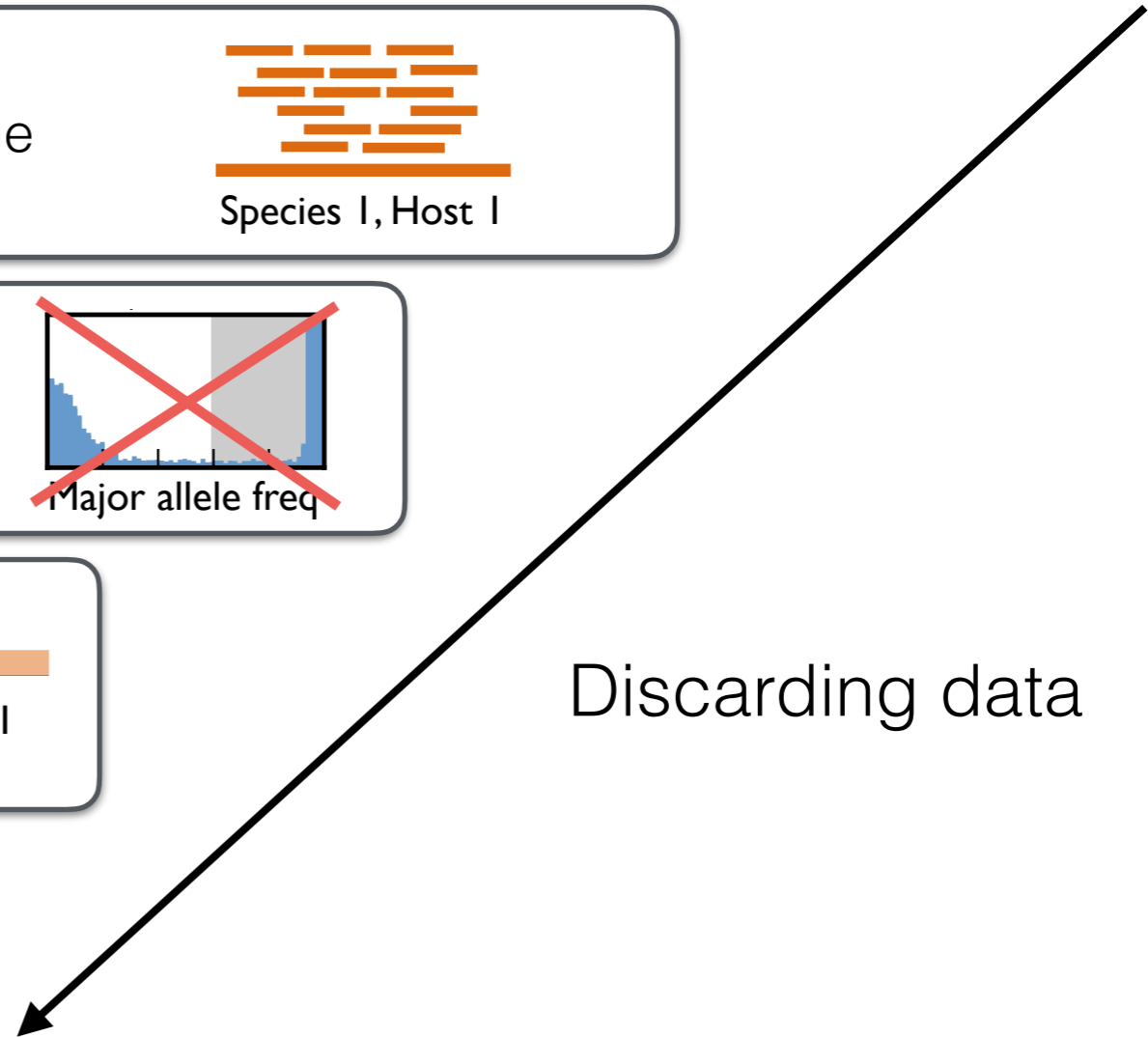


Major allele freq

Restrict to high-confidence part of coding genome and pangenome



Analyze SNV & gene differences that pass coverage & frequency thresholds



Discarding data