

Reconstructing the Embryo: Replacing Measured Data by Computed Data

~ Bioemergences Meeting, Málaga, Spain, December 2006 ~



René Doursat

Paul Bourgine

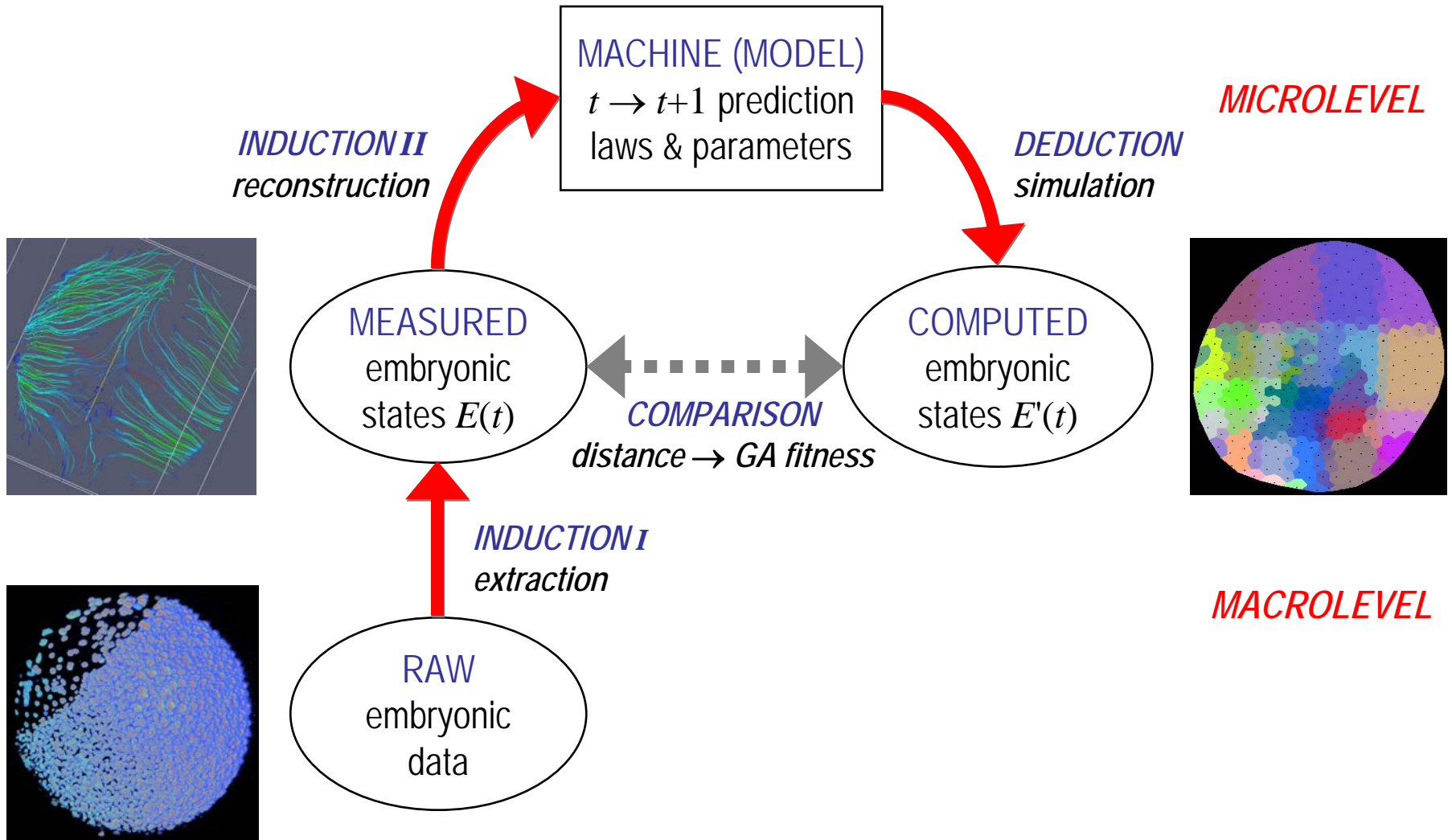
*Institut des Systèmes Complexes, CREA
CNRS & Ecole Polytechnique
1, rue Descartes, 75005 Paris*



Applied developmental biology



The big picture



Current extraction (Embryomics)

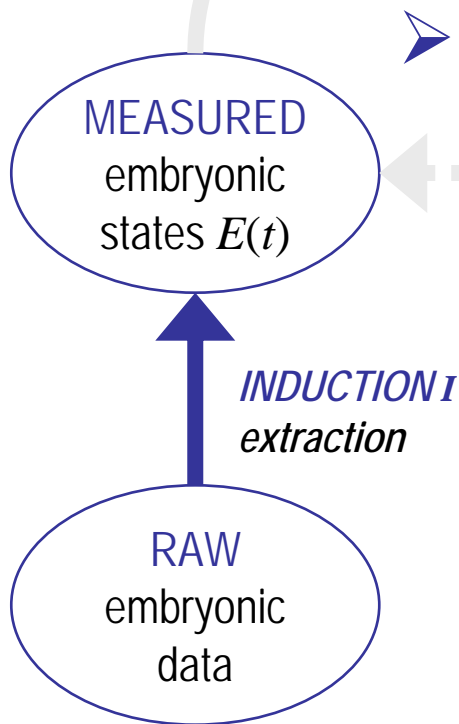
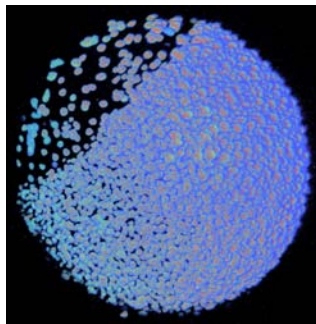
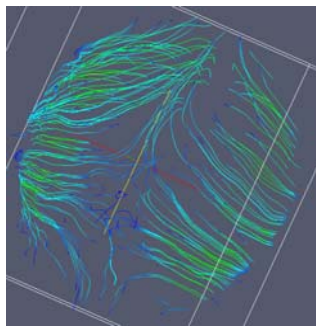
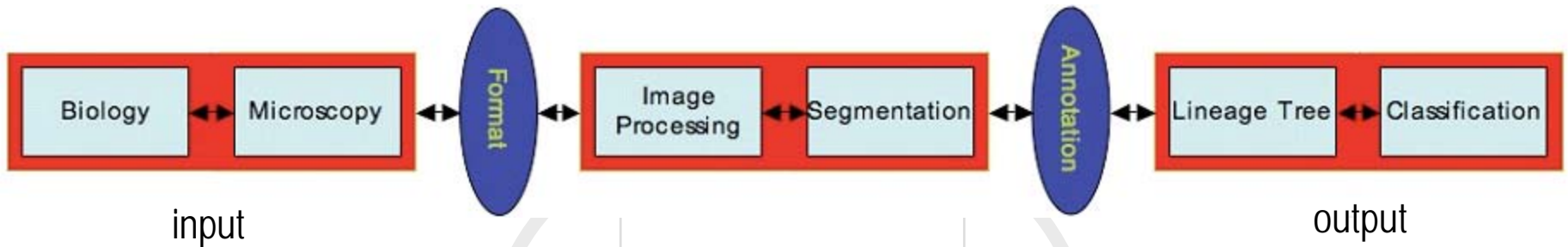
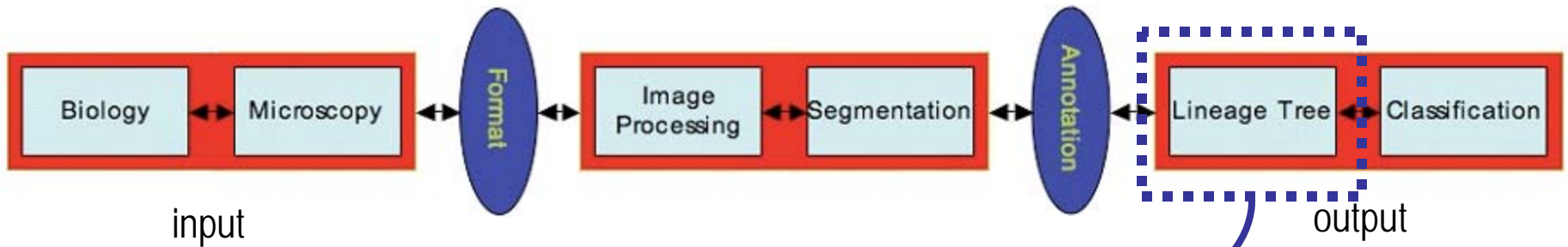


Image analysis

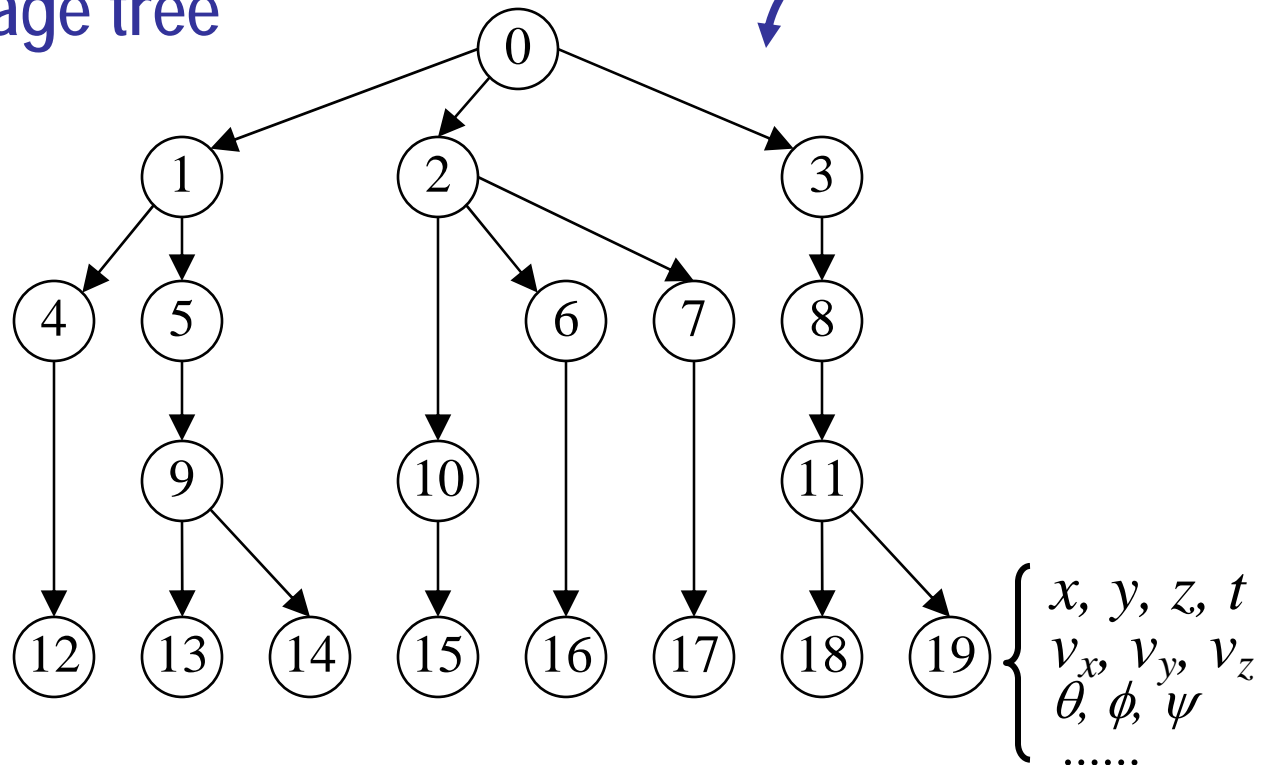
- ✓ input: images and movies
 - ✓ methods: segmentation, tracking
 - ✓ output: lineage tree labeled with dynamic variables (positions, velocities, division rates, etc.)
- *extensive* set of measured states that can be replayed "by rote"

Current extraction (Embryomics)

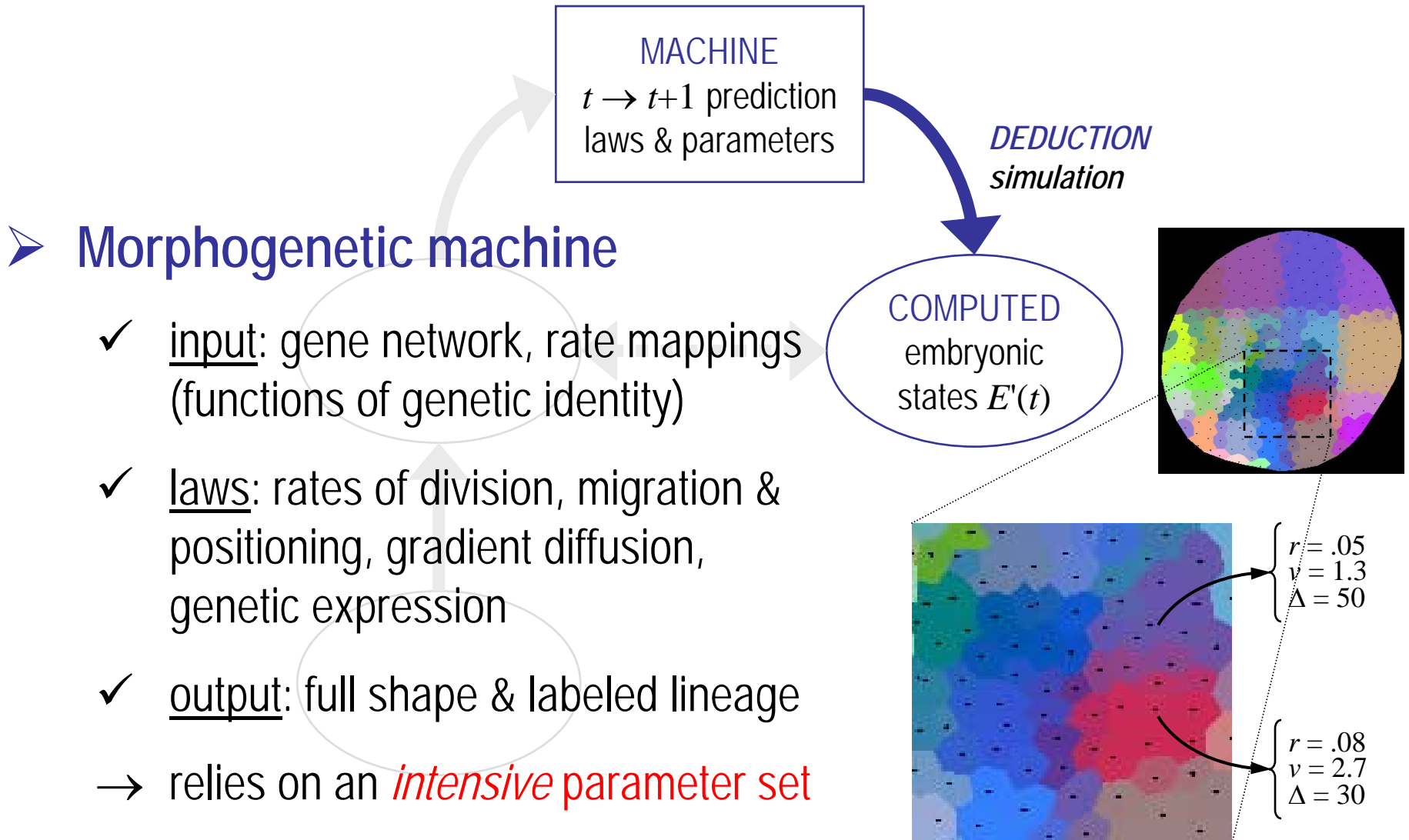


➤ Labeled lineage tree

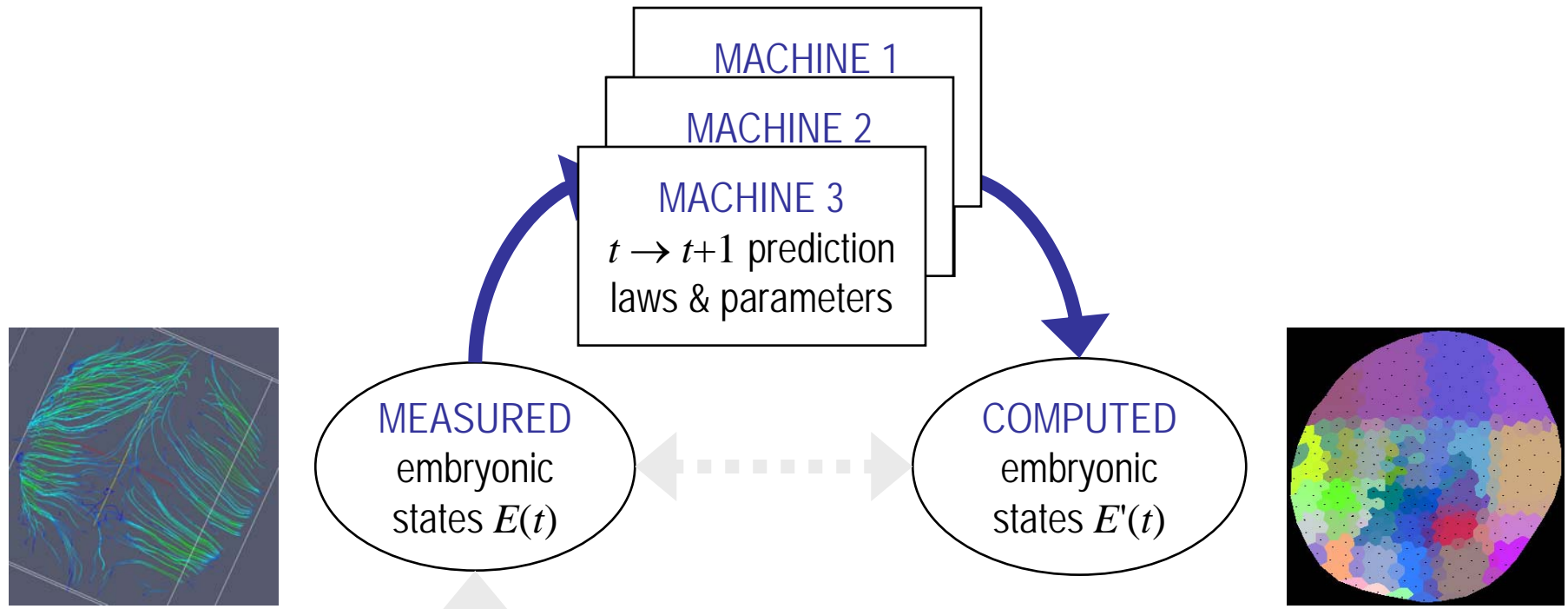
✓ complete measured state



Current morphogenetic machine (R. Doursat)



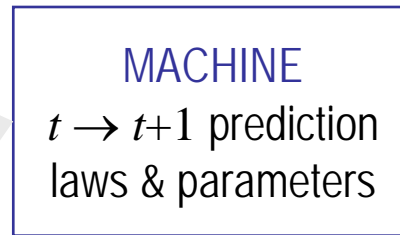
Predicting is modeling



➤ Different levels of generality vs. specificity for the machine

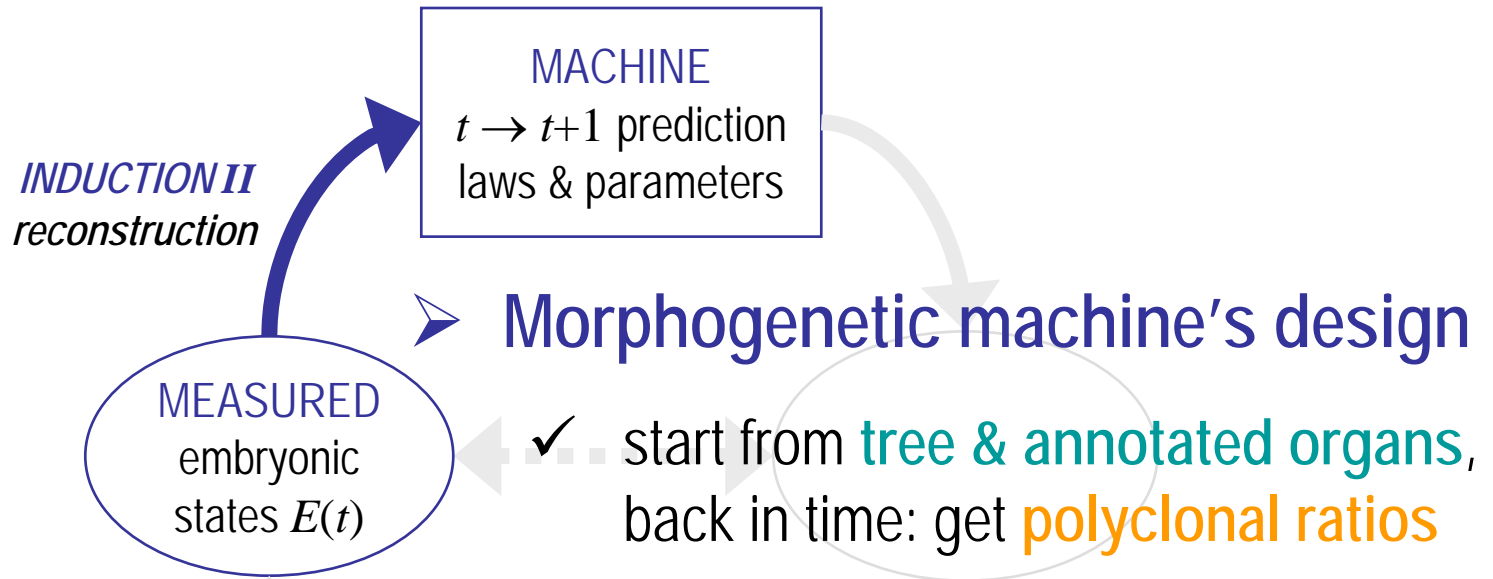
- ✓ too specific: lookup table or "rote playback". . . no generalization!
- ✓ too generic: agnostic statistical estimator. . . no convergence!
- best: heuristic **model**, with genetic-biomechanic laws & parameters

Predicting is modeling & optimizing



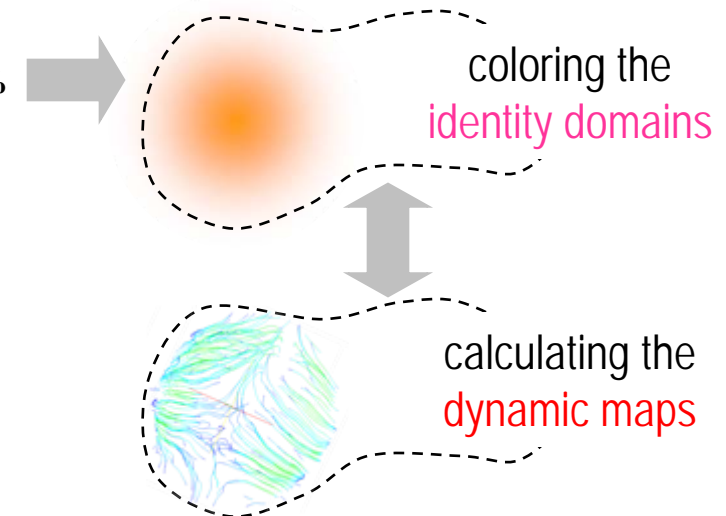
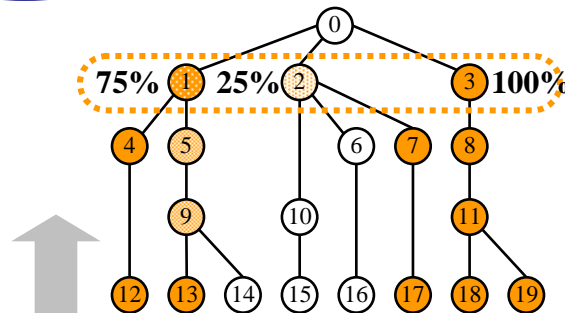
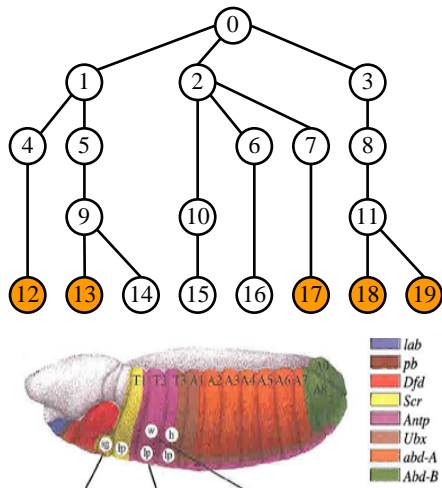
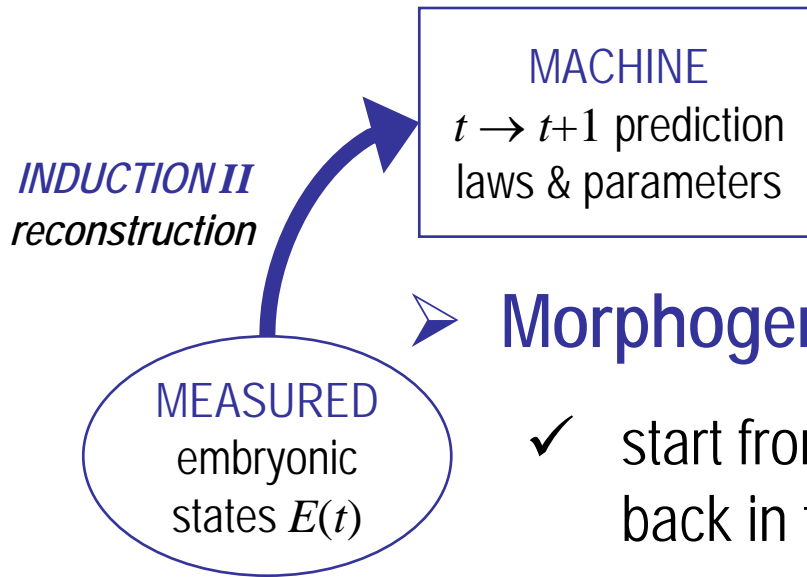
- **The morphogenetic machine is a parametrized function**
 - ✓ each state is “predicted” or “reconstructed” as a function of the previous state: $E(t+1) = F_{\lambda}(E(t))$ (or more past states)
 - ✓ this function relies on built-in mechanisms and parameters λ
 - ✓ the parameters are “learned” (by machine learning) or “optimized” (by genetic algorithms), etc.
- *learning does not occur directly on the extensive state variables, but on the intensive set of parameters*

Future morphogenetic machine: design methodology

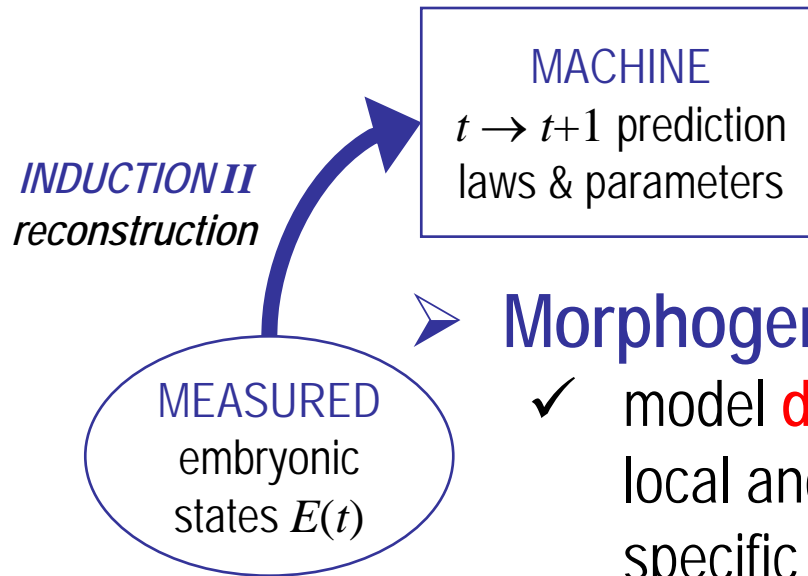


- ✓ from the polyclonal ratios, induce the **identity domains**, the basic components of the reconstruction
 - ✓ from the identity domains, induce the **dynamic mappings** (field functions): division rates, velocity vectors, deformation tensors, etc.
- *model dynamic maps by { mechanisms + parameter } computation*

Future morphogenetic machine: design methodology

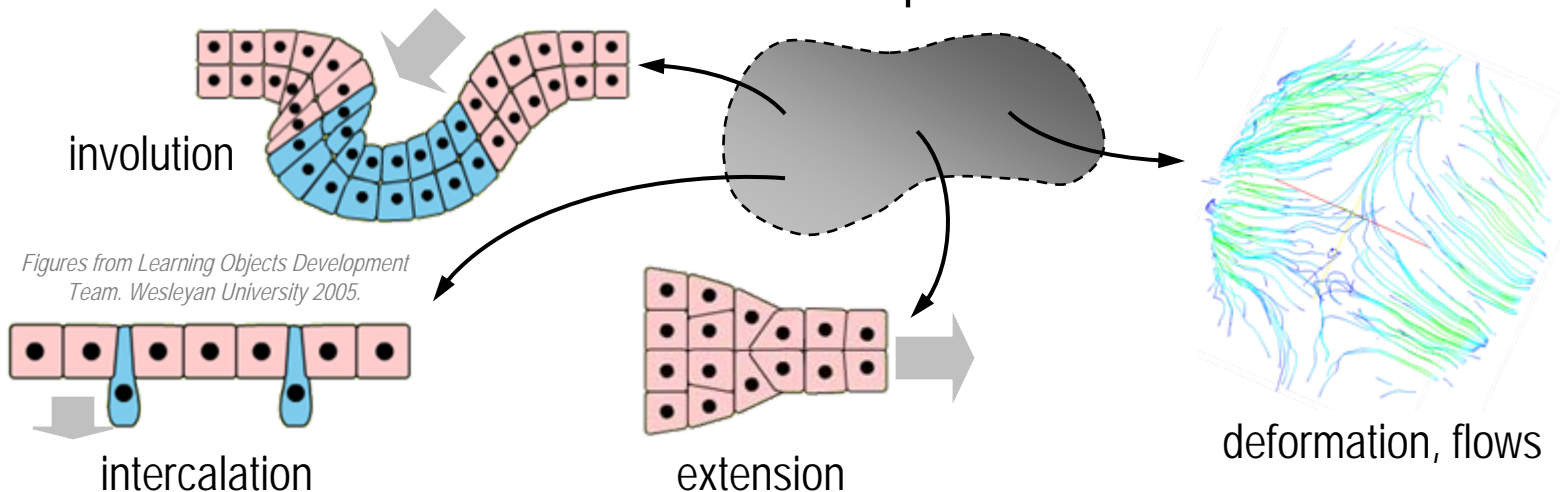


Future morphogenetic machine: design methodology



Morphogenetic machine's design

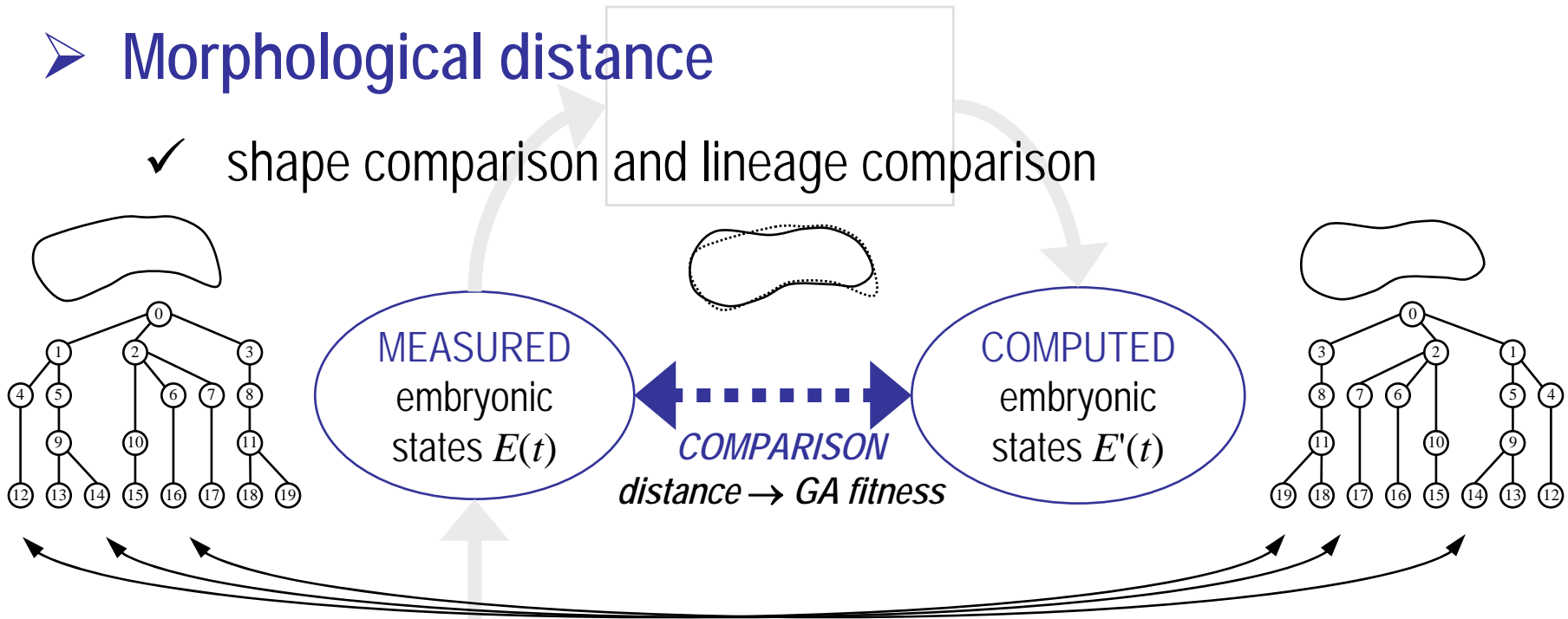
- ✓ model **dynamic maps** by execution of local and global transformations at specific locations and times



Comparing measured and computed embryos

➤ Morphological distance

- ✓ shape comparison and lineage comparison



- ✓ compare 2 measured embryos \rightarrow variability, BioEmergences
- ✓ compare a measured embryo with a computed embryo \rightarrow error-correction (in learning), fitness (in evolutionary optimization)