

End-Start Constraint Element

*Add the **End-Start constraint** to some two *algorithm elements*. Lets denote these elements as **alg1** and **alg2**.*

Parameters in GUI

| Parameter | Description | Default value |
|---------------------|---|---------------|
| Min distance | Minimum distance between an alg1 annotation end and an alg2 annotation start. | 0bp |
| Max distance | Maximum distance between an alg1 annotation end and an alg2 annotation start. | 0bp |

Constraint Explanation:

Let:

alg1_annot_end := the last nucleotide of an annotation obtained from the **alg1**.

alg2_annot_start := the first nucleotide of an annotation obtained from the **alg2**.

The result annotations should comply with the rule:

Min distance <= Distance(**alg1_annot_end**, **alg2_annot_start**) <= **Max distance**

Parameters in Schema File

Type: distance

Distance-type: end-to-start

| Parameter | Parameter in the GUI | Type |
|-----------|----------------------|----------------|
| min | Min distance | <i>numeric</i> |
| max | Max distance | <i>numeric</i> |