

regentrans input data

Genetic data:

Perform whole-genome
sequencing of isolates
from different facilities



Identify groups of
closely related isolates
(e.g. sequence type [ST],
clonal complex [CC])



For each group of closely related isolates:

Align to reference
genome of same
ST/CC



Mask
recombinant
sites



Create
**variant site
alignment**



Create
phylogeny



Create **genetic
distance matrix**

Input type:

Pre-input / **Required** / *Optional*

Isolate metadata:

- **Facility**
- **Patient**
- *Collection date*

Network data:

- *Patient transfer network*
- *Physical distance*
- *Drive time*