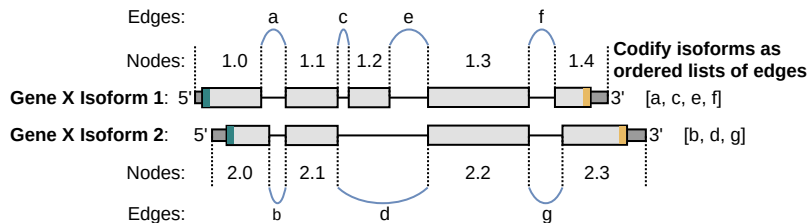
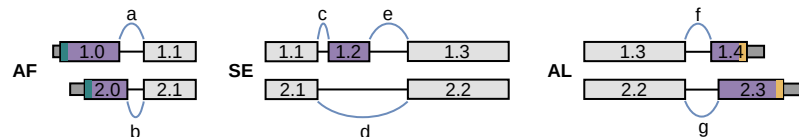


**A**

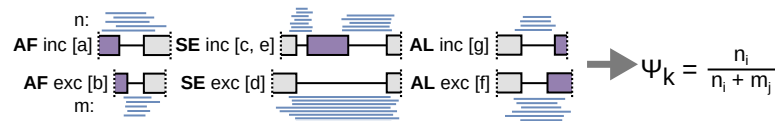
Compare overlapping transcripts as sets of exon  
boundary-defined nodes connected by edges (junctions)

**B**

Define the minimal set of binary events that distinguish alternative isoforms

**C**

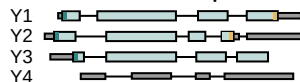
Assign mapped junction reads to events based on  
overlaps with edges unique to their included/excluded forms

**D**

Identify exons containing  
start codons



Match annotated CDS  
to transcripts



Identify poison exons



Record transcript characteristics

- CDS, 3'UTR and 5'UTR length
- putative protein sequence
- PTC presence and location

**E**

Match events to isoforms by edges

- AF [a] → Gene X Isoform 1 [a, c, e, f]
- AF [b] → Gene X Isoform 2 [b, d, g]

Identify exons  
unique to each form

- AF inc [a] 1.0
- AF exc [b] 2.0
- Predict switch events  
from CDS & PTC info
- NMD □ NSD
  - coding-to-noncoding
  - CDS-altering