

# .IML intron models

Intron model files describe the format of splice site combinations that are considered as potential intron. Discriminatory attributes of biological introns are (1) the distance of the donor/acceptor pair, (2) the combination of their splice site sequences. Each model block is introduced by a header line.

```
#MODEL minDist maxDist
```

where #MODEL introduces a new model, and minDist respectively maxDist delimit the boundaries on the lengths of valid introns that are described by the model. Subsequently, a list of donor/acceptor sequences that may co-occur in valid introns is provided.

donorSeq1	acceptorSeq1
donorSeq2	acceptorSeq2
...	...

The sequences are the strings directly adjacent to exons, and may be redundant — as combinations are evaluated — as their length may vary, even amongst donors and acceptors.