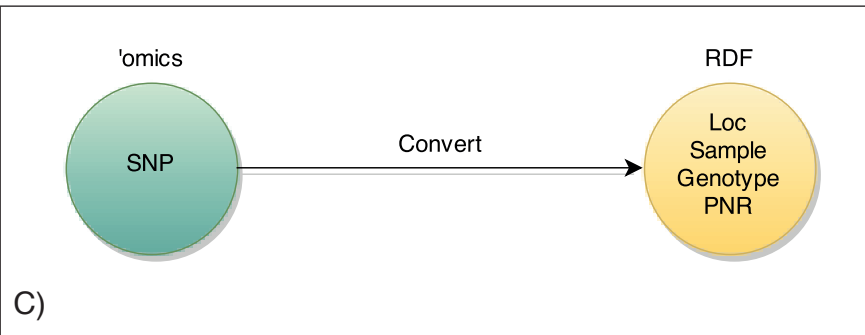
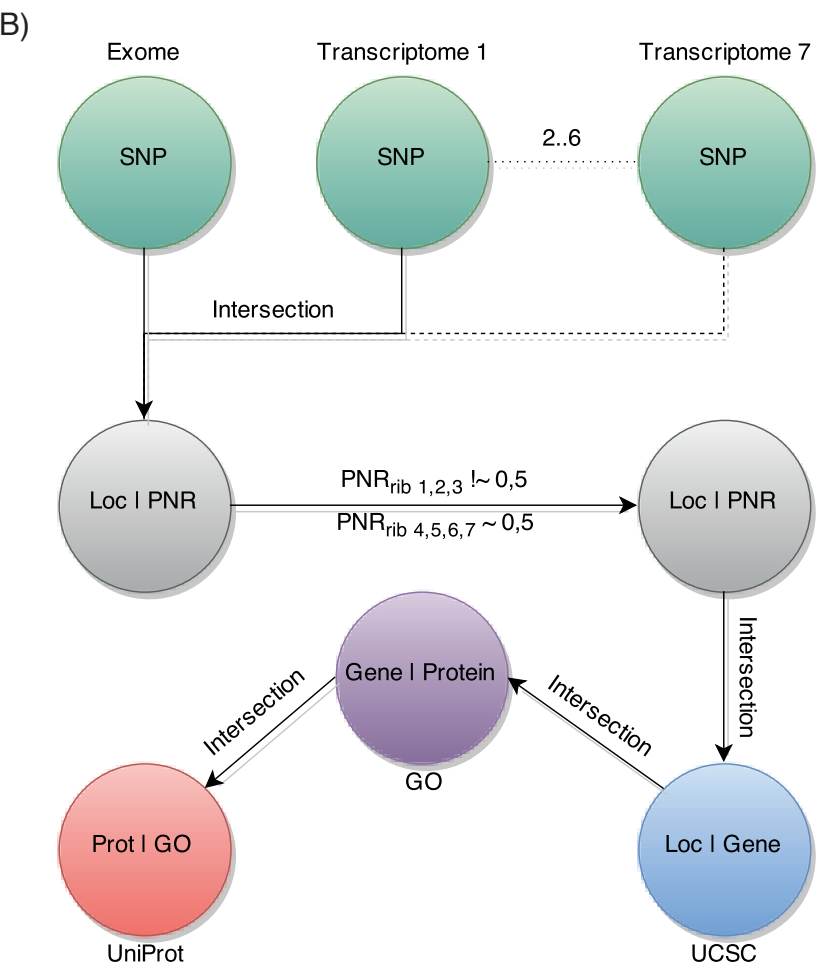


A) Extract all ontology-terms of all SNPs with an allelic bias in only transcripts bound to maximal 3 ribosomes.



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
}
```