

My research as of 2015-04-16

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Research question

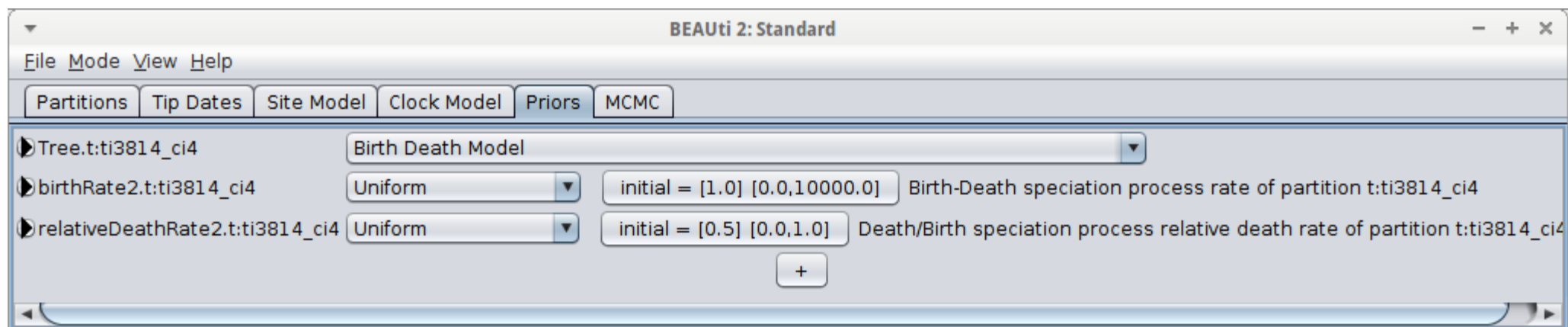
- How do species assemblages form?
- How can DNA sequences help in increasing our understanding of this process?
- Why DNA?
 - DNA is measured in huge quantities nowadays
 - Creates better phylogenies than a single trait (Pigot & Etienne, 2015)
- Which parameters?
 - Speciation and extinction rate
 - Migration rates
 - Number of species 'carrying capacity'
 - Geographical distribution/situation

Possibilities

- Extend joint inference?
- Extend individual-based models?
- Lineage-based modeling?

Joint inference

- Conclude a phylogeny hand-in-hand with the parameters that affected the phylogeny creation
- Uses a Bayesian approach
- Some models implemented in BEAST2
 - I could add more

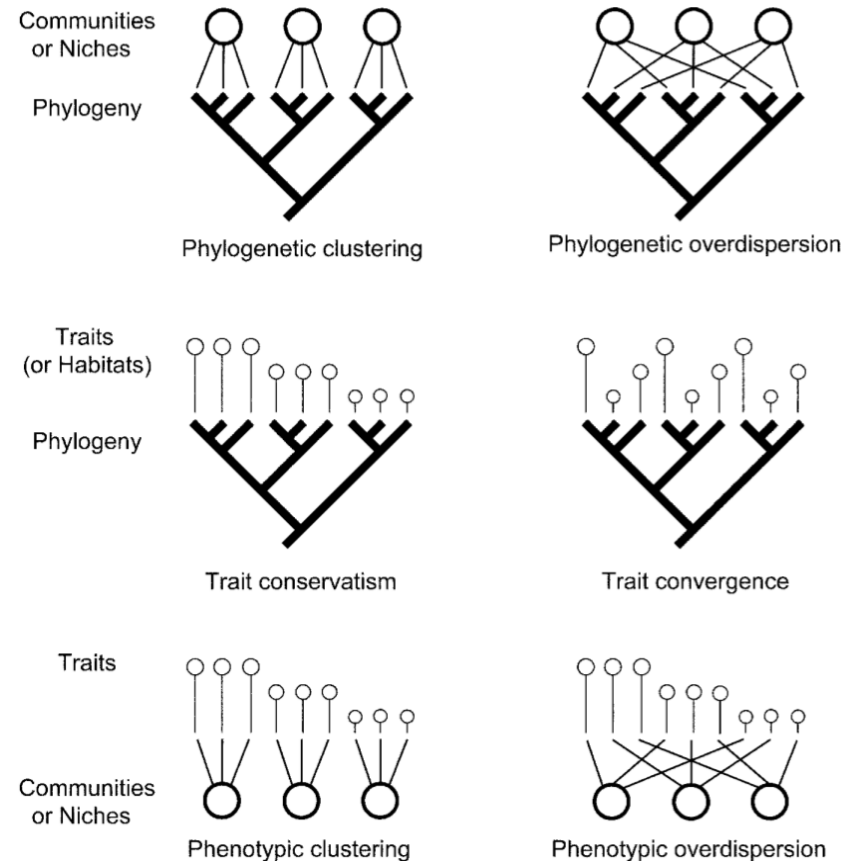


Individual-based modeling

- Use existing models, give all individuals DNA. Redo the analysis with DNA. Will the results be the same?
 - Null hypothesis: yes
- Models to expand
 - Webb et al., 2002: competition versus habitat filtering
 - Avise et al., 1987: biogeography
 - Ricklefs, 1987: species saturation
 - Rosindell & Etienne, 2015: protracted speciation
- Some other ideas
 - Nowak's superstar
 - Non-neutral DNA

Webb et al., 2002

- Competition versus habitat filtering



Ecological traits phylogenetically

Conserved

Convergent

Dominant ecological force:

Habitat filtering (phenotypic attraction)

Clustered

Overdispersed

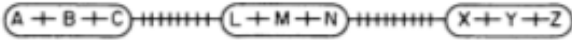
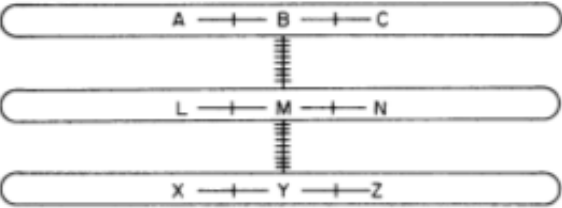
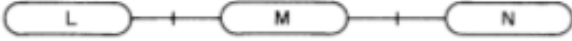
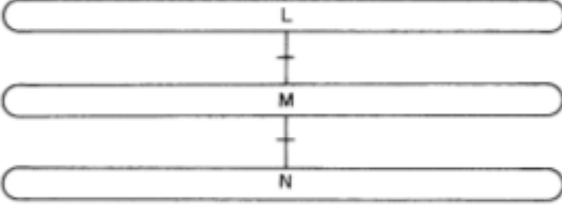

Competitive exclusion (phenotypic repulsion)

Overdispersed

Random

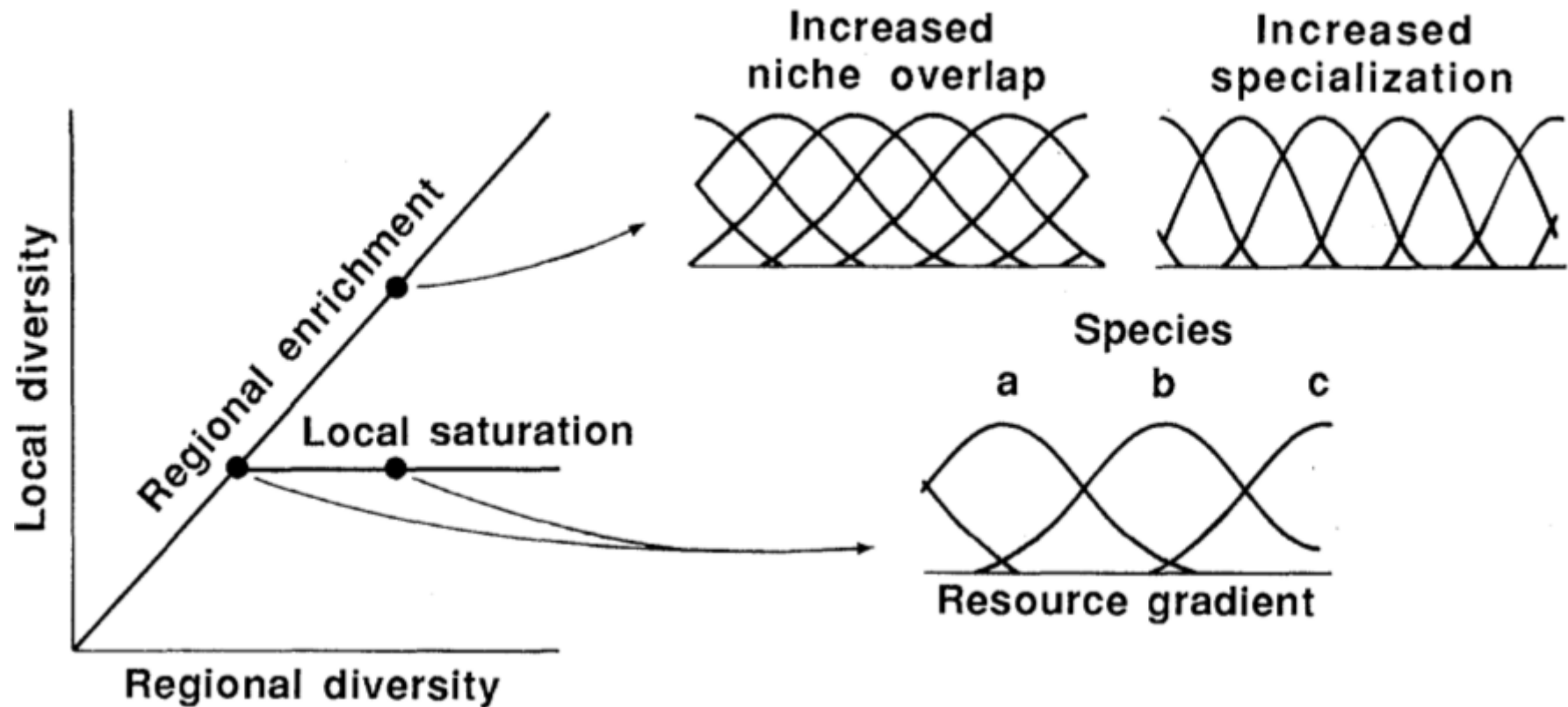
Avise et al., 1987

- Phylogeography

CATEGORY	GENETIC DIVERGENCE PATTERN	GEOGRAPHIC DISTRIBUTION			LIKELY EVOLUTIONARY CIRCUMSTANCE
		REGION 1	REGION 2	REGION 3	
I	discontinuous				<p>A) LONG-TERM EXTRINSIC (E.G. ZOOGEOGRAPHIC) BARRIERS TO GENE FLOW; AND/OR</p> <p>B) EXTINCTIONS OF INTERMEDIATE GENOTYPES IN SPECIES WITH LIMITED GENE FLOW.</p>
II	discontinuous				<p>A) RECENT, SECONDARY ADMIXTURE ZONES; OR</p> <p>B) INTRINSIC (E.G. REPRODUCTIVE ISOLATION) BARRIERS AMONG SYMPATRIC SIBLING SPECIES.</p>
III	continuous				LIMITED GENE FLOW IN A SPECIES NOT SUBDIVIDED BY LONG-TERM ZOOGEOGRAPHIC BARRIERS.
IV	continuous				VERY EXTENSIVE GENE FLOW IN A SPECIES NOT SUBDIVIDED BY LONG-TERM ZOOGEOGRAPHIC BARRIERS.
V	continuous				INTERMEDIATE GENE FLOW IN A SPECIES NOT SUBDIVIDED BY LONG-TERM ZOOGEOGRAPHIC BARRIERS.

Ricklefs, 1987

- Species saturation



Rosindell & Etienne, 2015

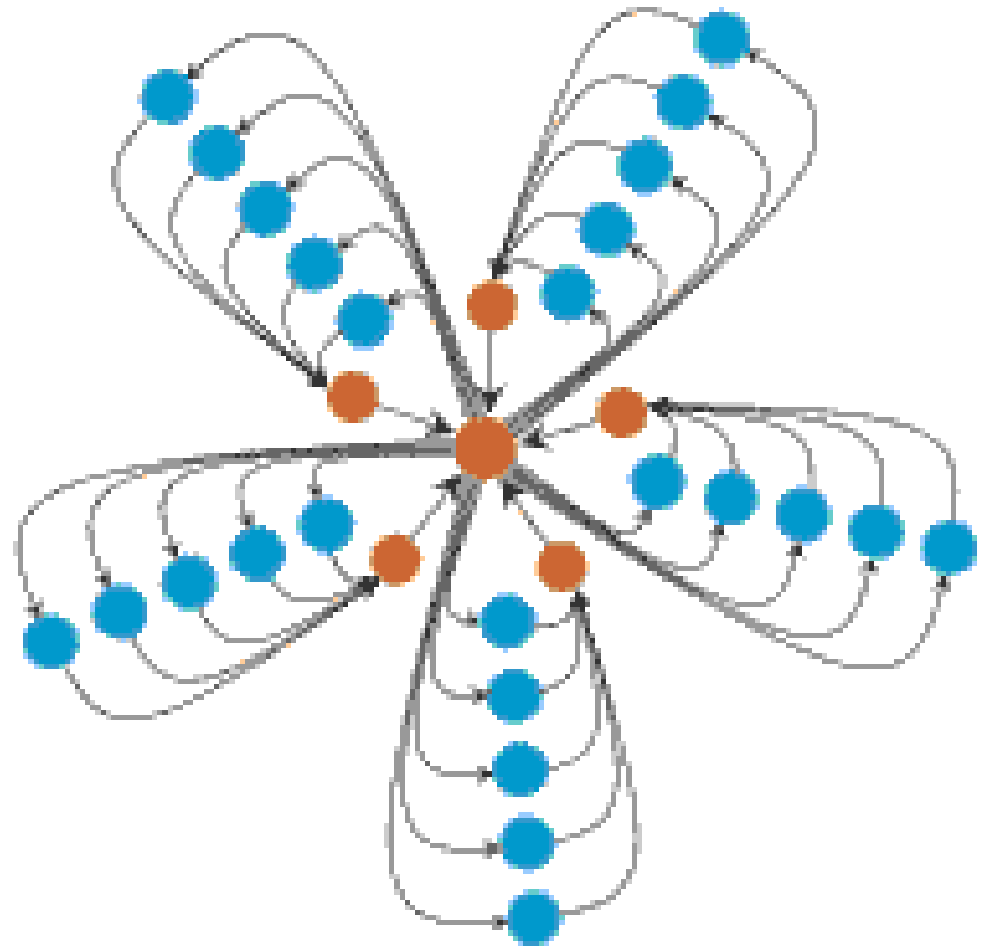
- Protracted speciation
- Incipient species become true species after n generations
- Extension:
 - Use DNA
 - DNA 0-97% similar: different species, no mating
 - 97-100% similar: same species, mating probability higher for high similarity

Non-neutral DNA

- Most DNA is assumed to be neutral towards a trait
- What if it is not?

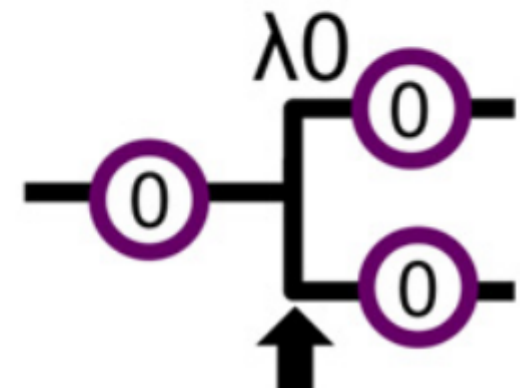
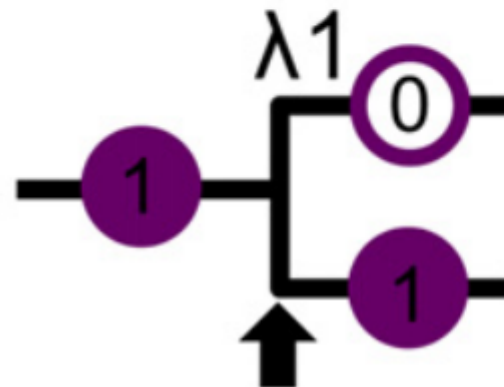
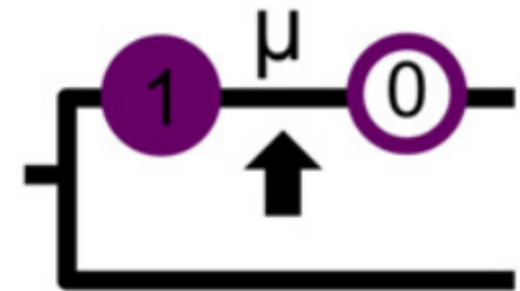
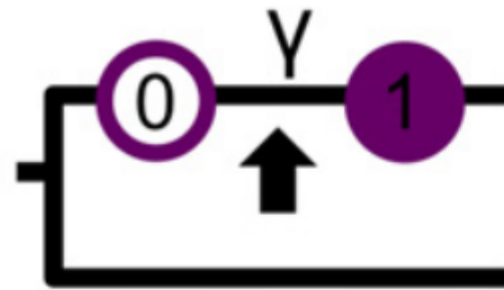
Nowak's graphs

- Certain population structures (e.g. superstar) can amplify selection



Lineage-based modeling

- Create better null-phylogenies using better phylogeny construction model, like Pigot & Etienne, 2015
- No idea for another extension yet



Conclusion

- A lot can potentially be done
 - What is scientifically relevant?
 - What is scientifically novel?