Genetic Networks

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The genetic architecture of ecosystems

Genetic connectivity and structure within and between populations.

Studying genetic spatial variation is important for making informed decisions in conservation management efforts.

But what features can we study from it?

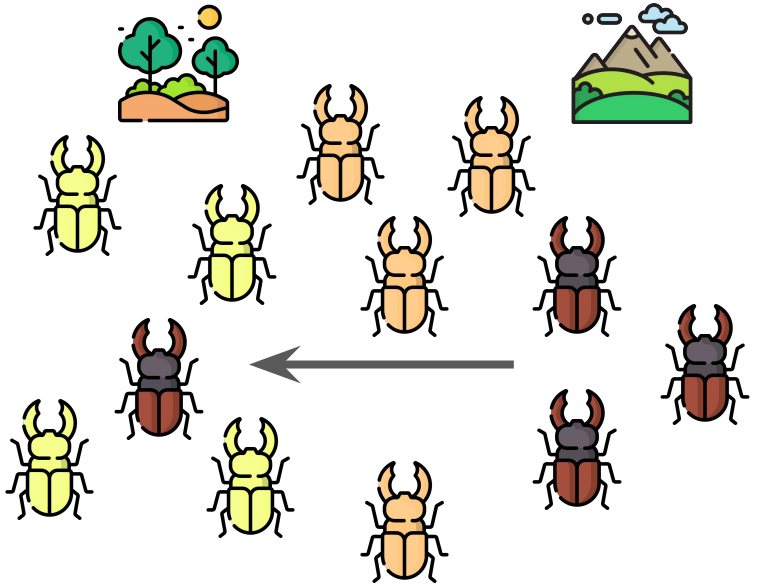
What processes shape it?

Basic concepts

Dispersal: movement of individuals from one location to another.

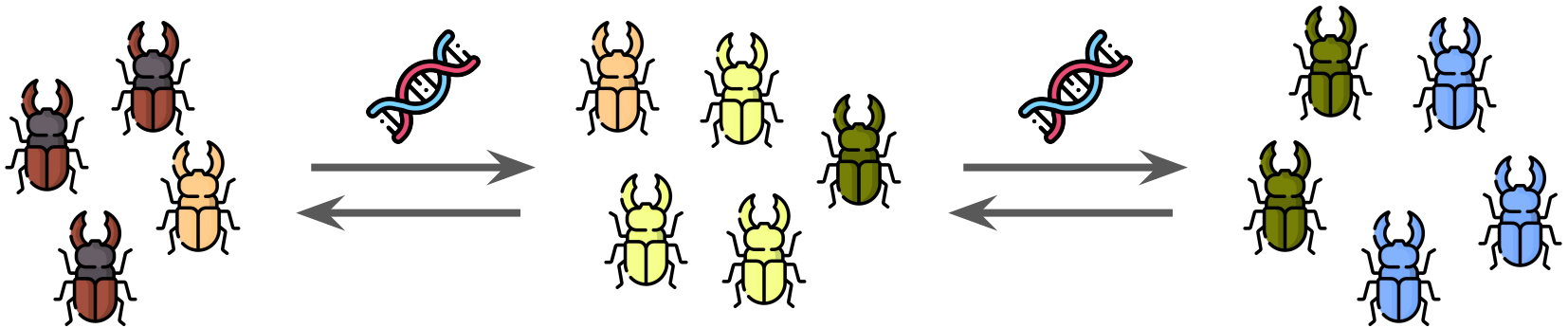
It can occur through a variety of mechanisms

- flight
- swimming
- movement of seeds or spores.



Basic concepts

Gene flow: movement of genes between different populations of the same species. Usually involves reproduction.



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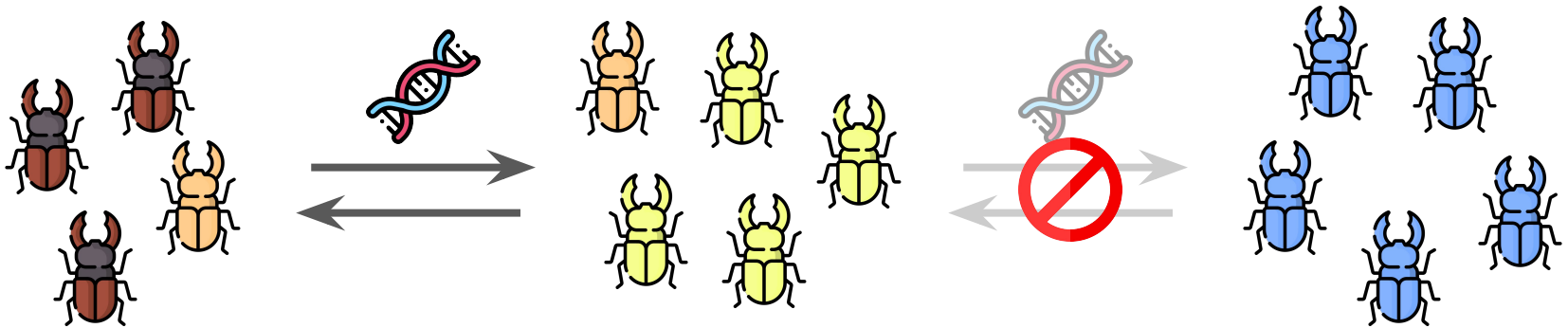
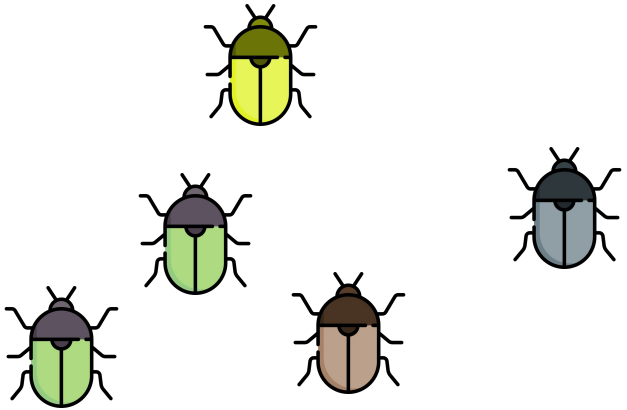


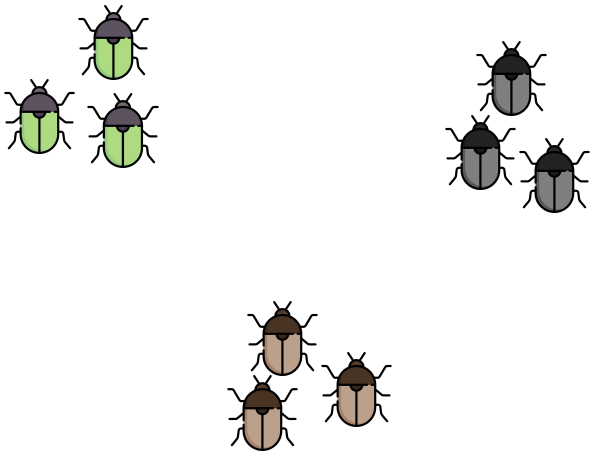
The genetic architecture of ecosystems

Different biological scales for genetic relatedness.

individual



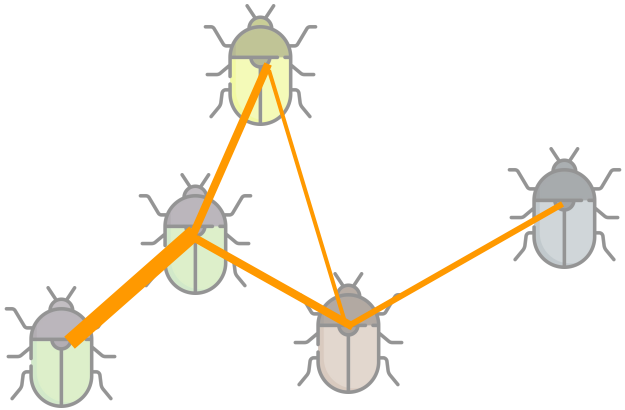
population



‘Genetic networks’

Different biological scales for genetic relatedness.

individual



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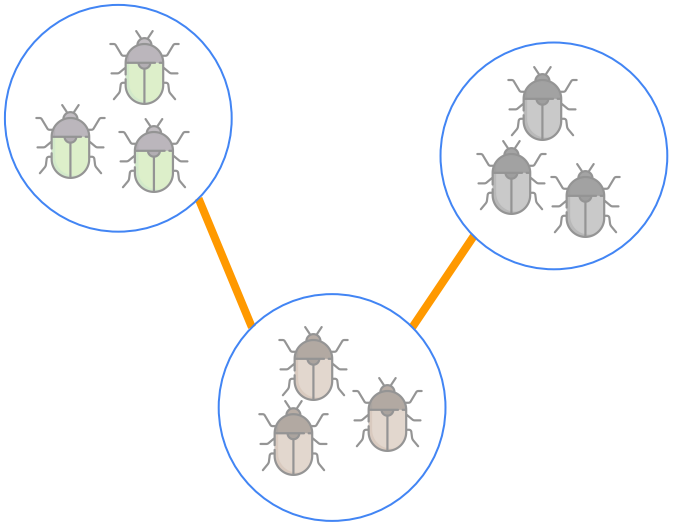
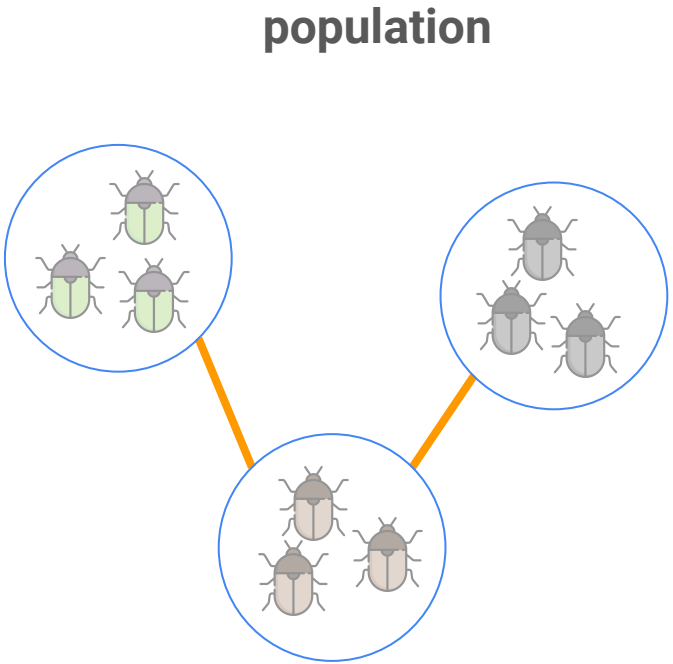


Population-based

Genetic networks

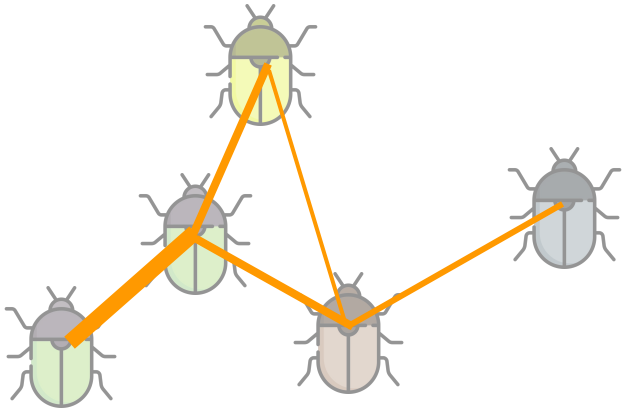
Useful for studying gene flow.

Advantage: no a priori assumptions about metapopulation structure.

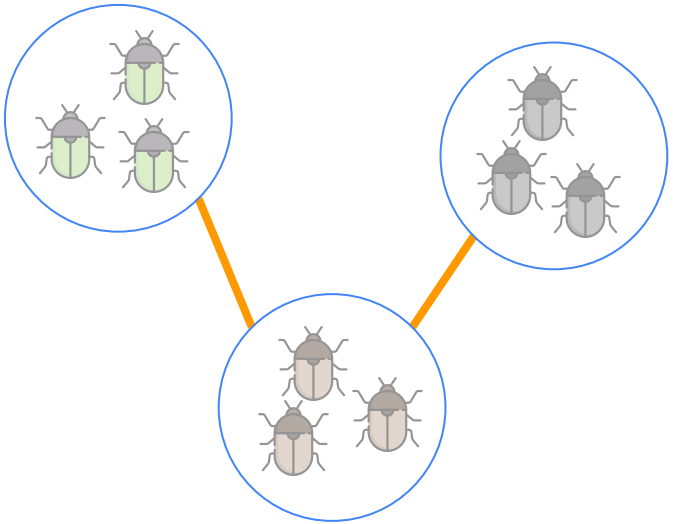


Genetic networks

individual

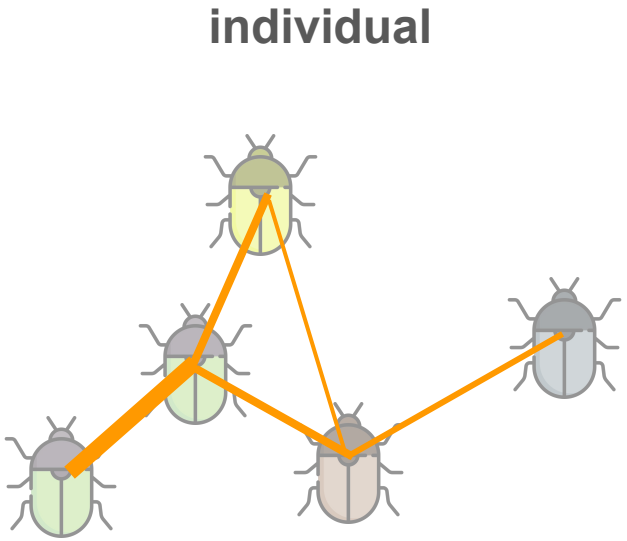


population



Individual-based

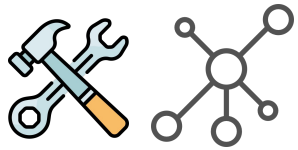
Genetic networks



Useful for studying dispersal.

More definition, less bias

Network Construction



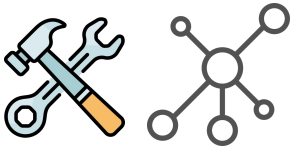
Genetic data: the raw material for building the networks.

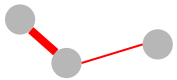
Useful for estimating relatedness

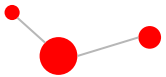
- Microsatellites
- SNPs

Forster et al. 2015

Network Construction



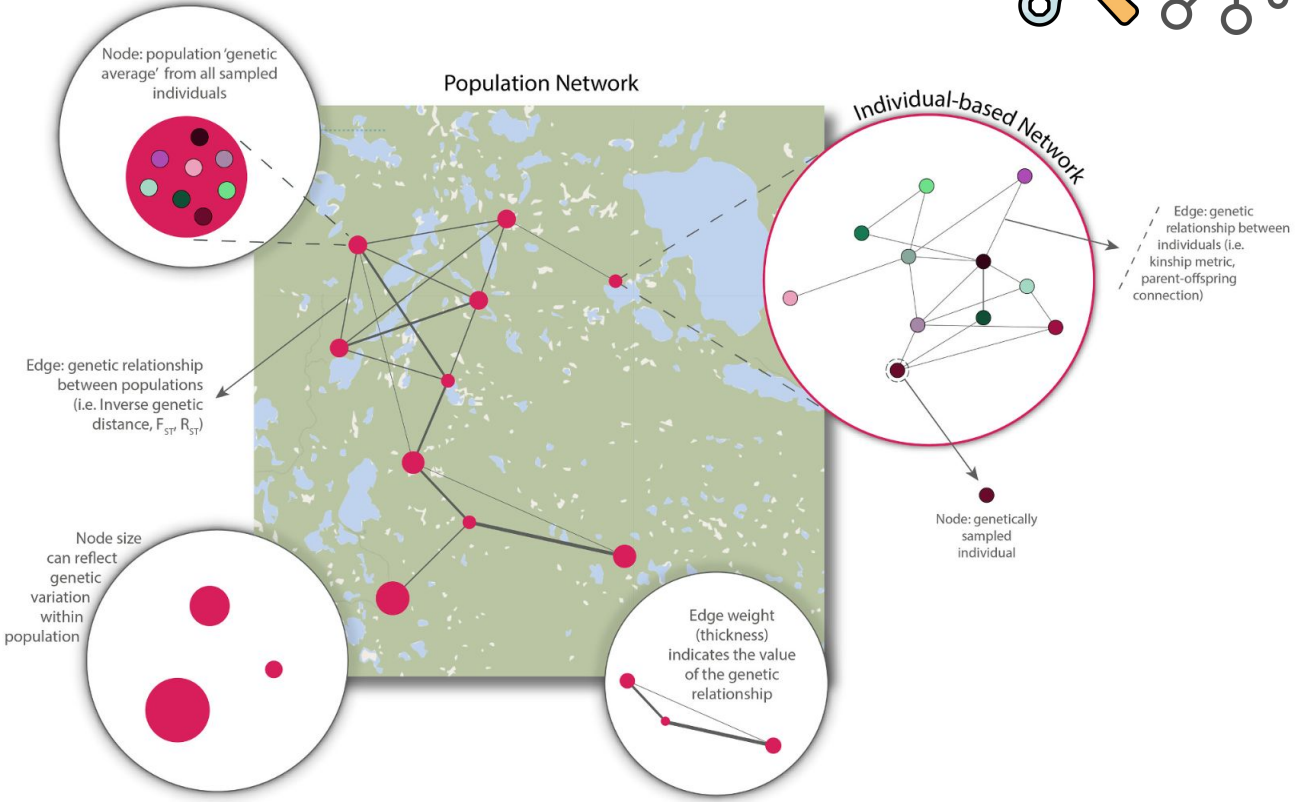




	Population network	**Individual network**
Node	Genetic average of a sampling location.	Individual or clonal unit.
Edge weights	Genetic covariance between populations.	Relatedness (many different measures).
Node weights	Genetic covariance within the population.	-

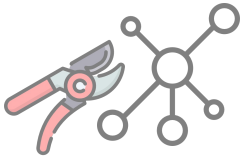
Network Construction

Summary



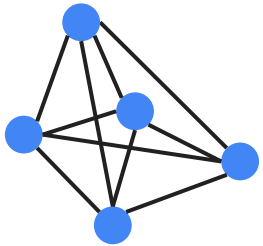
Jones, T. B., & Manseau, M. (2022). Genetic networks in ecology: A guide to population, relatedness, and pedigree networks and their applications in conservation biology. *Biological Conservation*, 267, 109466.

Network Pruning



All nodes are similar to some degree → Fully connected network

To perform topological analyses we want to keep only meaningful links.



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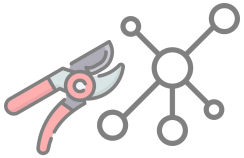

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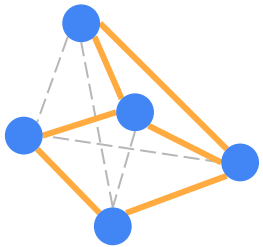
BUT

What does ‘meaningful’ mean?



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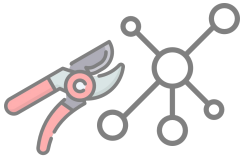


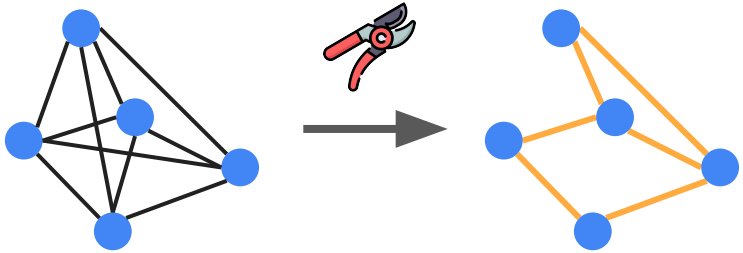
different strategies → different resulting topologies

Population-based

- Minimum covariance
- Percolation point
- Fixed threshold

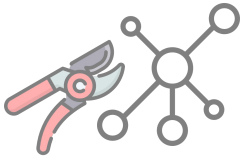
Individual-based

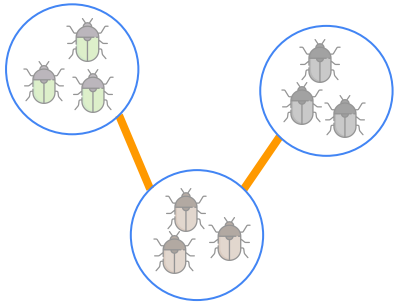
- Fixed threshold



Population-based

Network Pruning



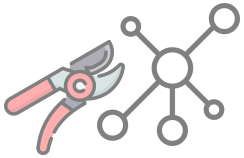


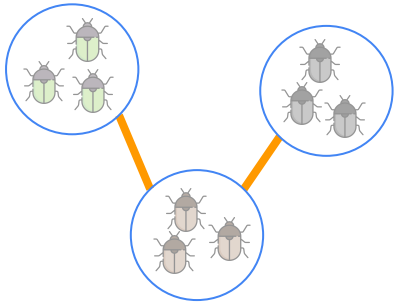
- Minimum covariance
- Percolation point
- Fixed threshold

Minimum set of links explaining total genetic variation among the populations.

Population-based

Network Pruning





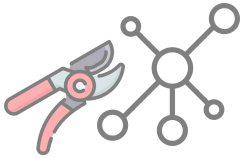
- Minimum covariance
- Percolation point
- Fixed threshold

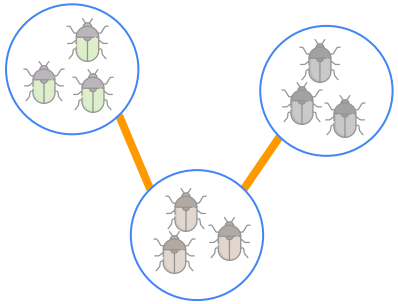
Sequentially remove low similarity links until a percolation point is reached.

The point after which the network splits into two smaller components.

Population-based

Network Pruning





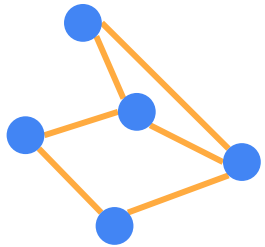
- Minimum covariance
- Percolation point
- Fixed threshold

Remove all links lower than a particular value.

Network analysis

Different approaches:

- Network metrics (incl. modularity)
- Incorporate landscape features to nodes
- Multilayer analysis



Population-based

Incorporating spatial features

Used for determining dispersal probability across the network.

Common for population-based networks.

Landscape information:

- Resistance surfaces
- Spatial distance

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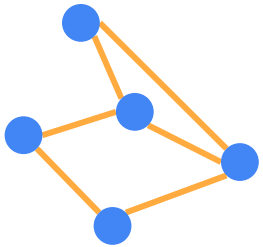
Network analysis - Hypothesis testing

- Null models
  - Random rewiring (edge swap)
  - Random re-weighting
- Assortativity coefficient: test for gene-flow barriers in the network
- Mantel Test:
  - Correlation Genetic distance ~ Physical distance
  - Compare layers in a multilayer network.
  - Compare edge weights with other measures.



Conservation Applications

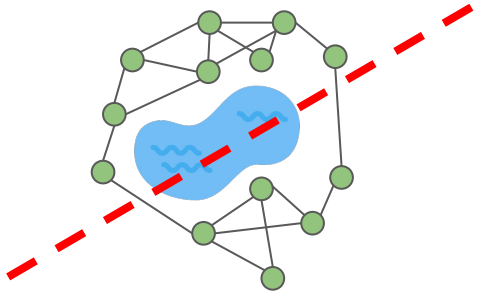
Metapopulation structure → identify genetic units for planning management

Population structure → identify dispersal

Conservation Applications - Dispersal

Assortativity coefficient: checks if nodes with similar attributes are connected.

Useful to identify geographical barriers.



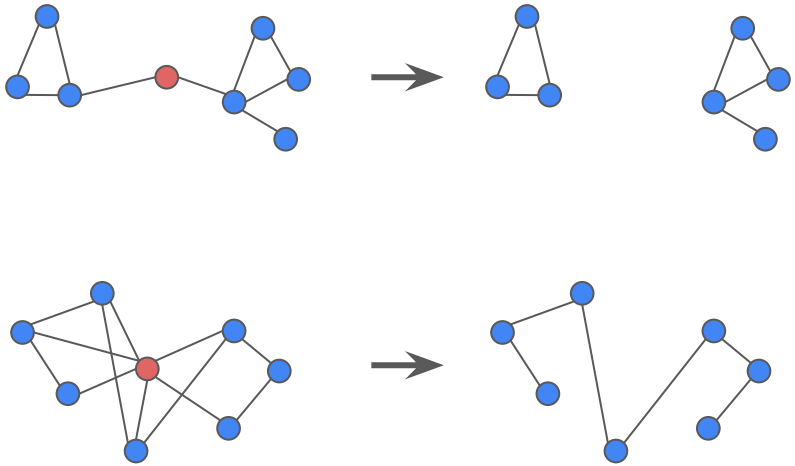
Suspected barrier

Conservation Applications - Gene Flow Structure

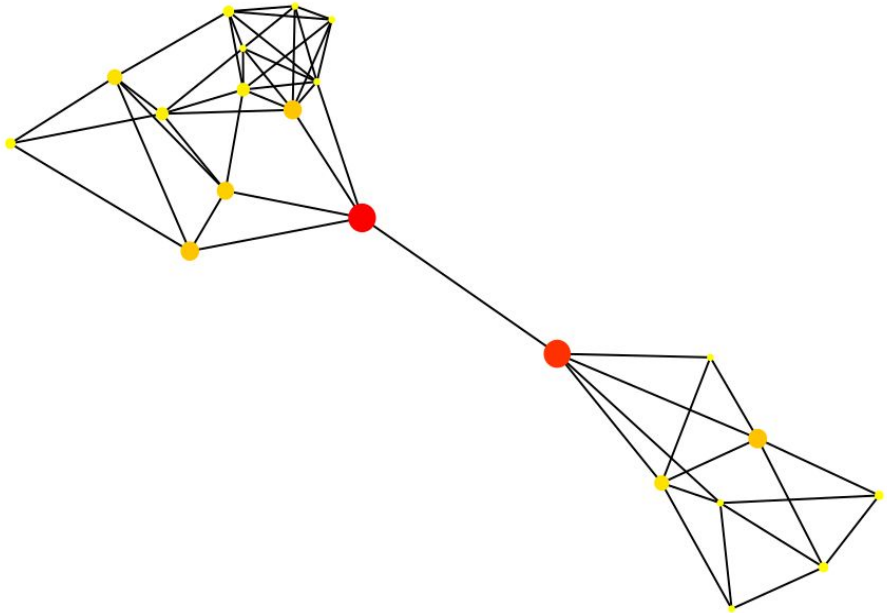
Genetic connectivity → studying gene flow

There are different types of keystone nodes:

- ‘bridge nodes’
- ‘hub nodes’

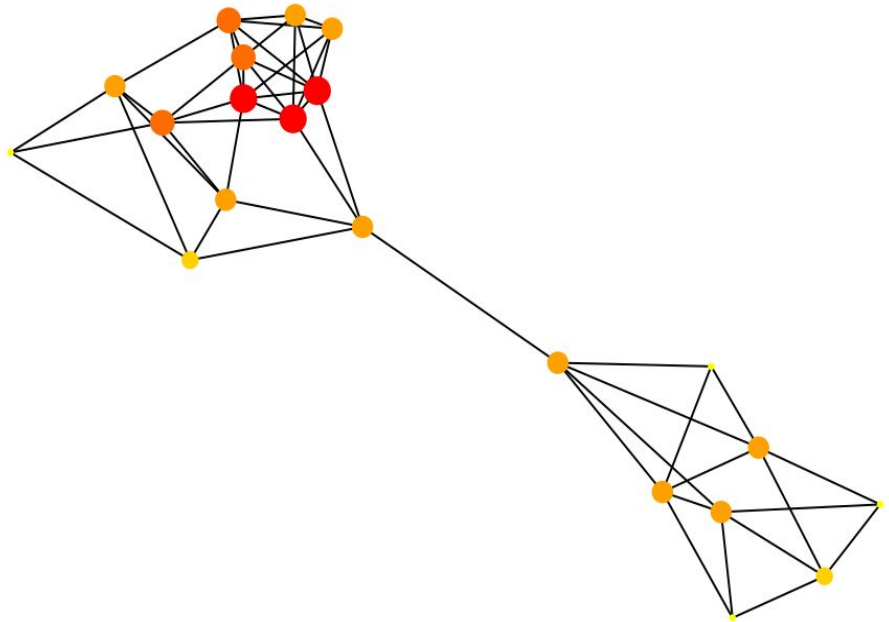


Conservation Applications - Gene Flow Structure



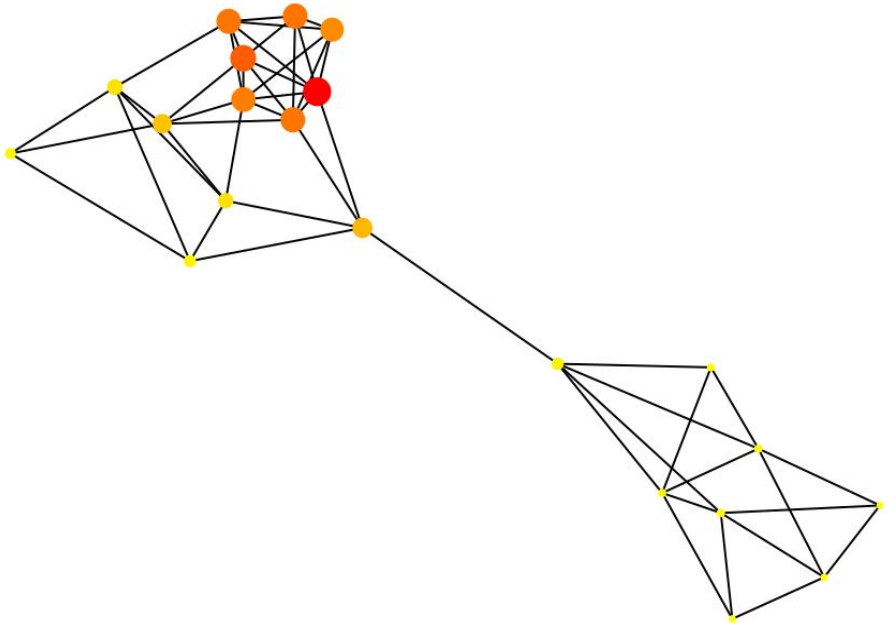
Betweenness centrality
to identify ‘bridge nodes’

Conservation Applications - Gene Flow Structure



Node degree to identify
‘hub nodes’

Conservation Applications - Gene Flow Structure

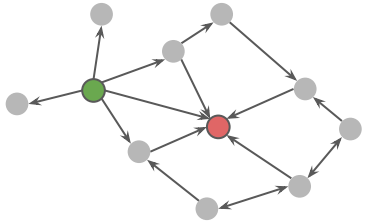


Eigenvector centrality to identify ‘hub nodes’

Conservation Applications - Source/Sink Dynamics

Direction of gene flow → targeted conservation efforts

Source and **sink** nodes in the metapopulation



Conservation Applications - High Fitness Families

Multilayer network (population/region + individual) helps to identify:

- highly connected families
- regions of high reproductive output

This gives clues to detect:

- asymmetric breeding
- potential source and sink regions

References & acknowledgements

- Jones, T. B., & Manseau, M. (2022). Genetic networks in ecology: A guide to population, relatedness, and pedigree networks and their applications in conservation biology. Biological Conservation, 267, 109466.
- Dyer, R. J., & Nason, J. D. (2004). Population graphs: the graph theoretic shape of genetic structure. Molecular ecology, 13(7), 1713-1727.

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