

- Get annotation data from public databases (Ensembl, Refseq, others...)

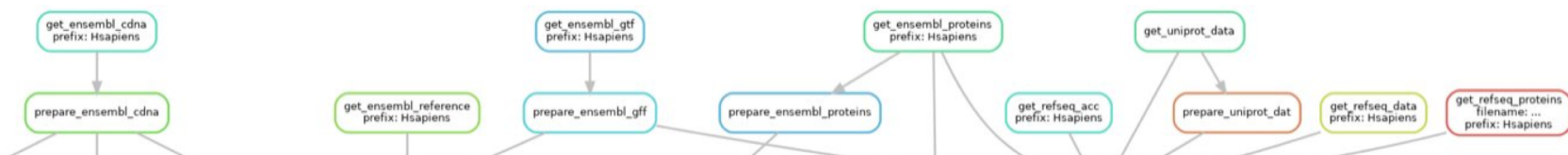
get\_ensembl\_cdna  
prefix: Hsapiens

get\_ensembl\_gtf  
prefix: Hsapiens

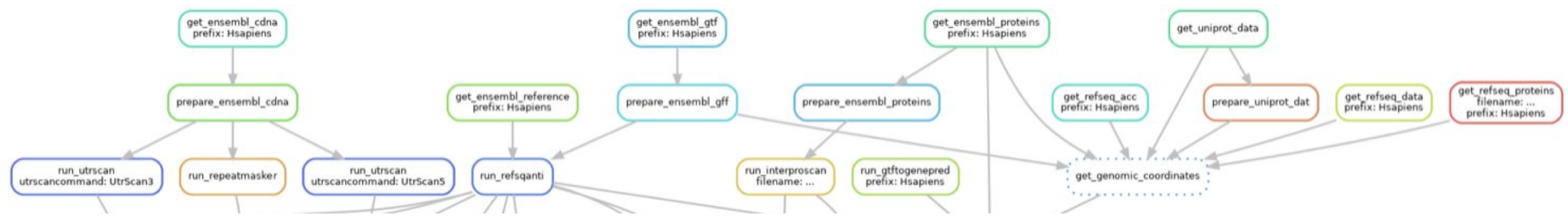
get\_ensembl\_proteins  
prefix: Hsapiens

get\_uniprot\_data

- Prepare data for function prediction and extract information from them.



- Run annotation algorithms (UTRscan, RepeatMasker, InterproScan, SQANTI...)





- Create a gff3 file with isoform-level functional labels

