

# Start-End Constraint Element

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

## Parameters in GUI

Parameter	Description	Default value
<b>Min distance</b>	Minimum distance between an <b>alg1</b> annotation start and an <b>alg2</b> annotation end.	0bp
<b>Max distance</b>	Maximum distance between an <b>alg1</b> annotation start and an <b>alg2</b> annotation end.	0bp

### Constraint Explanation:

Let:

**alg1\_annot\_start** := the first nucleotide of an annotation obtained from the **alg1**.

**alg2\_annot\_end** := the last nucleotide of an annotation obtained from the **alg2**.

The result annotations should comply with the rule:

**Min distance** <= Distance(**alg1\_annot\_start**, **alg2\_annot\_end**) <= **Max distance**

# Parameters in Schema File

Type: distance

Distance-type: start-to-end

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