Applications of EPIQUE tools for historians and philosophers of science: case studies and scientific change

Thibault RACOVSKI – IHPST, CNRS & Paris Pantheon-Sorbonne University

Outline

I – Case study: The phylomemy of biological research on evolutionary novelty

A - Methodological issues with doing the history of research on evolutionary novelty

B - The phylomemy of research on novelty, an illustration

II – The contribution of EPIQUE to the formulation and testing of theories of scientific change

I – Phylomemy of research on novelty

A - Methodological issues with doing the history of research on evolutionary novelty

Does evolutionary theory need a rethink?

Researchers are divided over what processes should be considered fundamental.

POINT

Yes, urgently

Without an extended evolutionary framework, the theory neglects key processes, say Kevin Laland *and colleagues.*

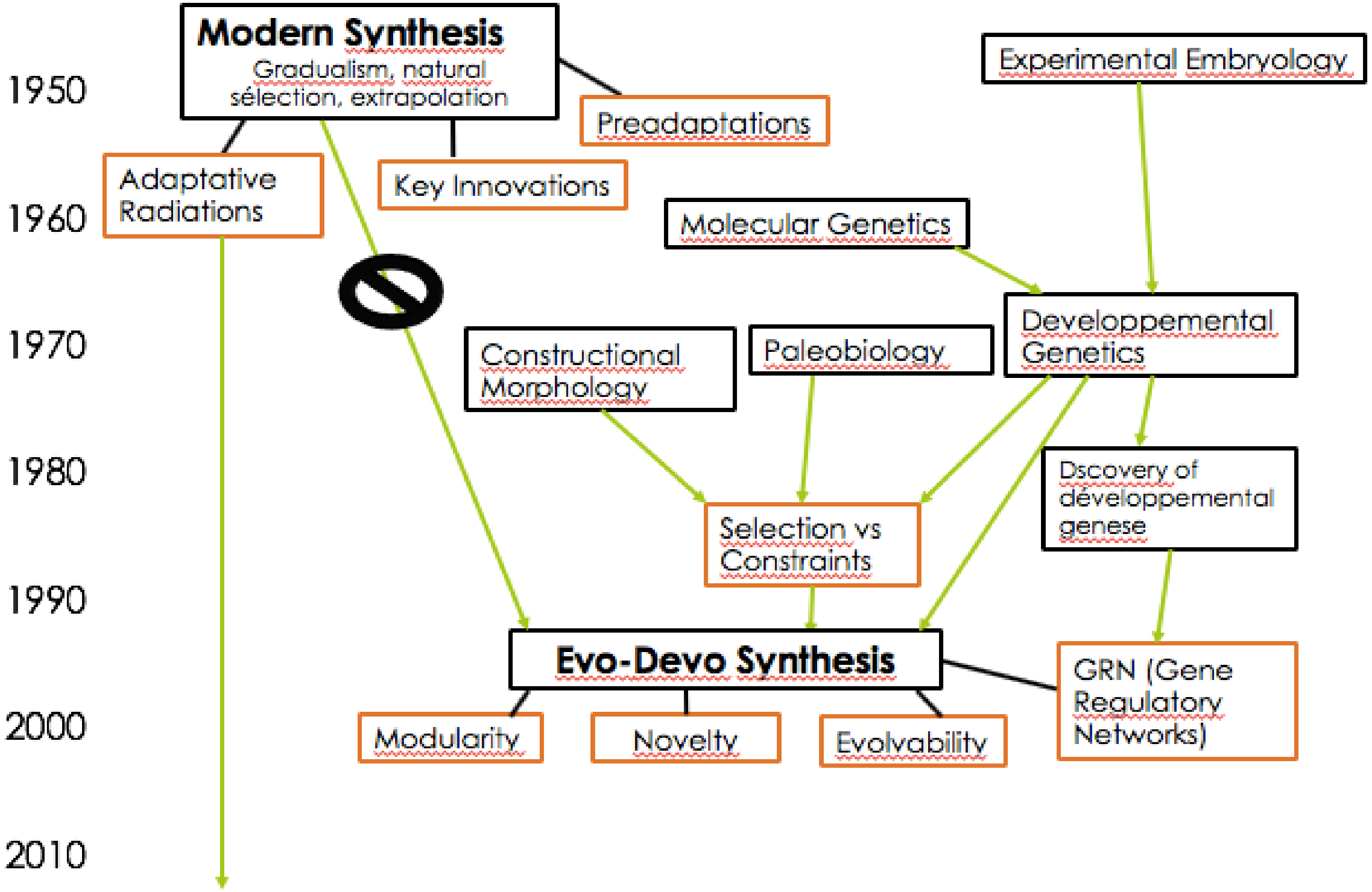
COUNTERPOINT

No, all is well

Theory accommodates evidence through relentless synthesis, say Gregory A. Wray, Hopi E. Hoekstra *and colleagues.*

The problem of the origin of novelty is currently embedded in a contemporary debate regarding the need for a paradigm shift in evolutionary biology that attracts a lot of attention from theoretical biologists and historians and philosophers of biology.

Overview of conceptual change in evolutionary biology in the last 70 years (the received view)



What is the relationship between the evolution of theoretical debates and the evolution of the whole novelty research landscape?

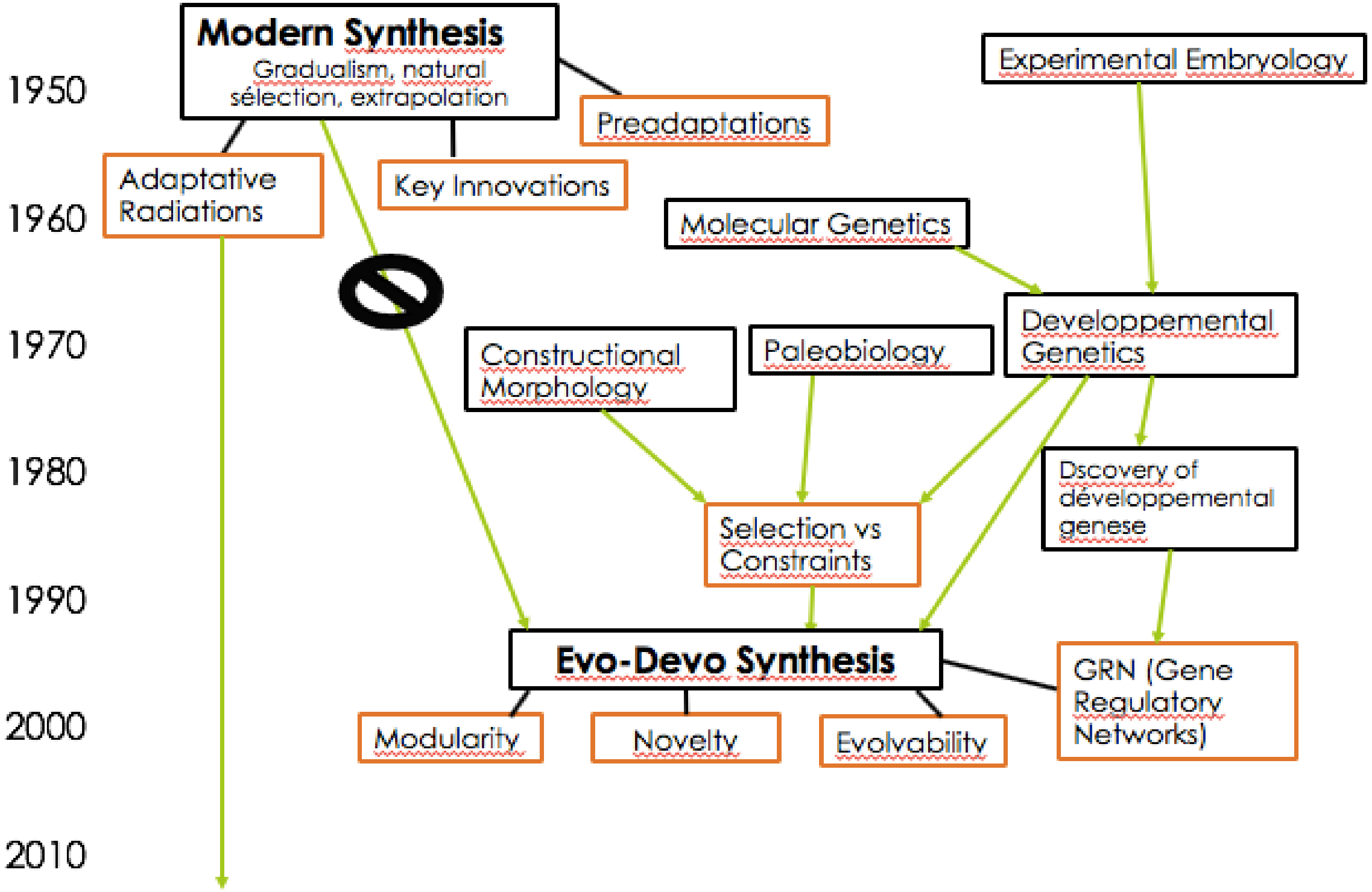
- How widely and at what pace do new concepts from the theoretical litterature spread (e.g. evolvability, modularity)?

- Do theoretical oppositions overshadow shared conceptual background and research practices?

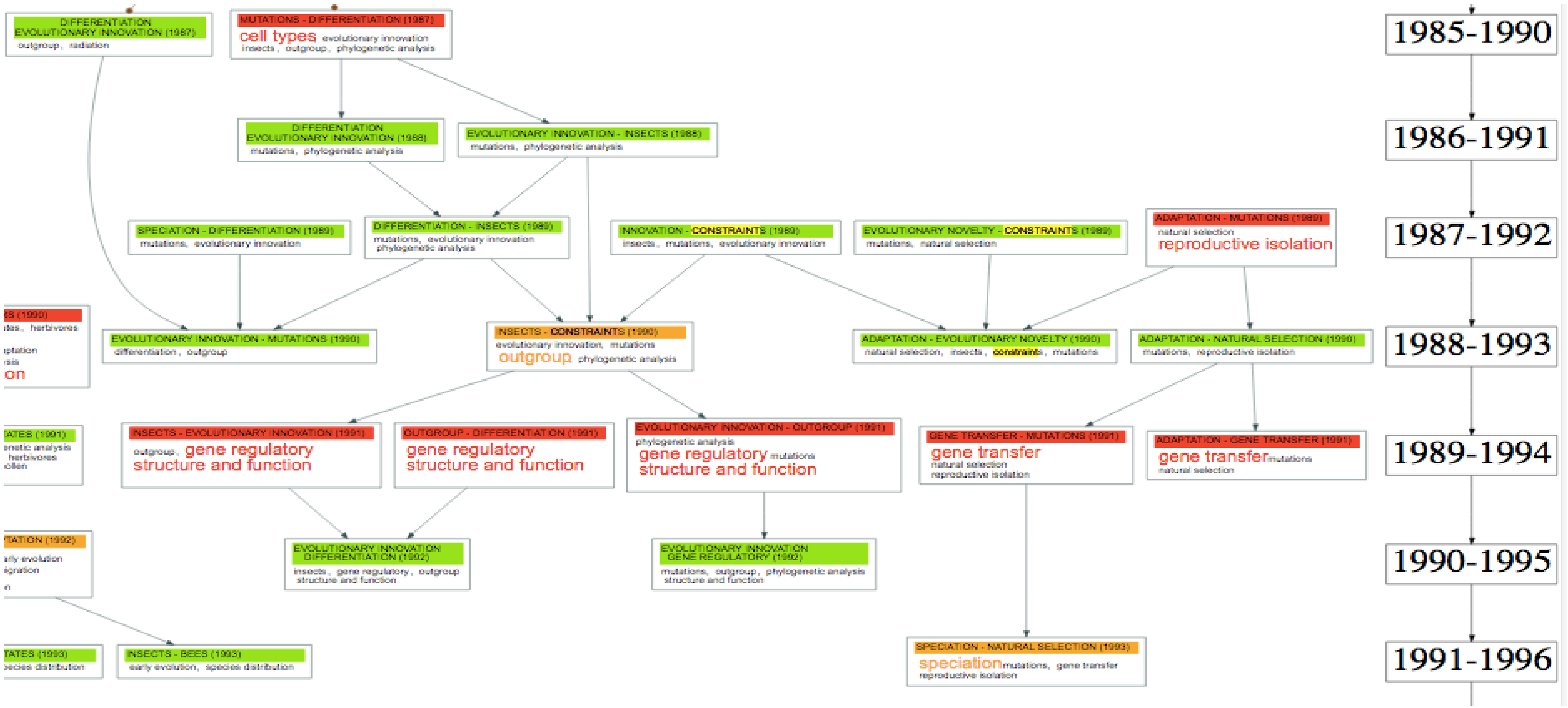
Historical hypotheses that can be tested with the phylomemetic analysis of a large corpus

- The decline of the research programs on adaptive radiations.
- The decline of the concept of preadaptation and the rise of the concept of exaptation from the 1980s
- The decline of the use of the concept of constraint from the 1990s onwards.

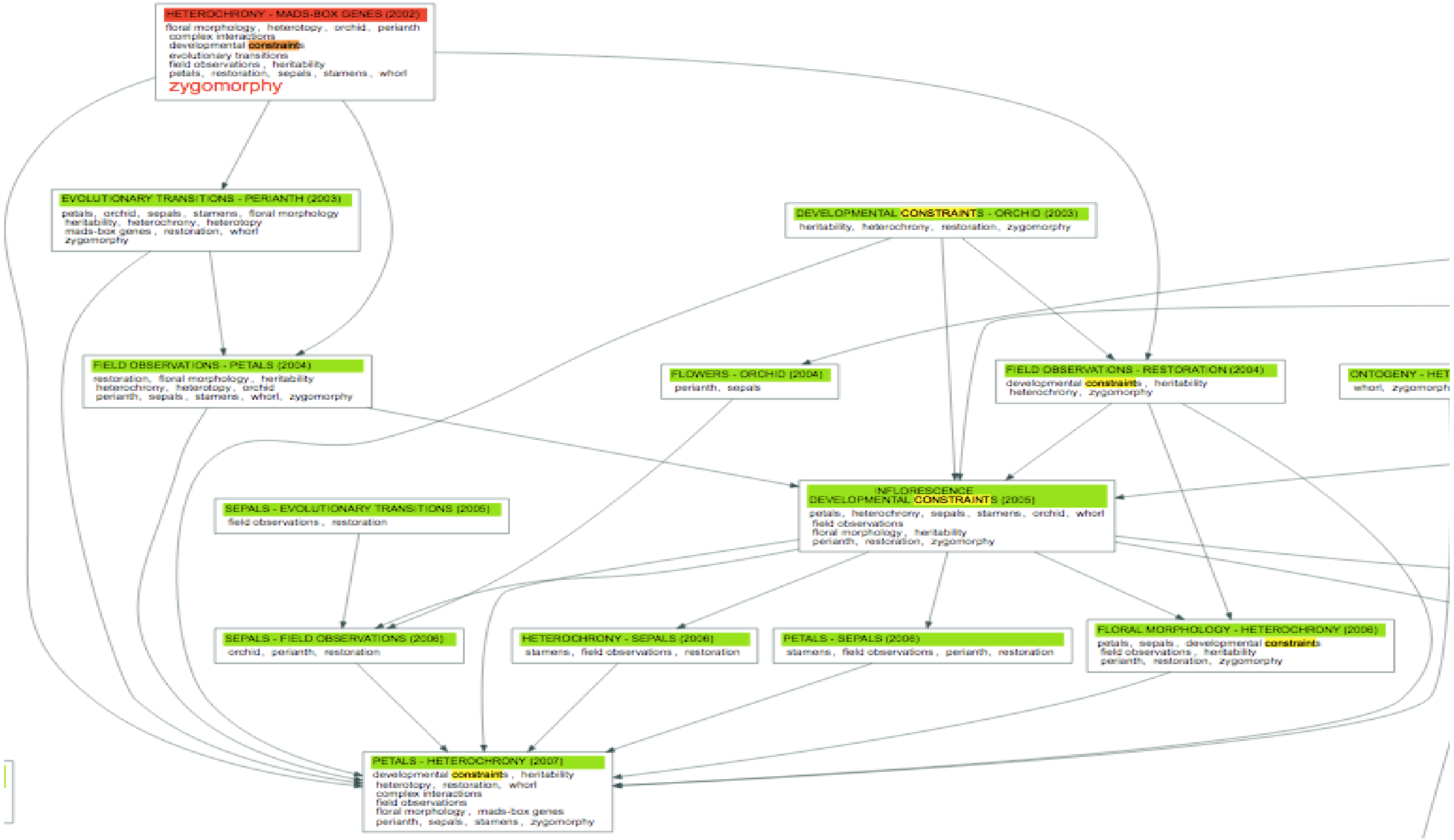
Illustration: the fate of the concept of constraint



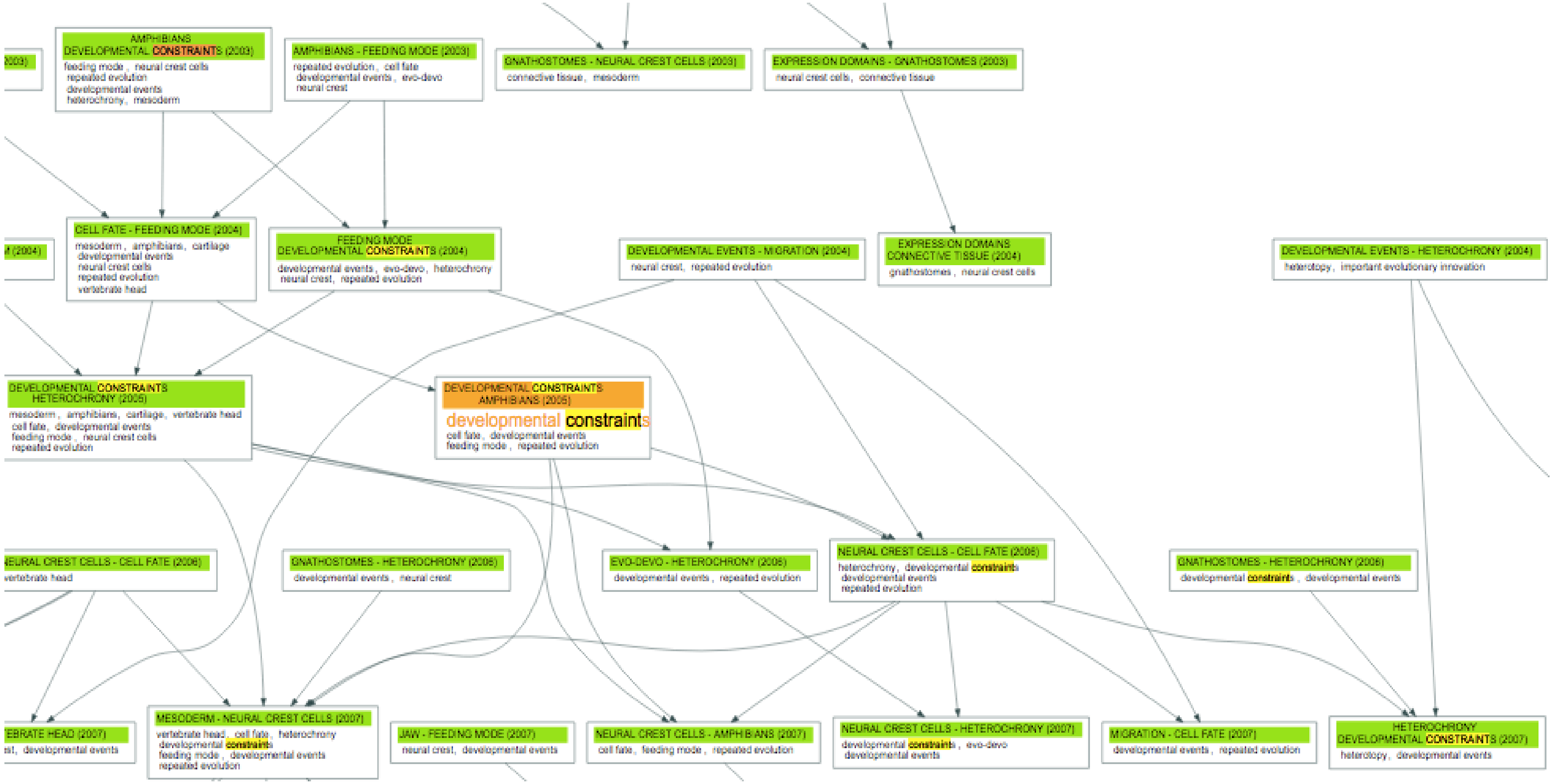
Constraint in the phylomemy



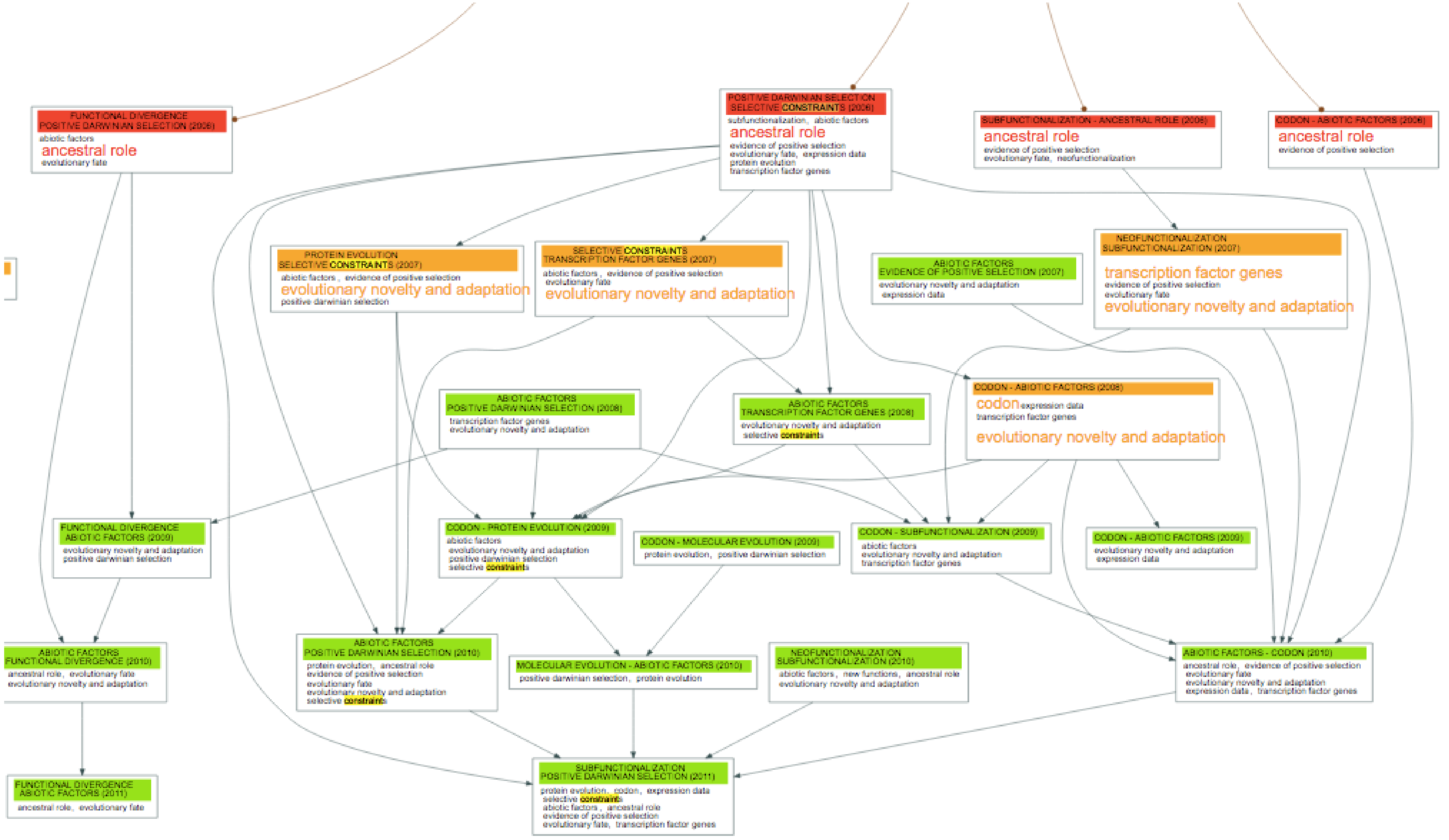
“Developmental constraint” is present in a branch (2002-2007) which captures a research program on the evolutionary developmental biology of the flower.



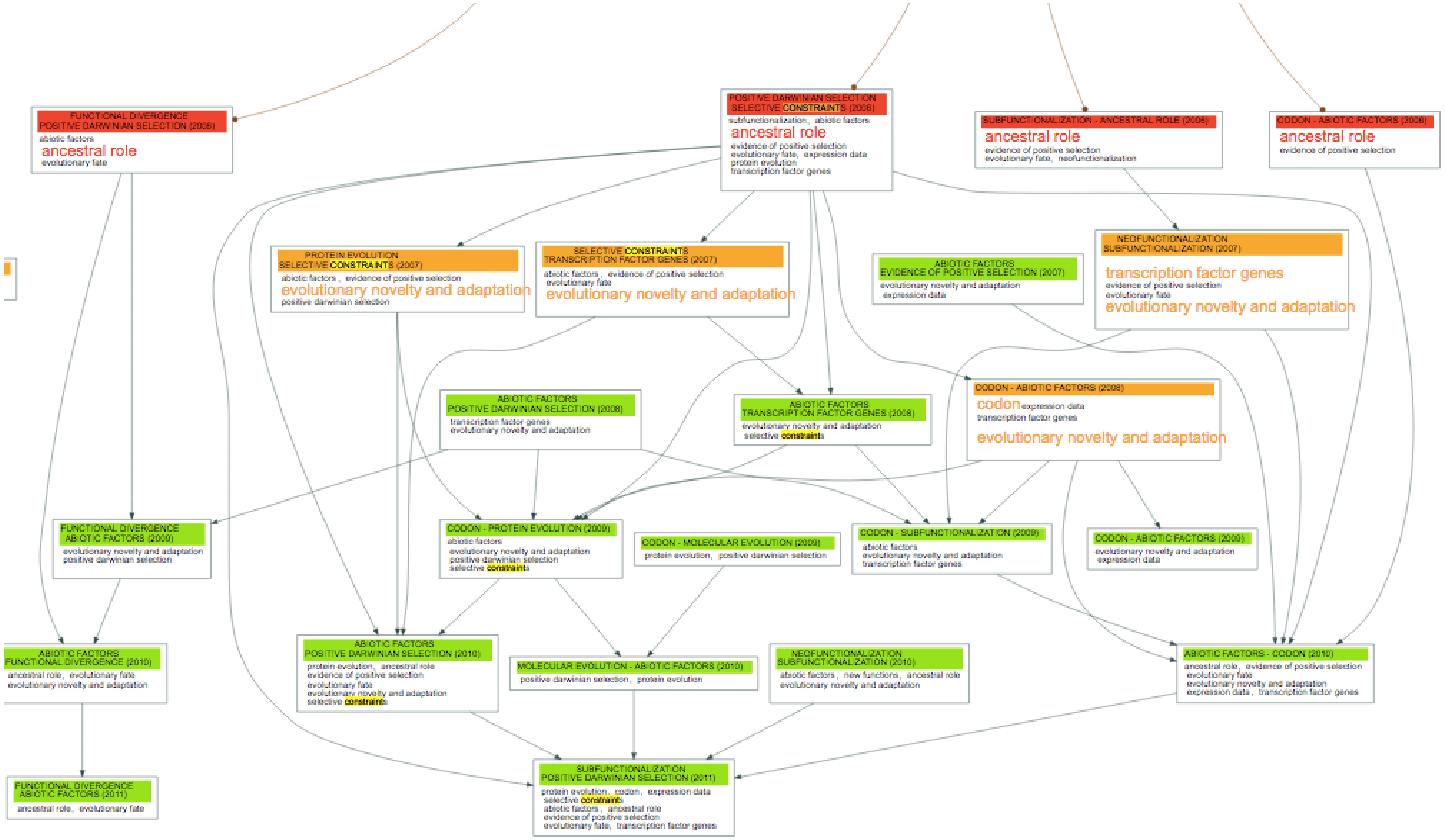
“Developmental constraint” is present in the branch entitled “Neural crest cells Vertebrate head”(2003-2007) which captures research programs on the evolutionary developmental biology of the vertebrate head and jaw.



“Selective constraint” is present in a branch (2006-2011) which captures research programs in genome evolution.



“Structural constraint” is present in a branch (2003-2008) which captures a research program on protein evolution.



- The phylomemy helps establish a fine-grain map of the evolution of the uses of the concept of constraint.

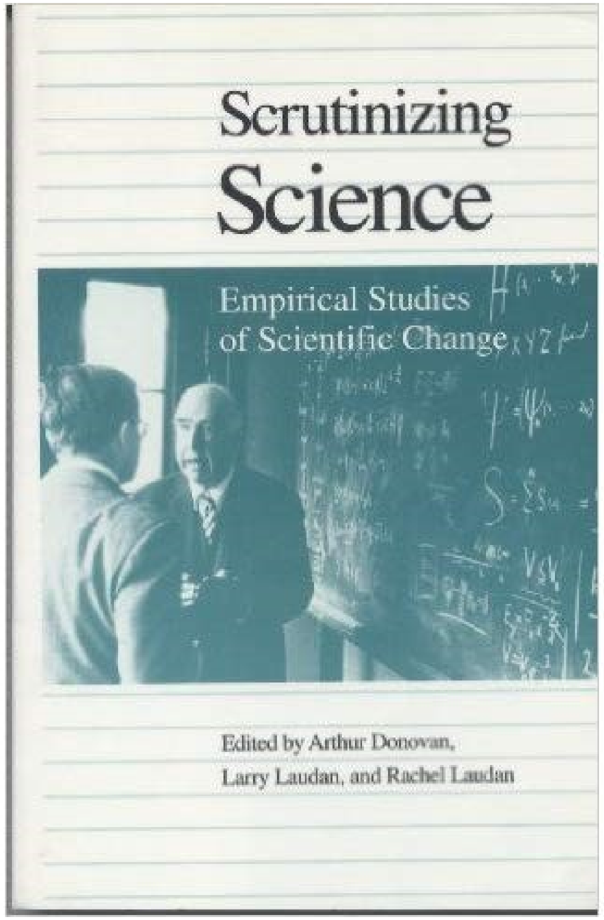
- This preliminary study undermines the thesis of a decline of the use of the concept of constraint.

II – Formulating and testing theories of scientific change

Rival theories of the evolution of science

- Bayesian theories change conjectures and refutations (Popper)
- Darwinian epistemology (Hull): social epistemology + selection of theories cumulative induction
- Research program (Lakatos)
- Paradigm shift (Kuhn)

Historical case studies as data to test theory of scientific change



The VPI project of Larry Laudan and colleagues is the most famous illustration of what has recently been called the “confrontation model” of the relationship between philosophy and history of science.

Methodological problems with the testing of philosophical theories with historical case studies

1) The Theory-Ladenness of historical case studies

2) Selection bias

3) Interpretation bias

ANR LIP6 UMR IRISA IHPST Institut des Systèmes Complexes Paris Île de France CNRS

Phylomemy: an approach in terms of patterns and processes of scientific change

- Identify the signatures of the evolutionary process of science:
  - the signature of a Darwinian selection of theories
  - the signature of a paradigm shift
  - the signature of selection in molecular evolution
- Discover and validate these signatures in the scientific corpus

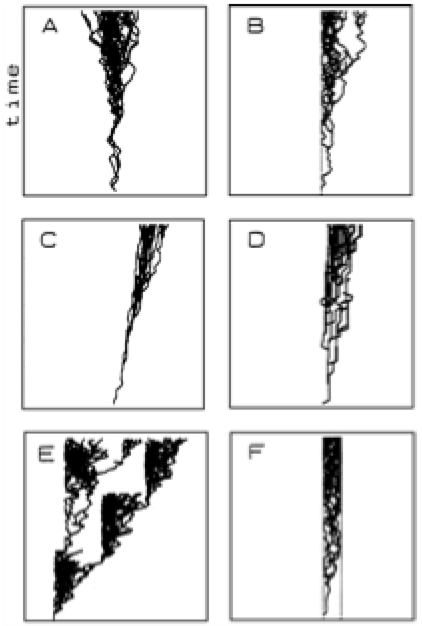


Figure 2 Output of a computer model for simulating the diversification of a group. The vertical axis is time and the horizontal axis is the state variable. In each figure, a group begins as a single species. In every time step, each lineage may increase (move right) or decrease (move left) in state space, speciate, and/or become extinct, each according to fixed probabilities. Boundaries (vertical lines in *B* and *F*) are "cushioning," meaning changes that would cause lineages to cross them are nullified. Biases are introduced (*C* and *D*) by setting the probability of moving right higher than that for moving left. (See 63 for further details.) (*A*) No trend—no boundary, no bias. (*B*) Passive trend—lower boundary, no bias. (*C*) Driven trend—no boundary, strong bias. (*D*) Weakly driven—no boundary, weak bias. (*E*) Driven, at the large scale (in that an increasing bias is present in the origin of groups, although change within groups is passive)—no boundary, strong bias. (*F*) No trend—upper and lower boundary, no bias.