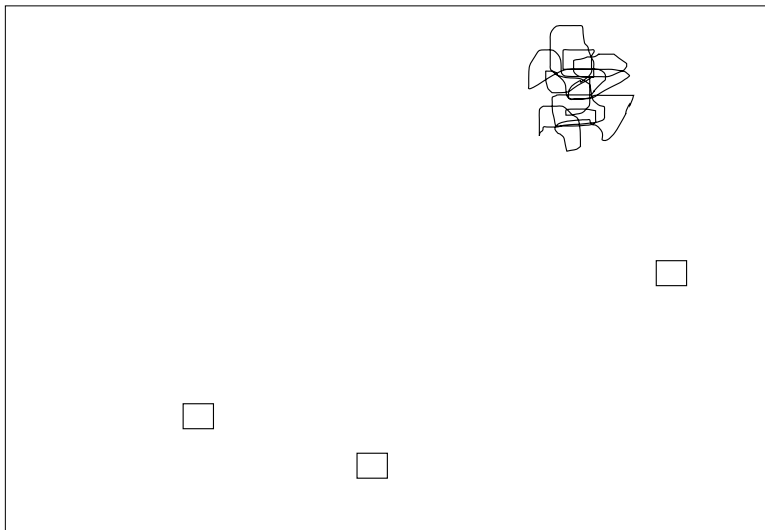


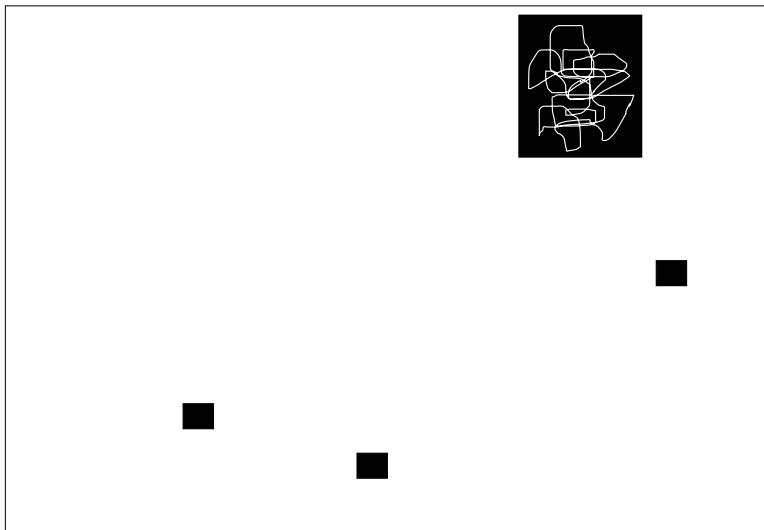
# Trap-spaces, attractor basins: towards a global attractor reachability map

# Approximation of complex attractors



A model can have multiple stable states and complex attractors

# Approximation of complex attractors

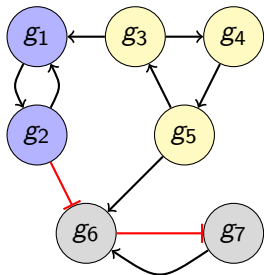


Wrapping each attractor into the smallest sub-space

# Attractors and trap-spaces

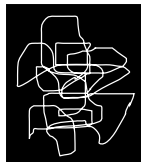
## Trap-space

Hypercube (partial assignment) in which the system can be trapped

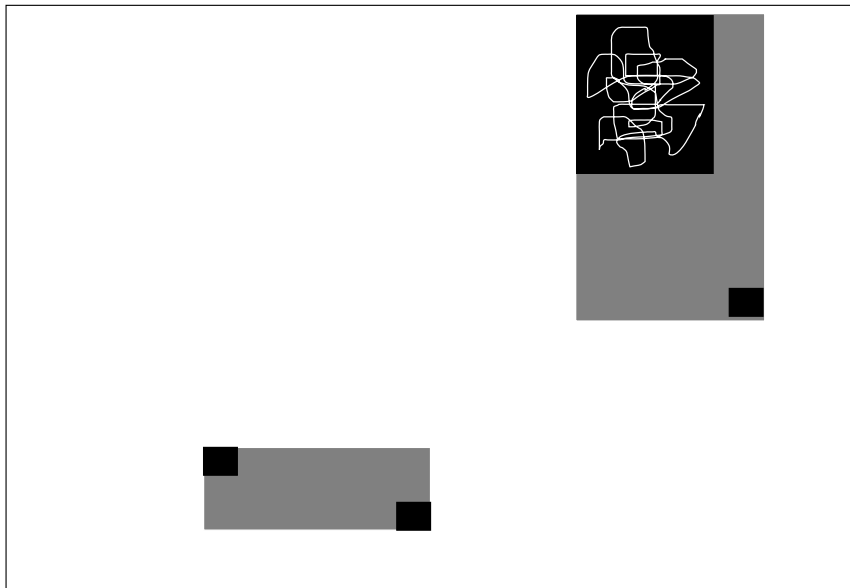


- Stability for some components  
 $g_3 = g_4 = g_5$
- Local dimension reduction
- Driven by positive circuits
- Identified by constraint solving

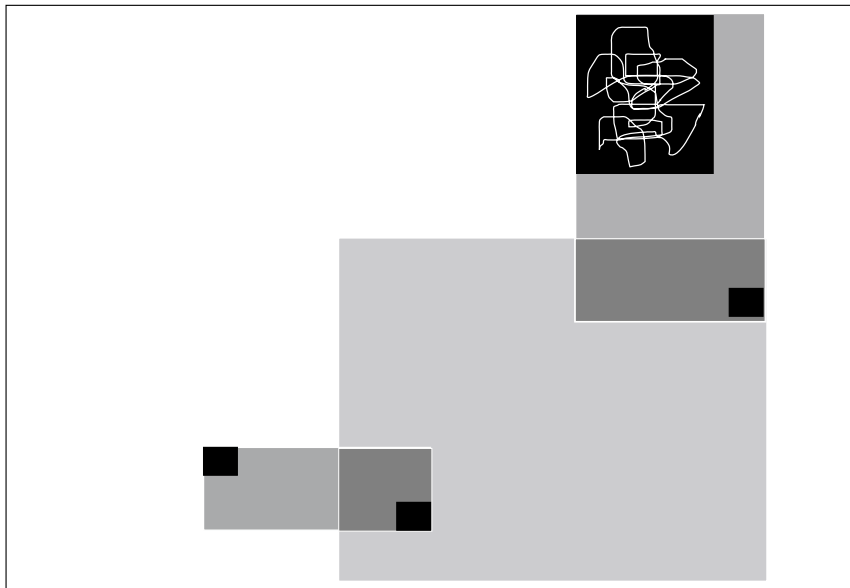
# Trap-spaces delineate iterative commitment



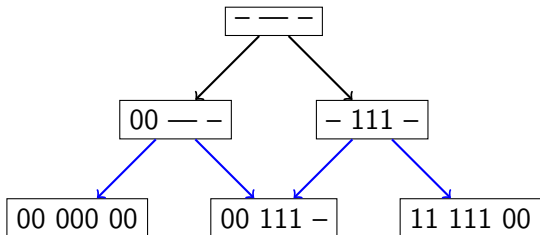
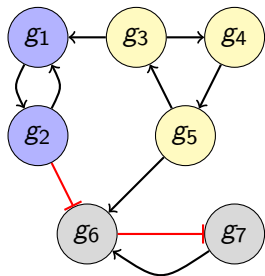
# Trap-spaces delineate iterative commitment



# Trap-spaces delineate iterative commitment



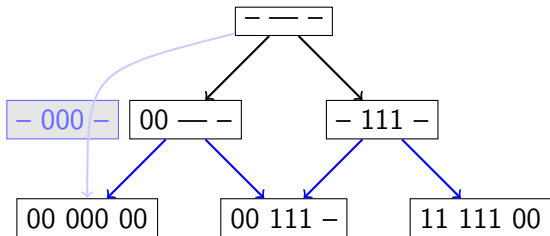
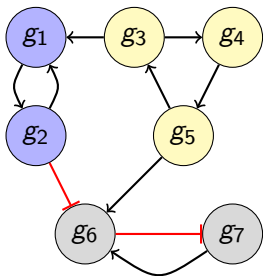
# Recent and ongoing refinements



- Inclusion tree provides reachability insights
- Percolation of downstream components
  - Reduce the number of trap-spaces
  - Percolated sub-space is always reachable
- Integration into GINsim



# Recent and ongoing refinements



- Inclusion tree provides reachability insights
- Percolation of downstream components
  - Reduce the number of trap-spaces
  - Percolated sub-space is always reachable
  - **Some commitment paths difficult to detect**
- Integration into GINsim

# Summary and practical use

- Catches most cyclic attractors in existing biological models
  - Can be checked and refined if needed
- Relation with circuits still unclear
- Works well on large models with few inputs
- Adding inputs: exponential number of attractors
  - Consider specific subsets of input combination
  - Identify inputs compatible with a "target" phenotype
- Coarse-grained global reachability map
  - Refinement strategies to be improved