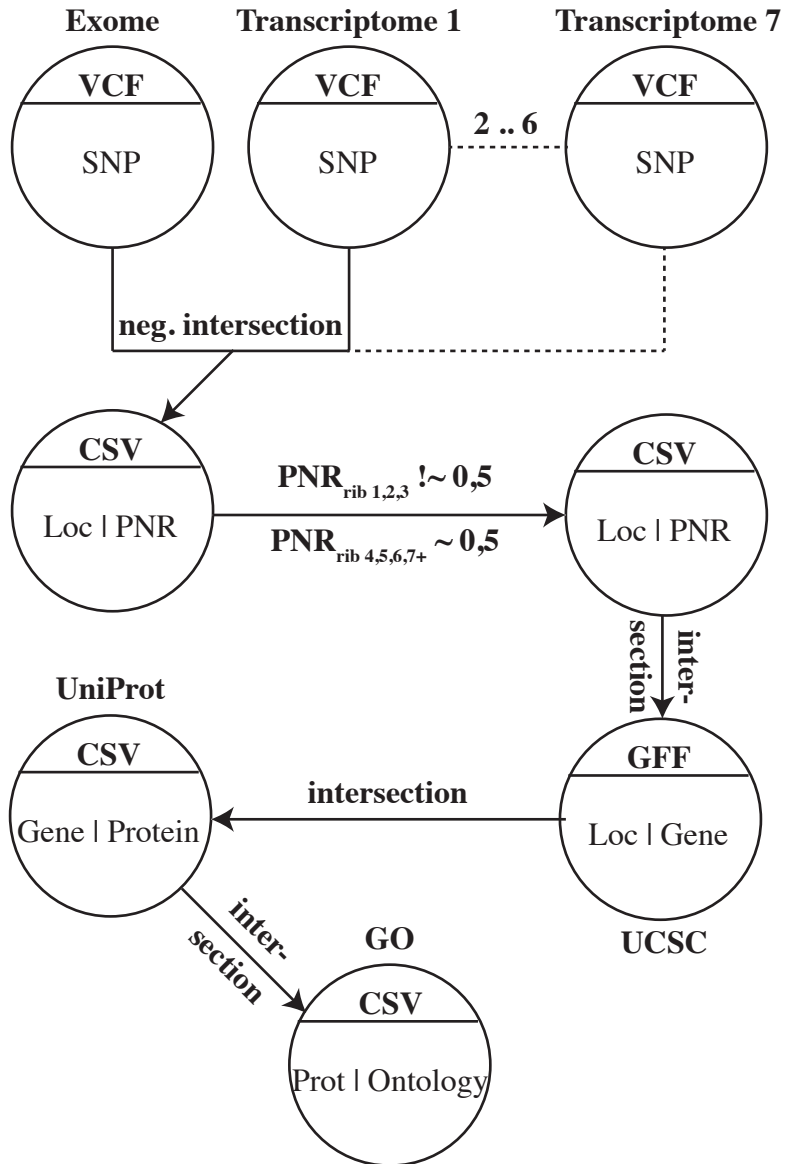
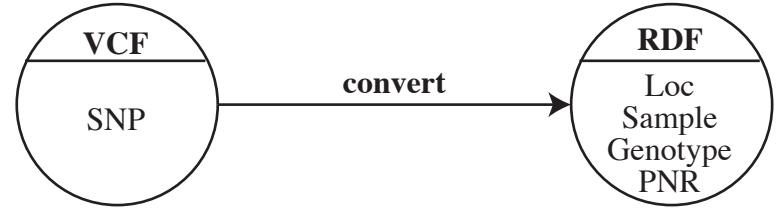


A) Extract all ontology-terms of all SNPs with an allelic bias in only transcripts bound to maximal 3 ribosomes.

B)



All



C)

D)

SPARQL

```
PREFIX go:http://www.geneontology.org/dtd/go.dtd
PREFIX uniprot:uniprot.org/pub/databases/uniprot/current_release/rdf/

SELECT go WHERE{
    ?y sample "exon",
        PNR is 0 or 1.
    ?y sample "Ribo1" or "Ribo2" or "Ribo3"
        PNR is not 0,5.
    ?y sample is not "exon" or "Ribo1" or "Ribo2" or "Ribo3",
        PNR is 0 or 1.
    ?y loc ?loc
    ?UniProt_id loc is ?loc.
    ?UniProt_id name is ?prot
    ?prot GO_id ?go
}
```