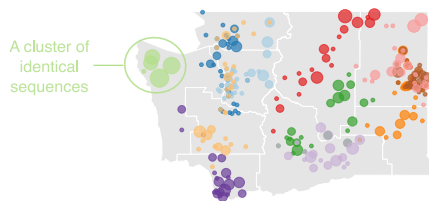
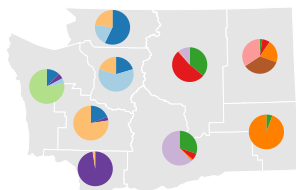


**A**

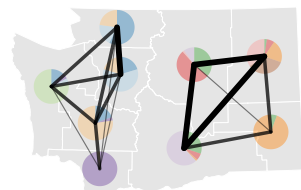
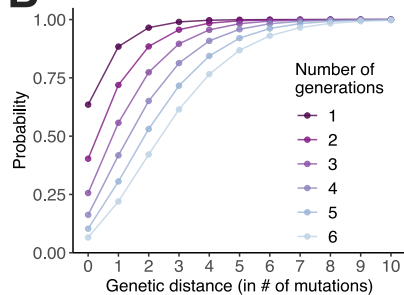
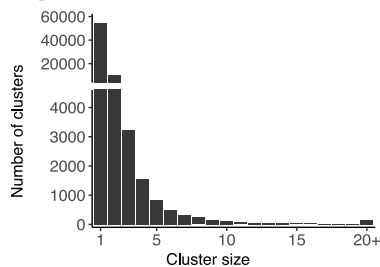
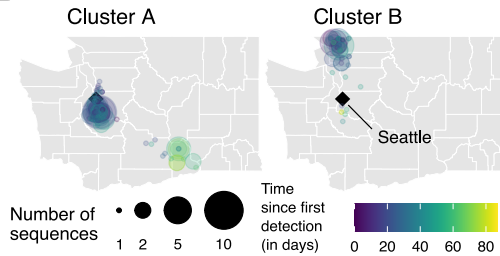
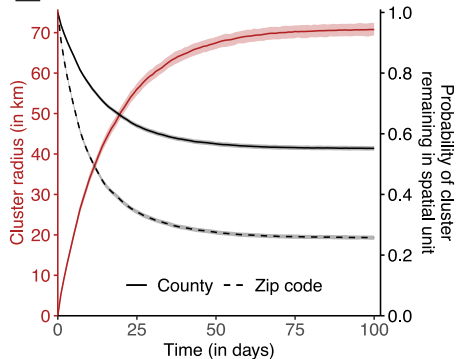
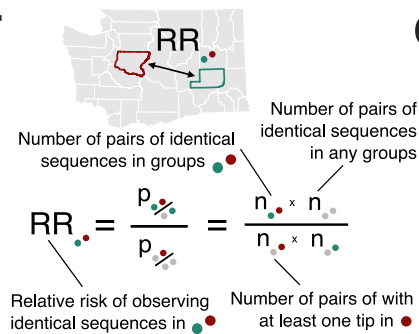
Identical sequences reflect  
epidemiologically linked individuals



Their geographic **clustering** is imprinted  
by underlying patterns of spread



This can be used to characterise  
**transmission between groups**

**B****C****D****E****F**

Measure of **enrichment**

RR > 1

**More** pairs than expected  
from the sequencing effort

RR = 1

**As many** pairs as expected

RR < 1

**Less** pairs than expected

**G**