RECON | vimes

An evidence-synthesis approach for detecting outbreak clusters

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4-6th September 2018

London School of Hygiene and Tropical Medicine
Imperial College London

Context...

Sustained transmission vs repeated introductions

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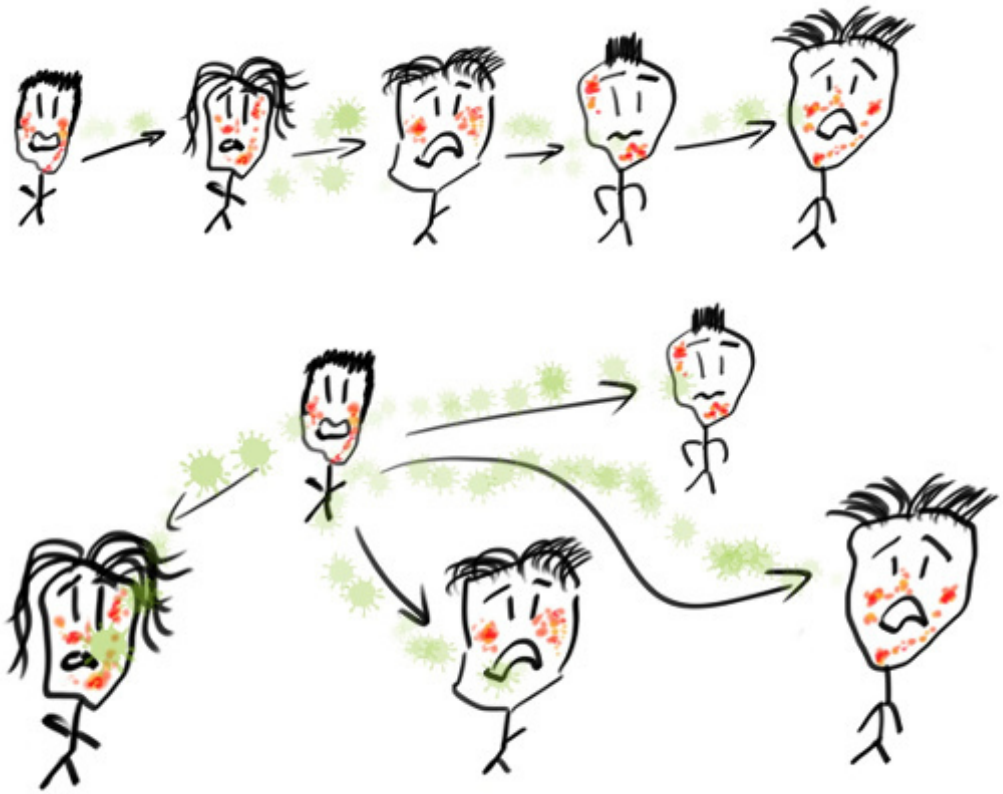

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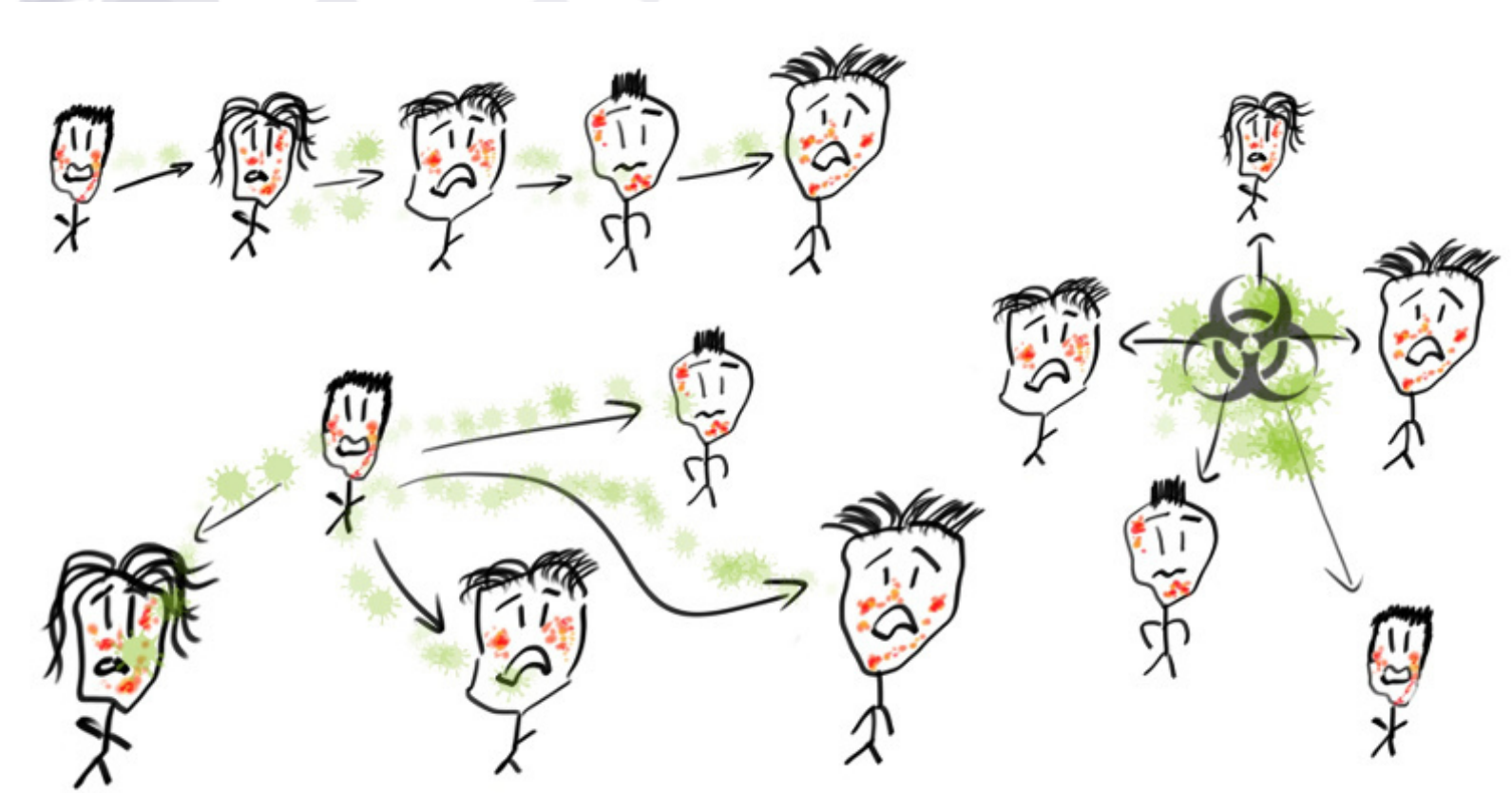

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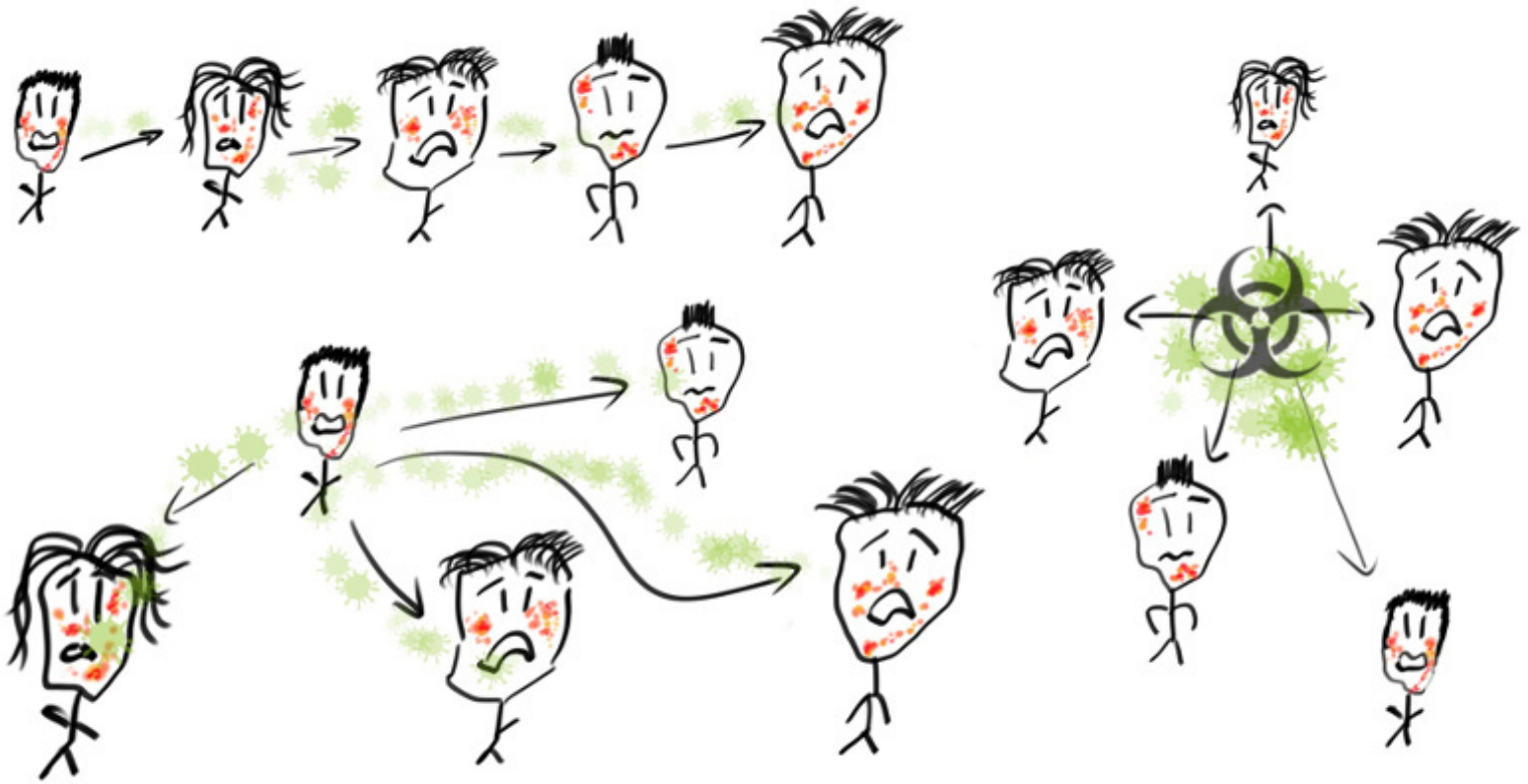

Different transmission patterns call for different interventions

Can we use data to identify these patterns?

One outbreak... how many introductions?

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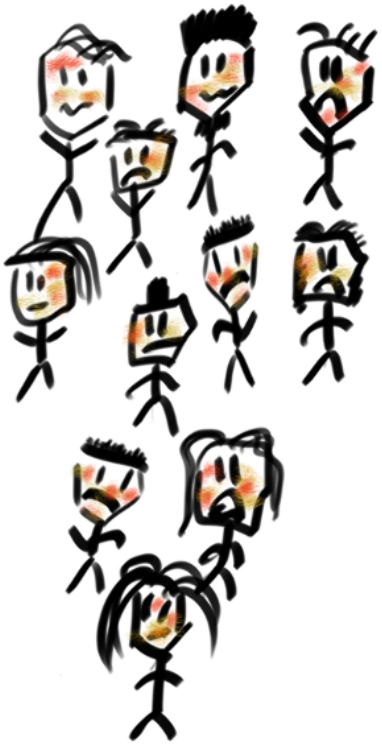

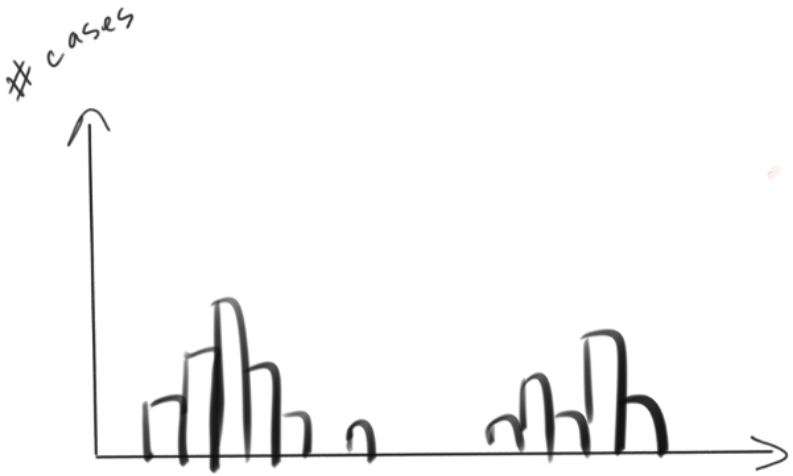

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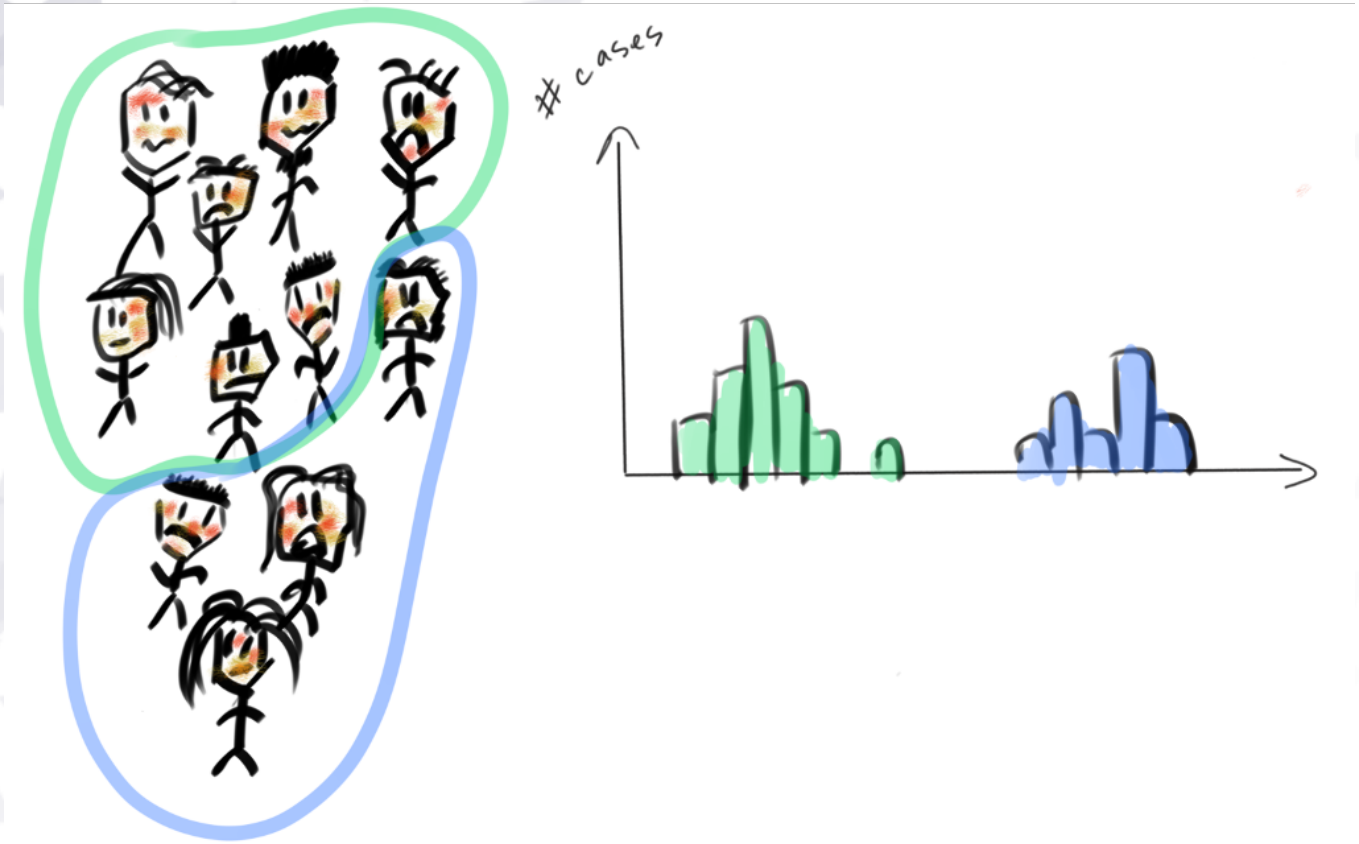

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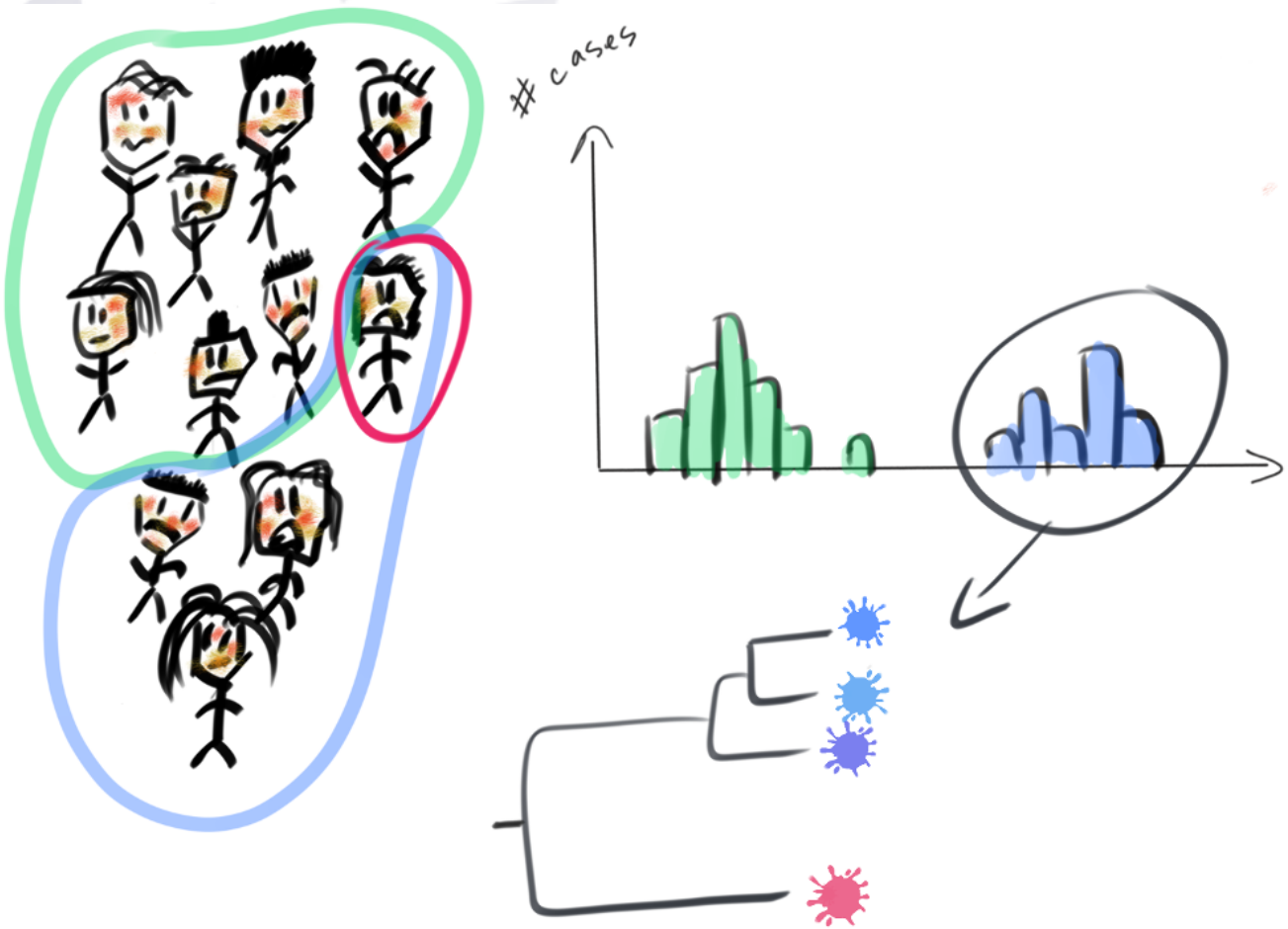

Combined data sources can detect outbreak clusters

VIMES: VIsualisation and Monitoring of EpidemicS [1]

Aims: develop a new method which...

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- integrates different data: temporal, spatial, genetic, etc.
- works fast, scales well: so that it can be used for real-time outbreak detection

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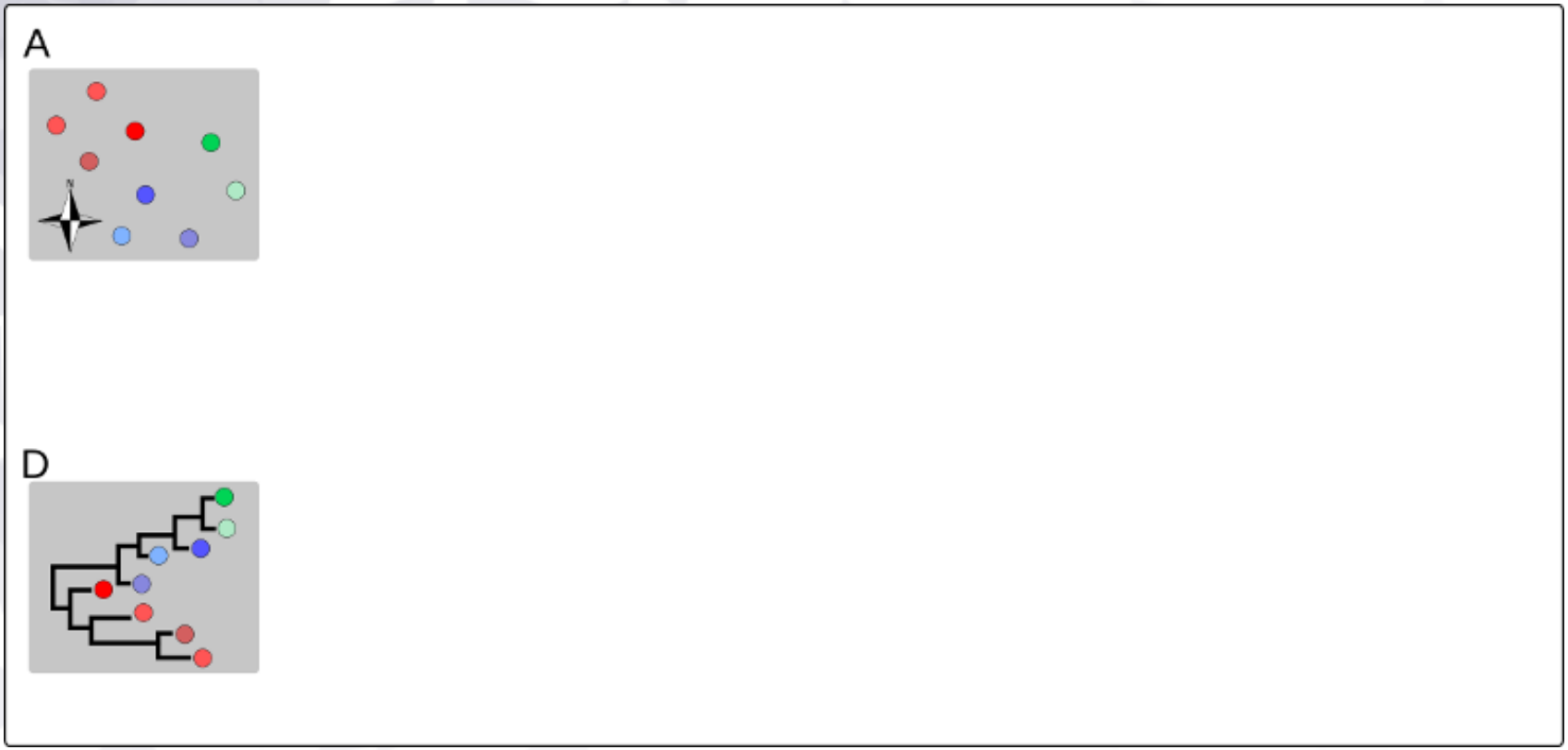
A graph-based evidence synthesis approach



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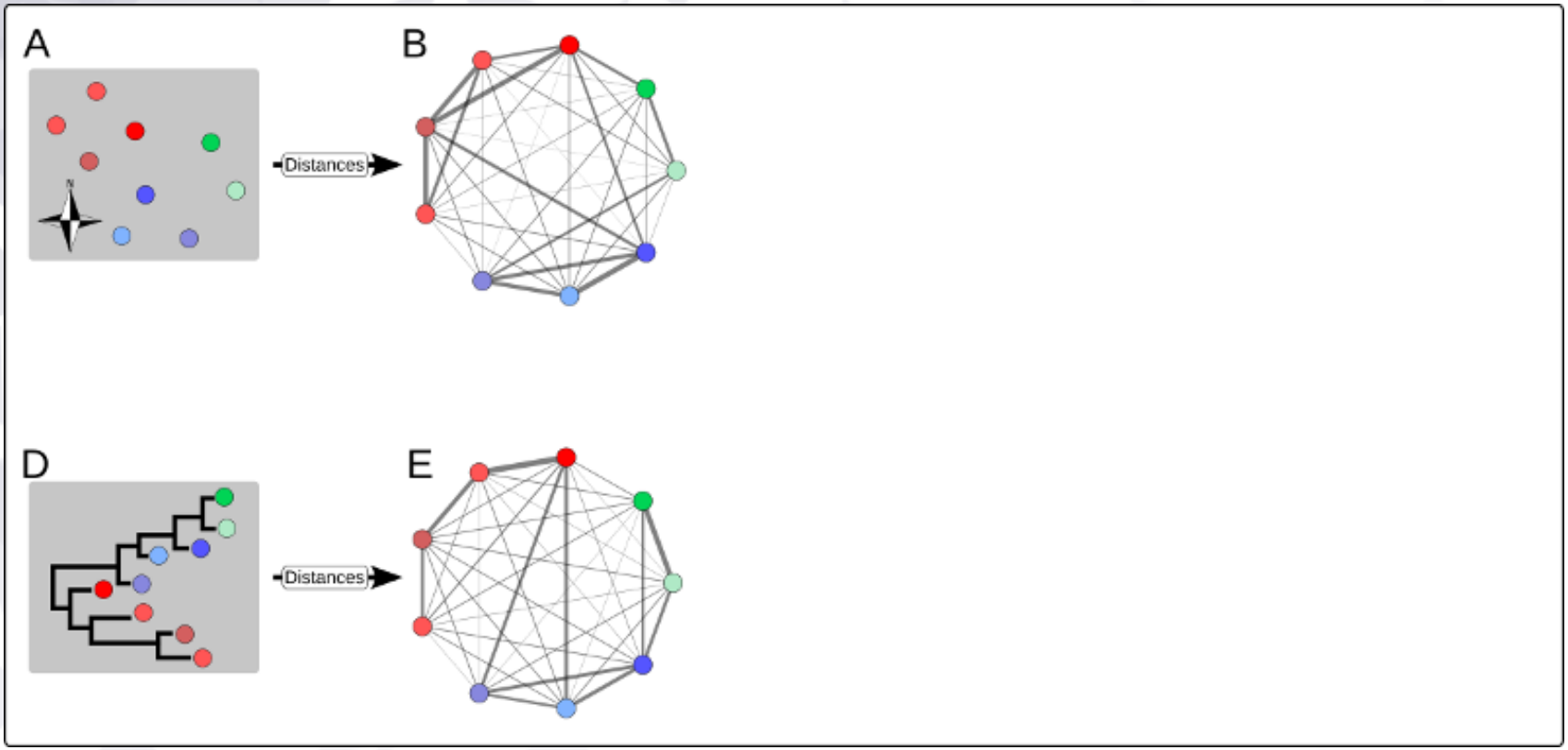

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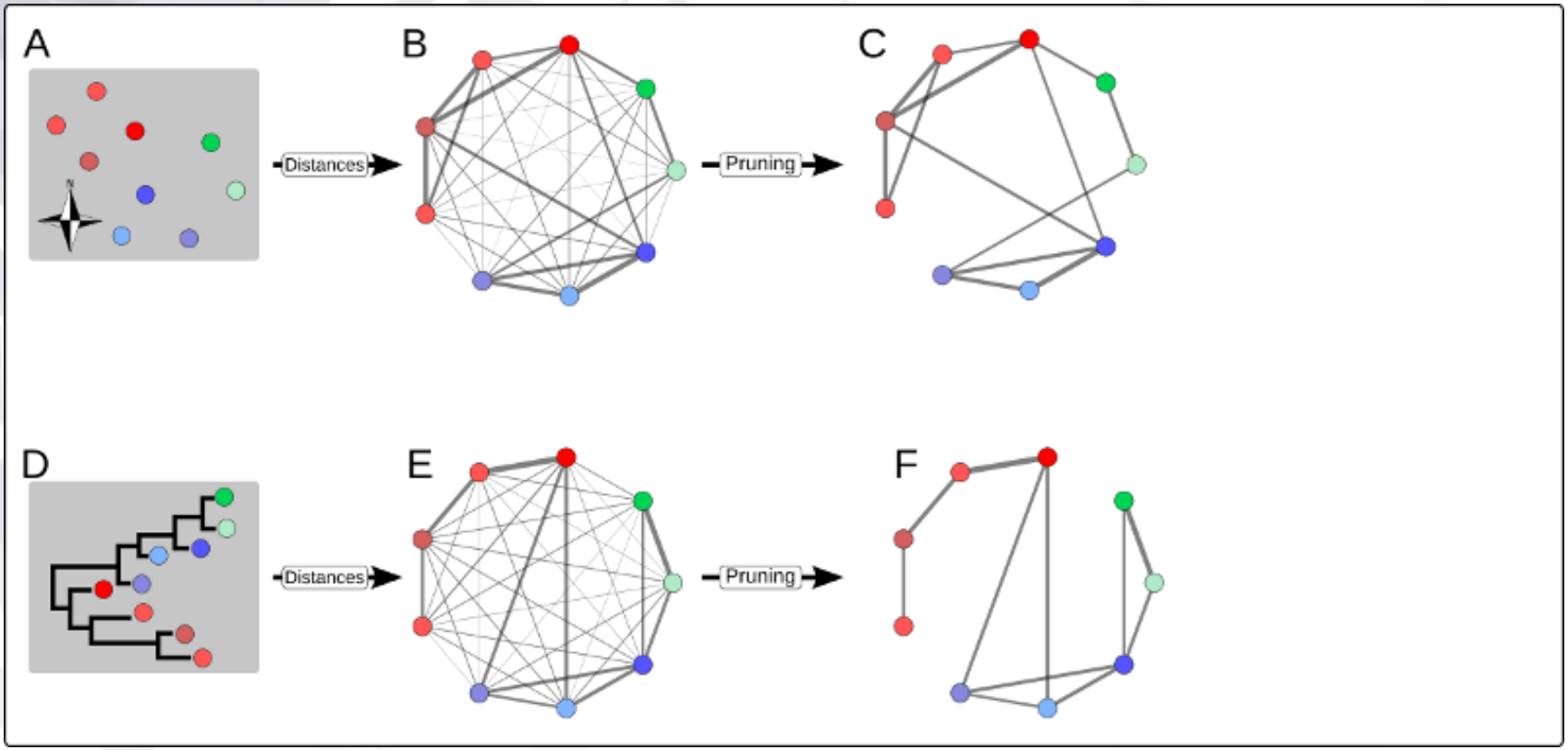

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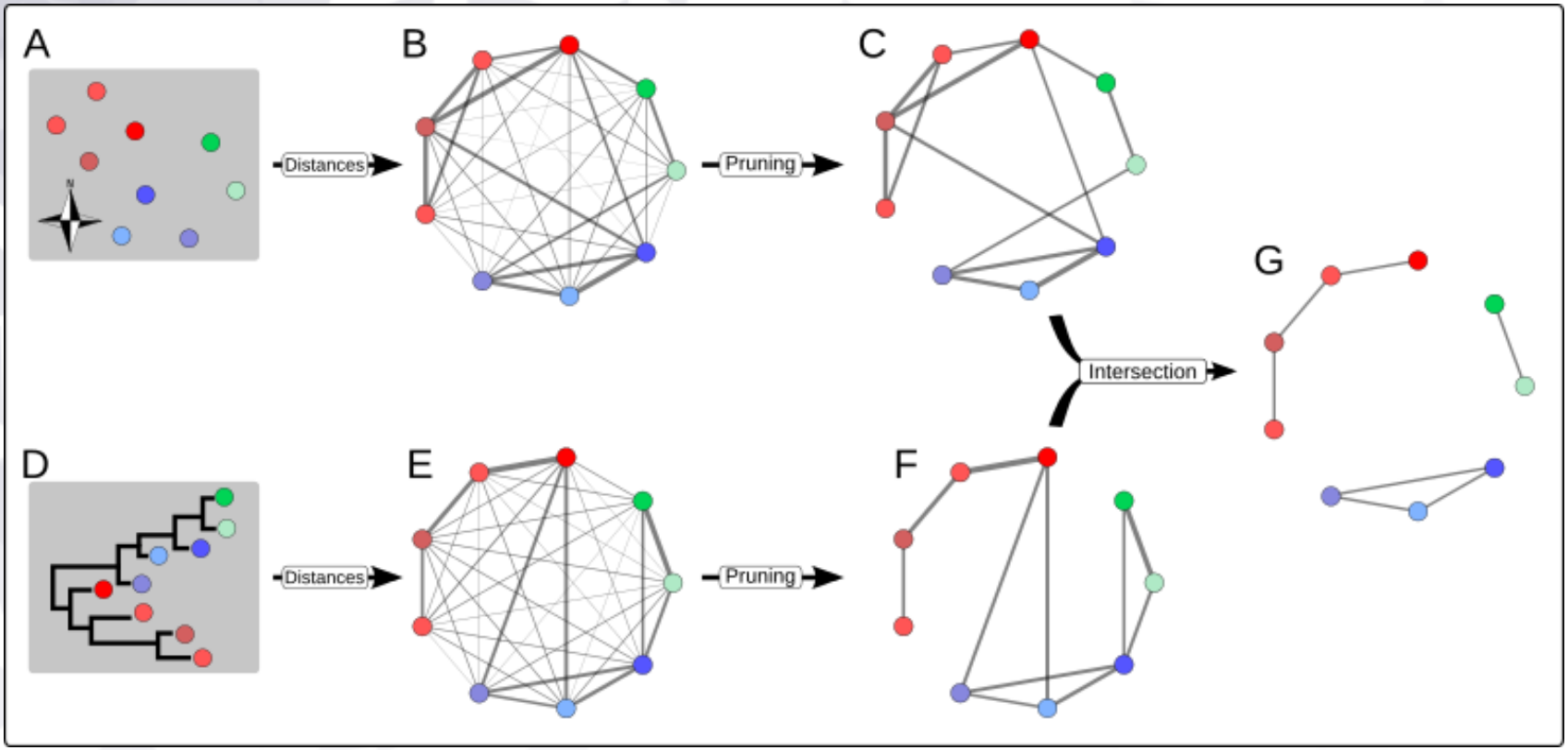

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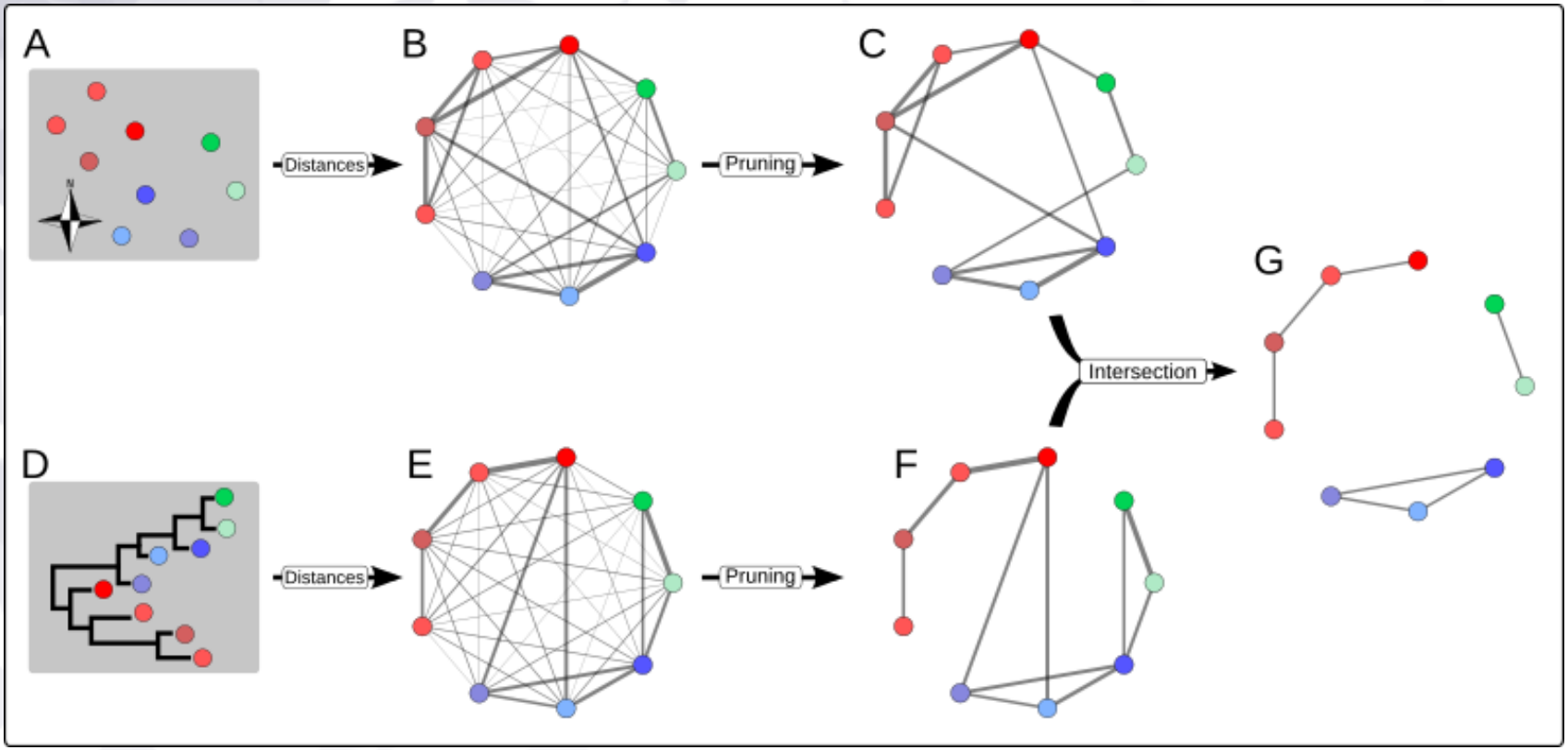
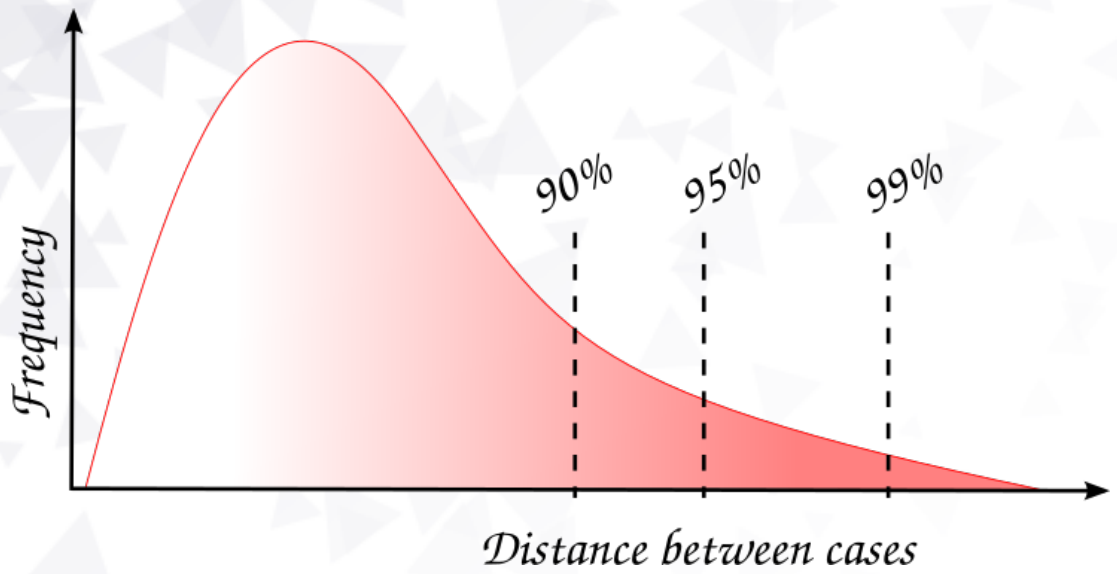


Can be extended to any number of data sources.

But it seems too simple...

Pruning graphs: where to cut?

Assuming a known expected distribution between pairs of cases (e.g. serial interval, spatial kernel, molecular clock), different quantiles can be used:



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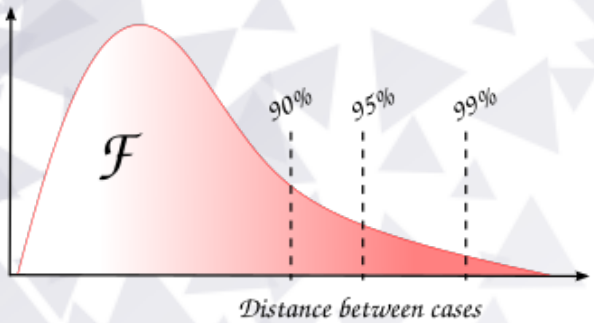

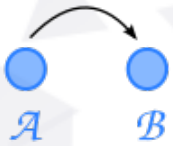

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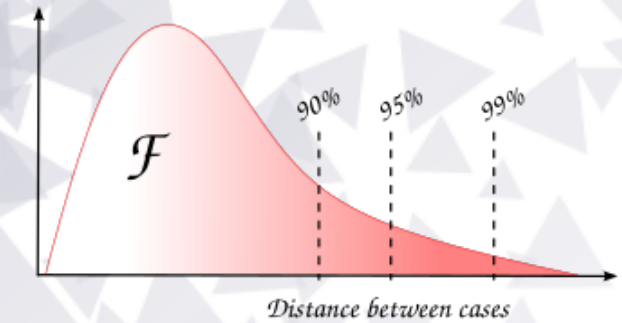

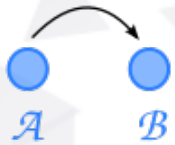

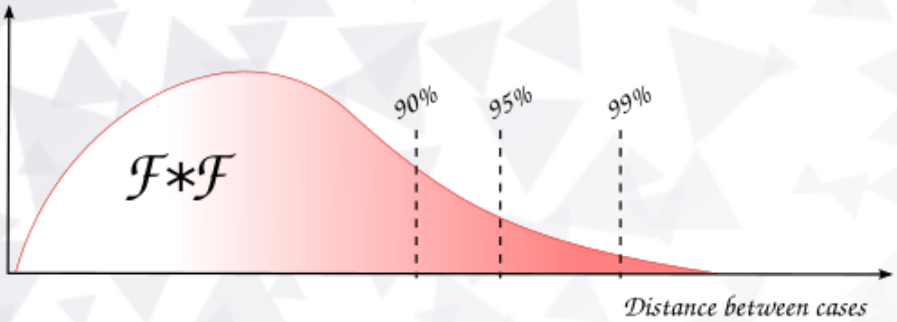

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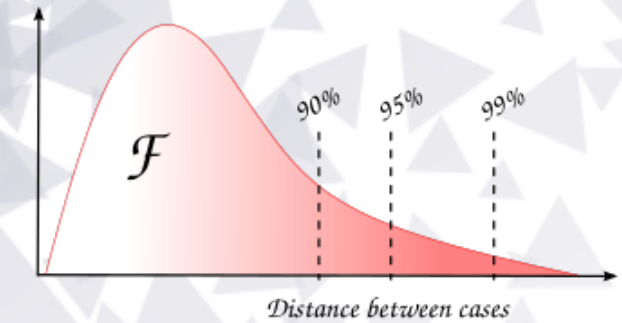

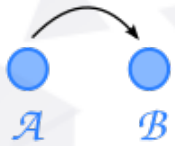

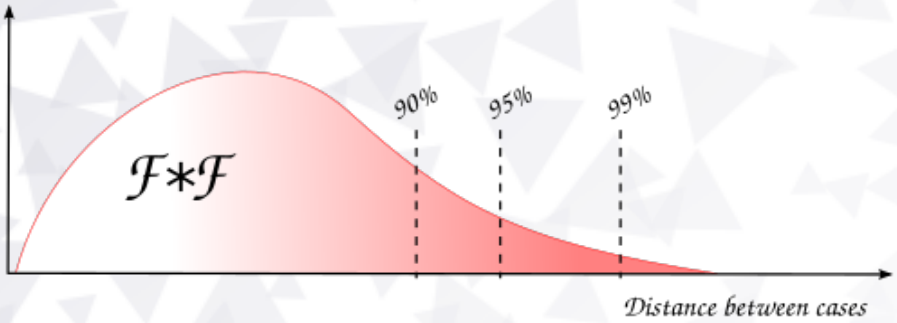

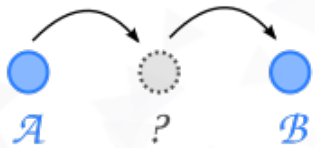

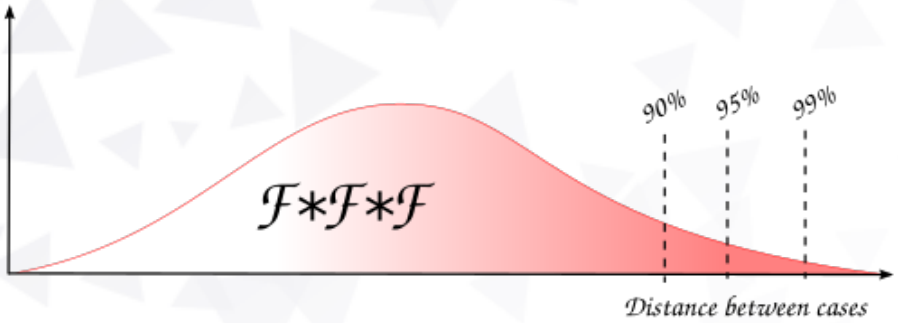

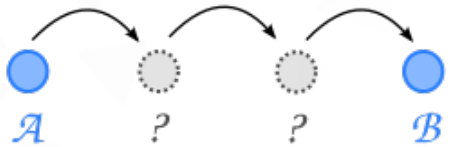

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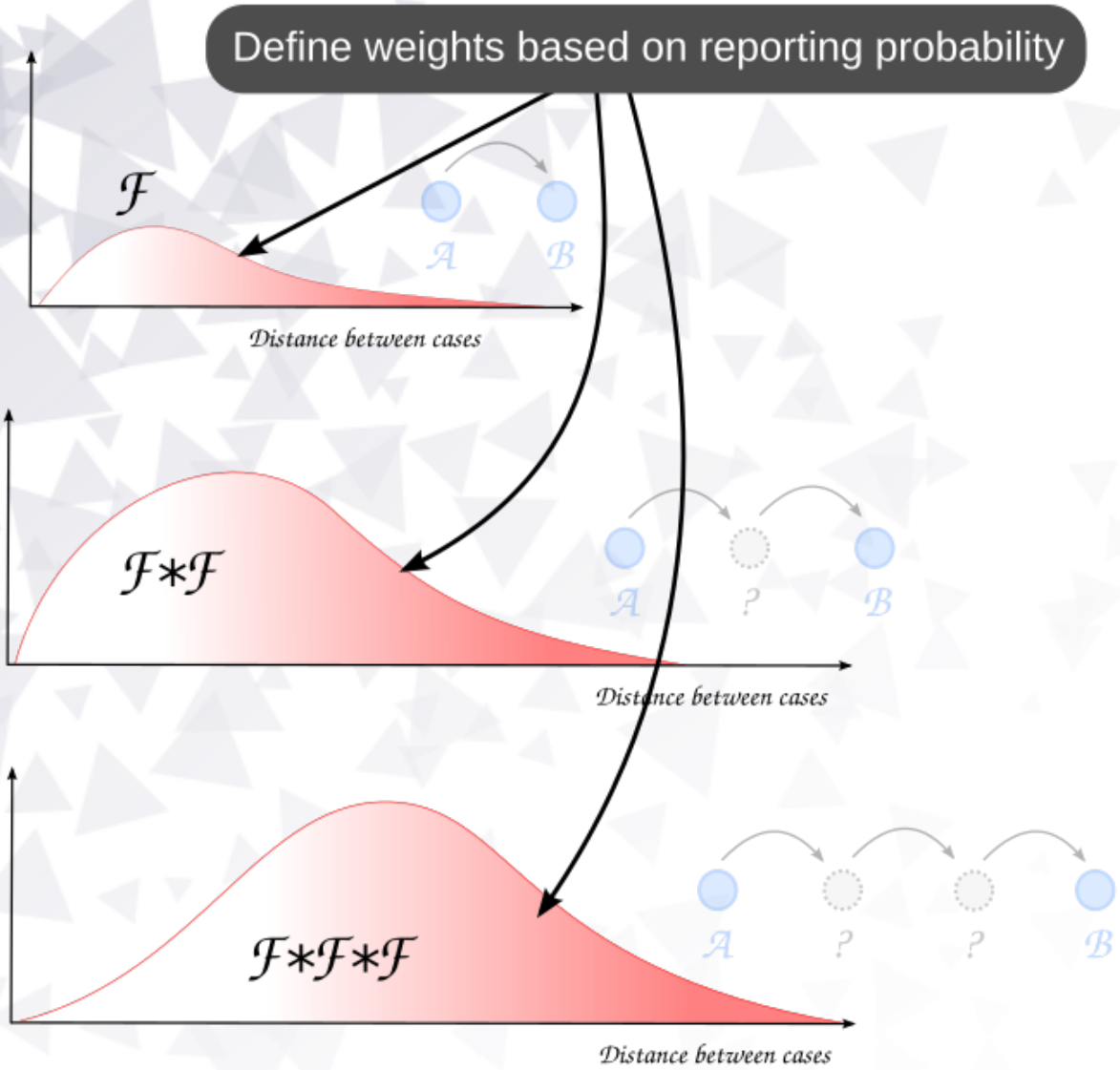

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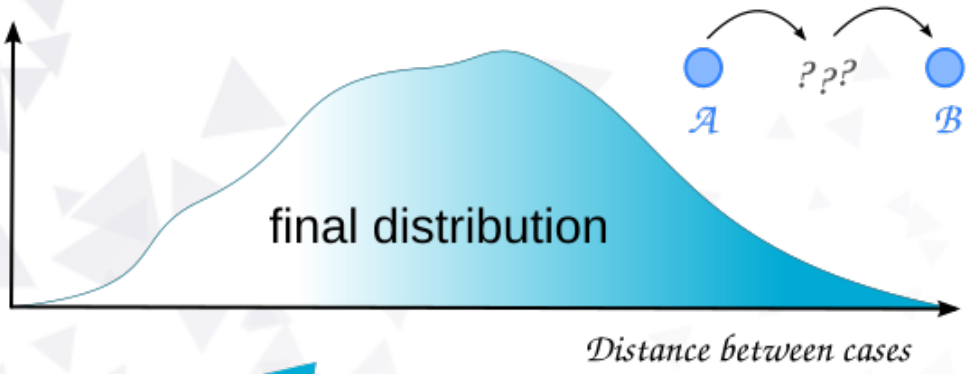
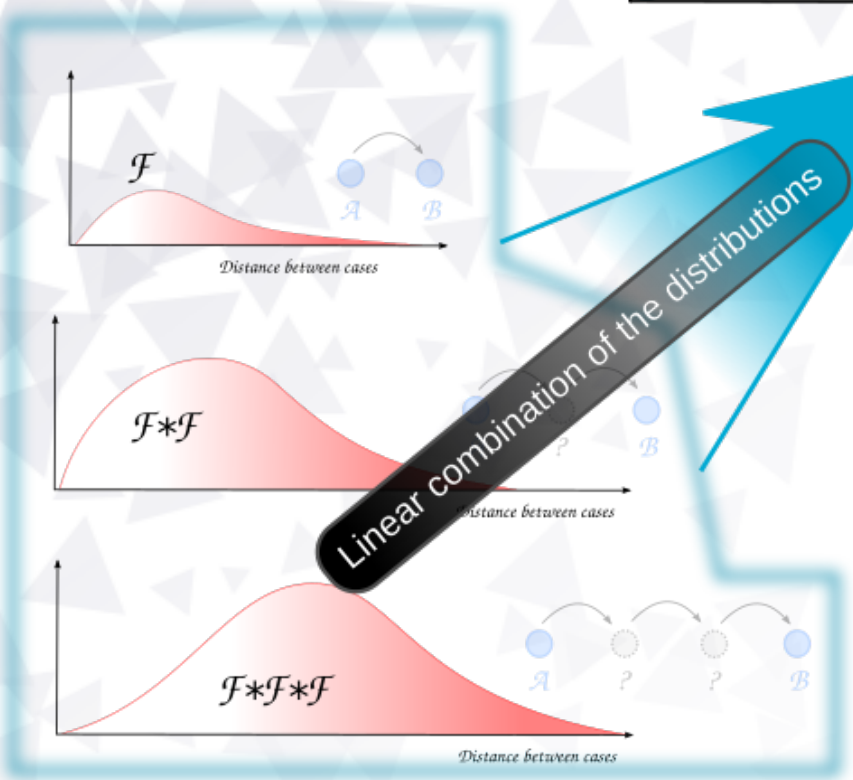




Linear combination of the distributions

idea by
Pierre Nouvellet

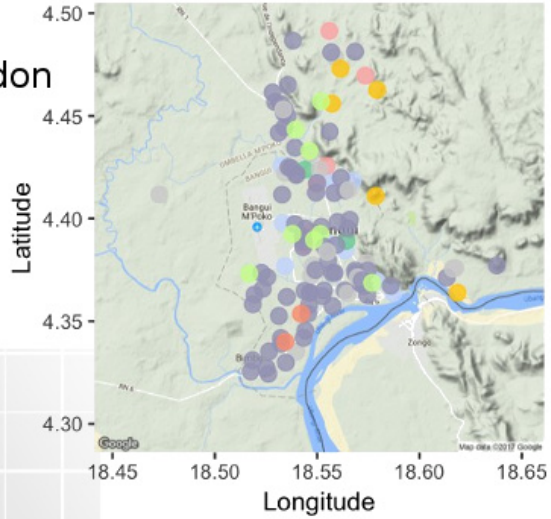
analytical results by
Anne Cori

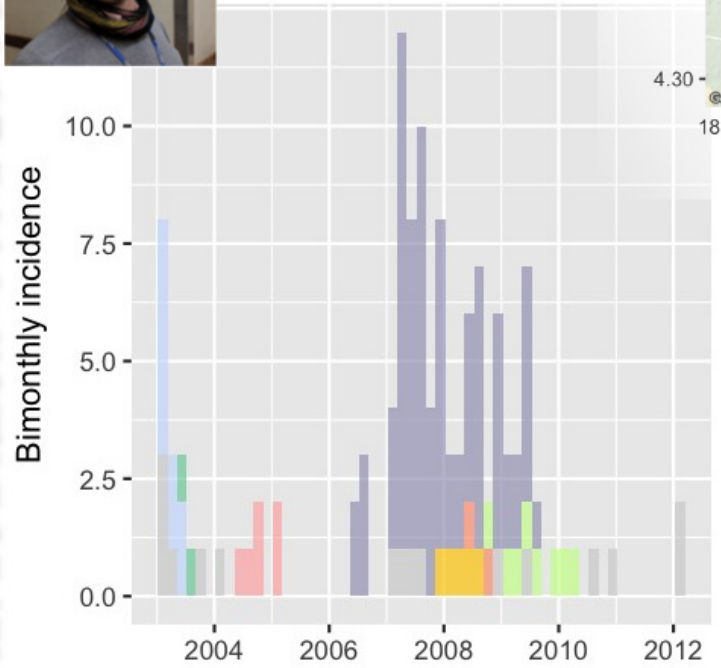
What does it look like in practice?

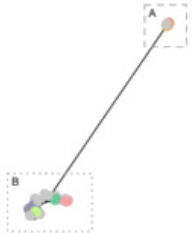
Application: dog rabies epidemics, Central African Republic

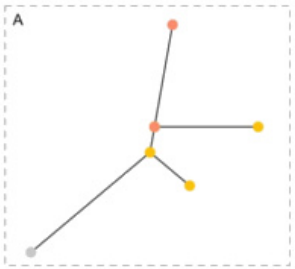
Anne Cori
Imperial College London

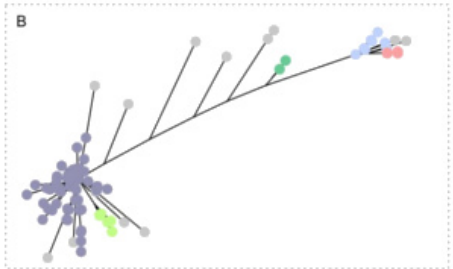
Pierre Nouvellet
University of Sussex



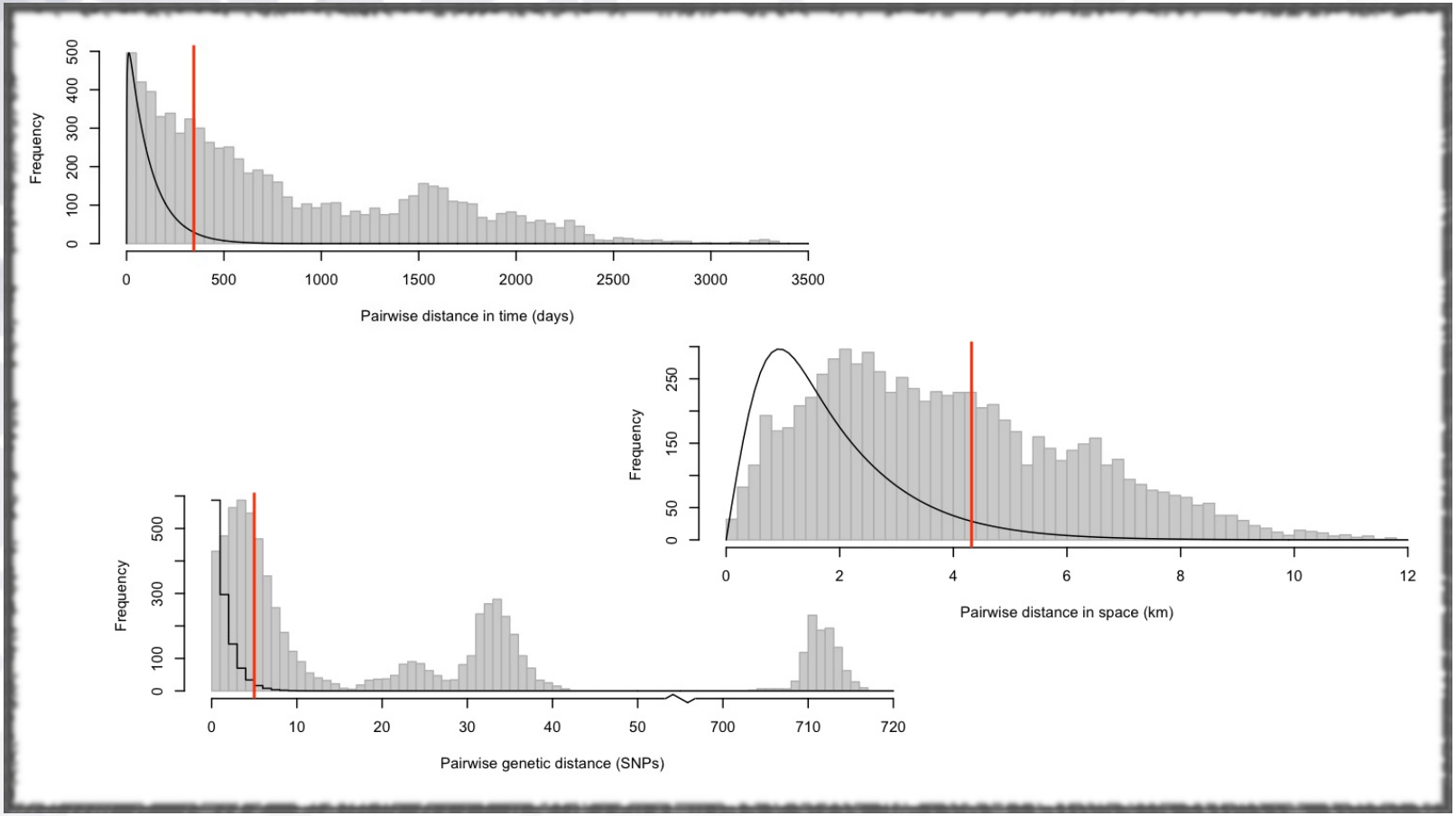




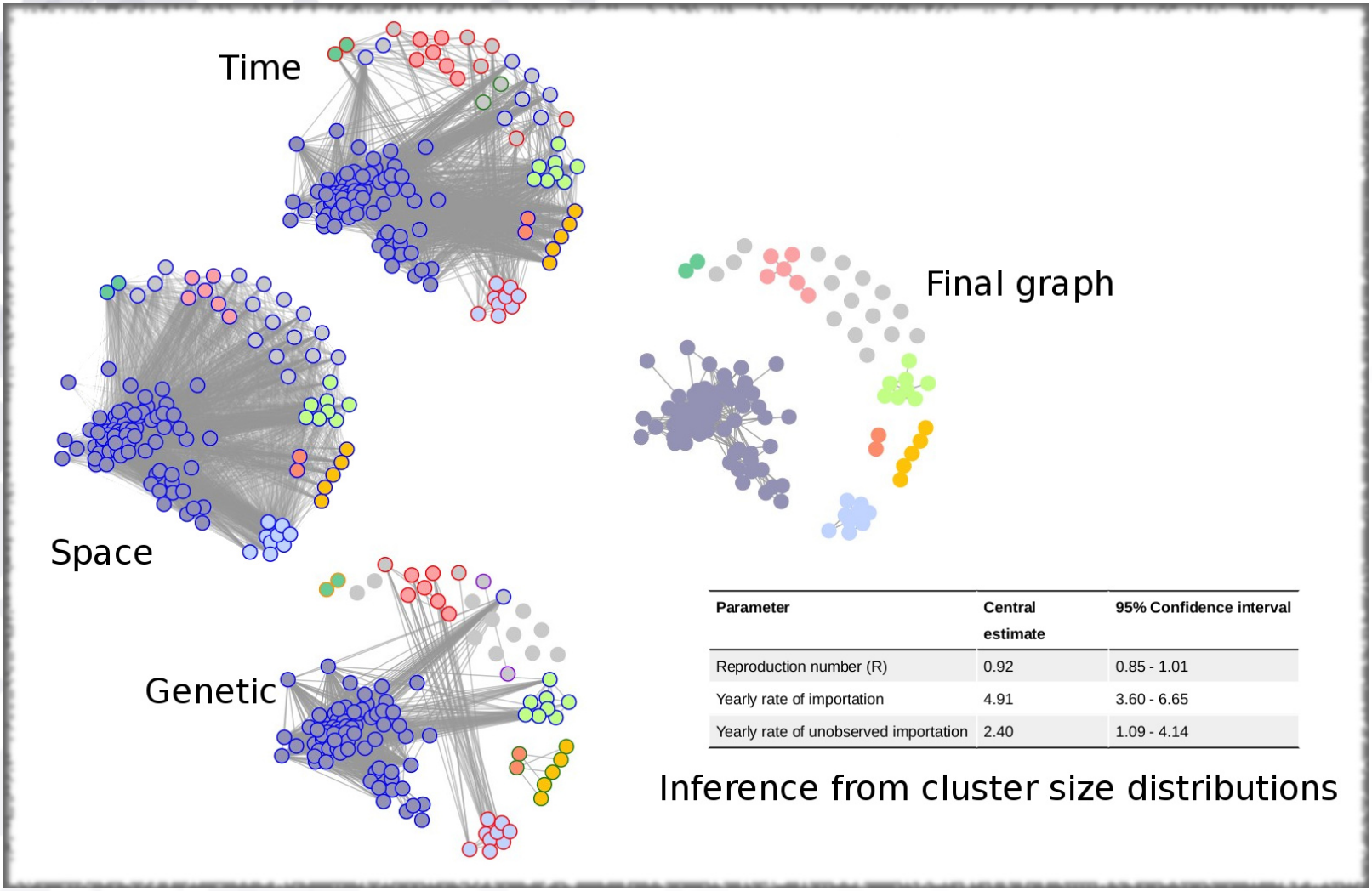




Distributions of distances between cases



Results



Parameter	Central estimate	95% Confidence interval
Reproduction number (R)	0.92	0.85 - 1.01
Yearly rate of importation	4.91	3.60 - 6.65
Yearly rate of unobserved importation	2.40	1.09 - 4.14

Inference from cluster size distributions

What's the take home message?

Summary

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- can integrate different data sources to detect outbreak clusters
- need arbitrary threshold: unsatisfying, but sensitivity study easy
- is fast, and can integrate data pipelines easily

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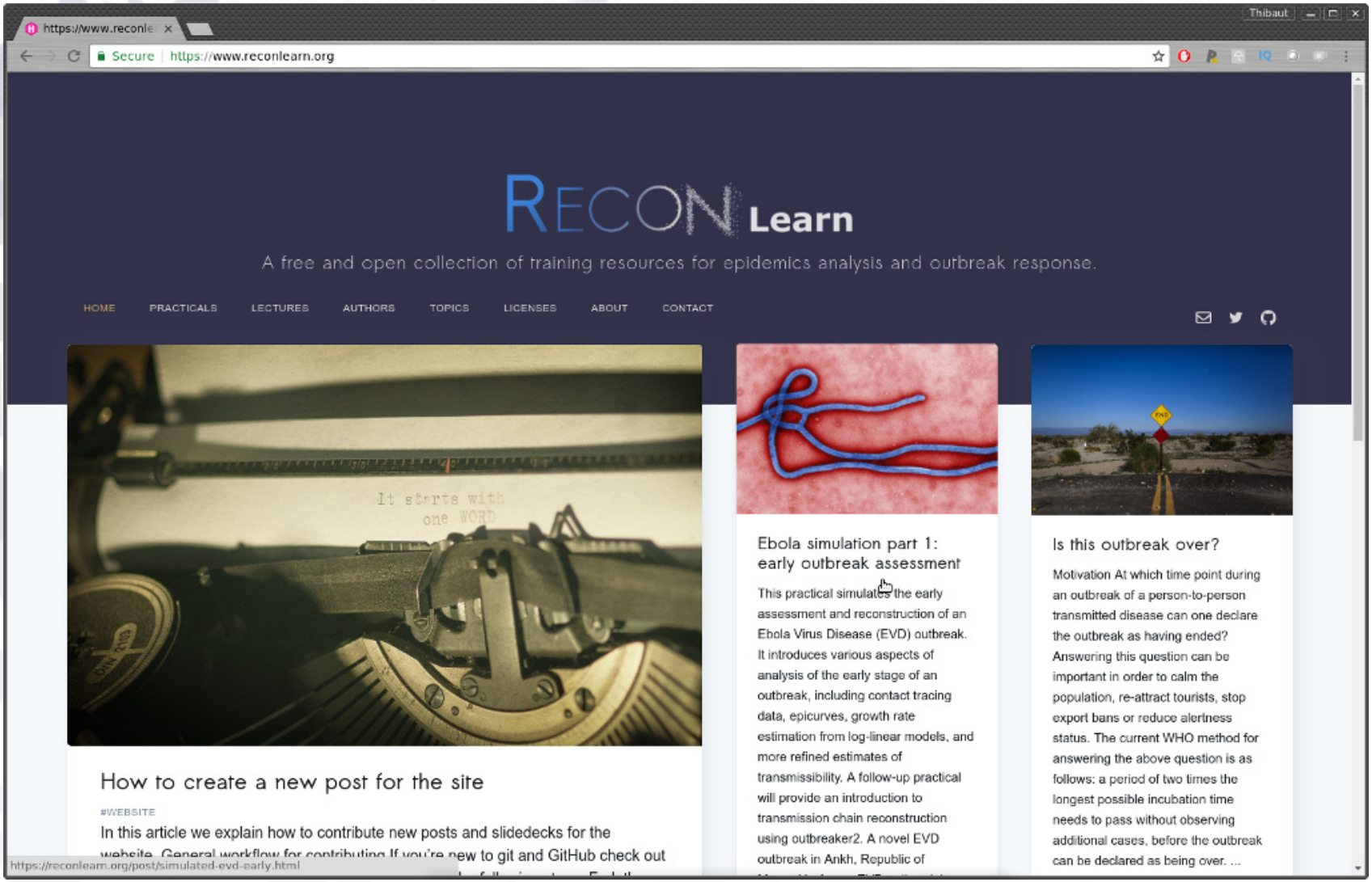
On our TODO list:

- integration in genomic surveillance systems (PHE)
- improve scalability (sparse matrices)
- objective criteria for automated threshold selection

Tutorials and lectures on this coming soon on...

RECON learn 2.0 (freshly online!)



www.reconlearn.org

Thanks

- **Conference organisers**
- **Colleagues:** Anne Cori, Pierre Nouvellet, Tini Garske, Hervé Bourhy, Emmanuel Nakouné
- **funding:** HPRU-NIHR, MRC

vimes

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