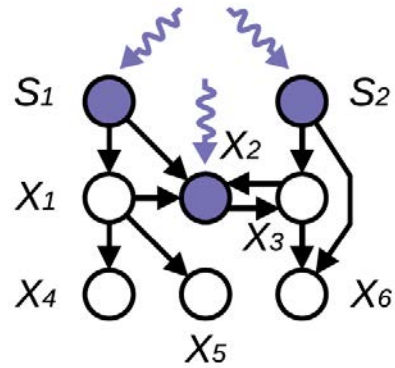
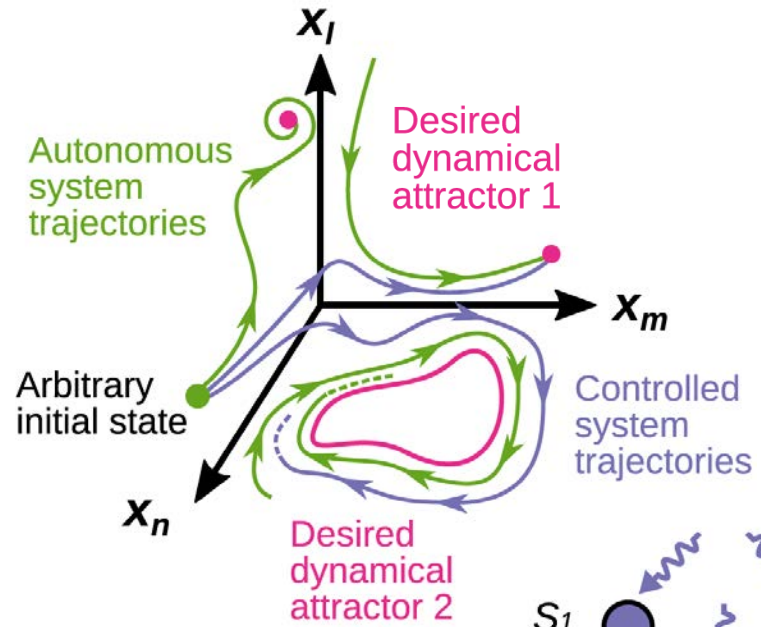


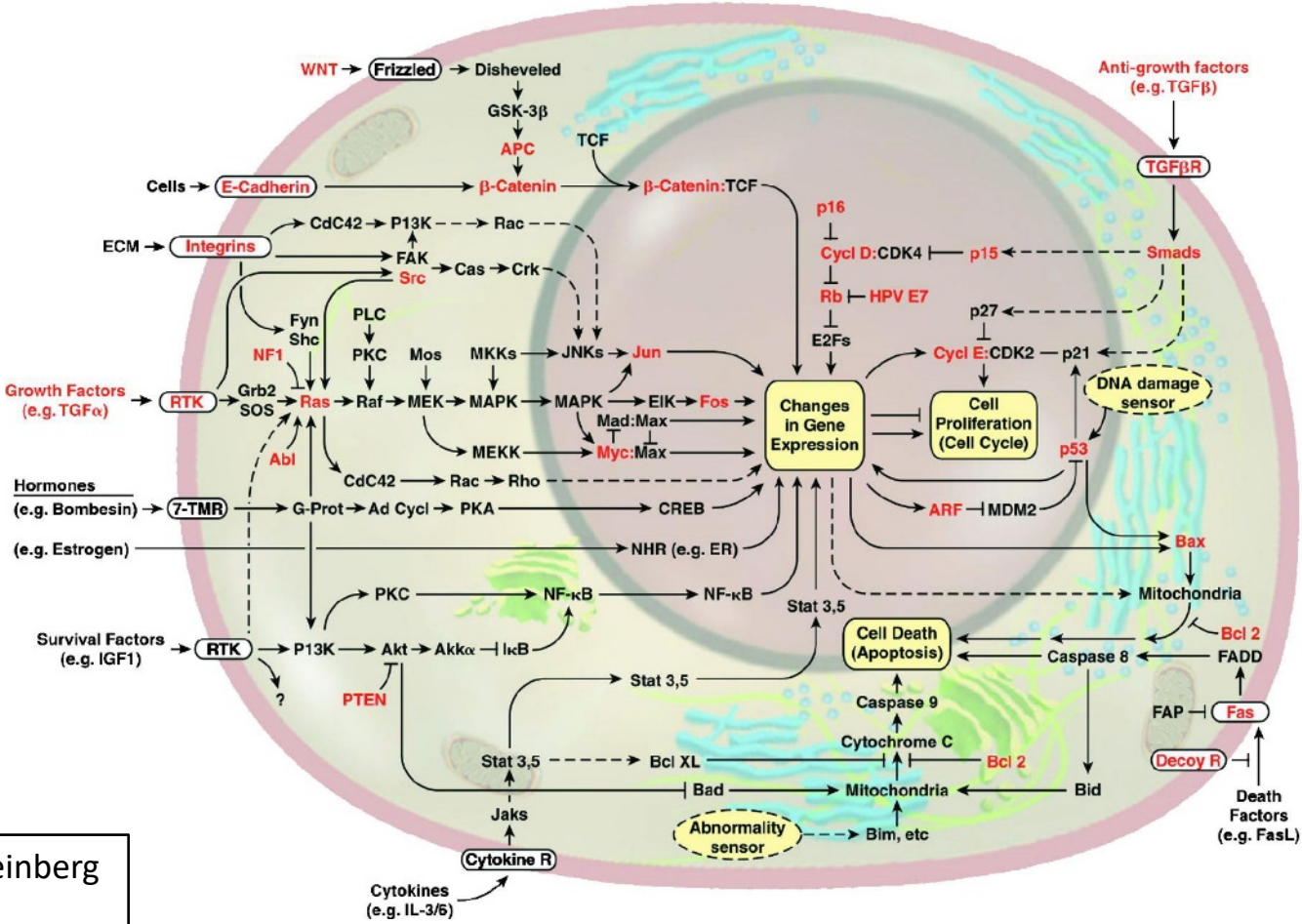
Model-dependent and model-independent control of biological network models



Jorge Gómez Tejeda Zañudo
Postdoctoral researcher
Broad Institute of MIT and Harvard
Dana-Farber Cancer Institute

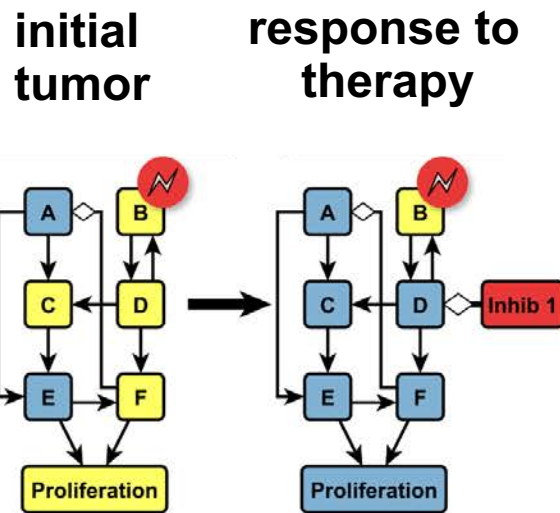
Cellular phenotypes arise from a complex molecular network

Network model: Dynamics of information propagation through cellular pathways and their connection to cellular behaviors

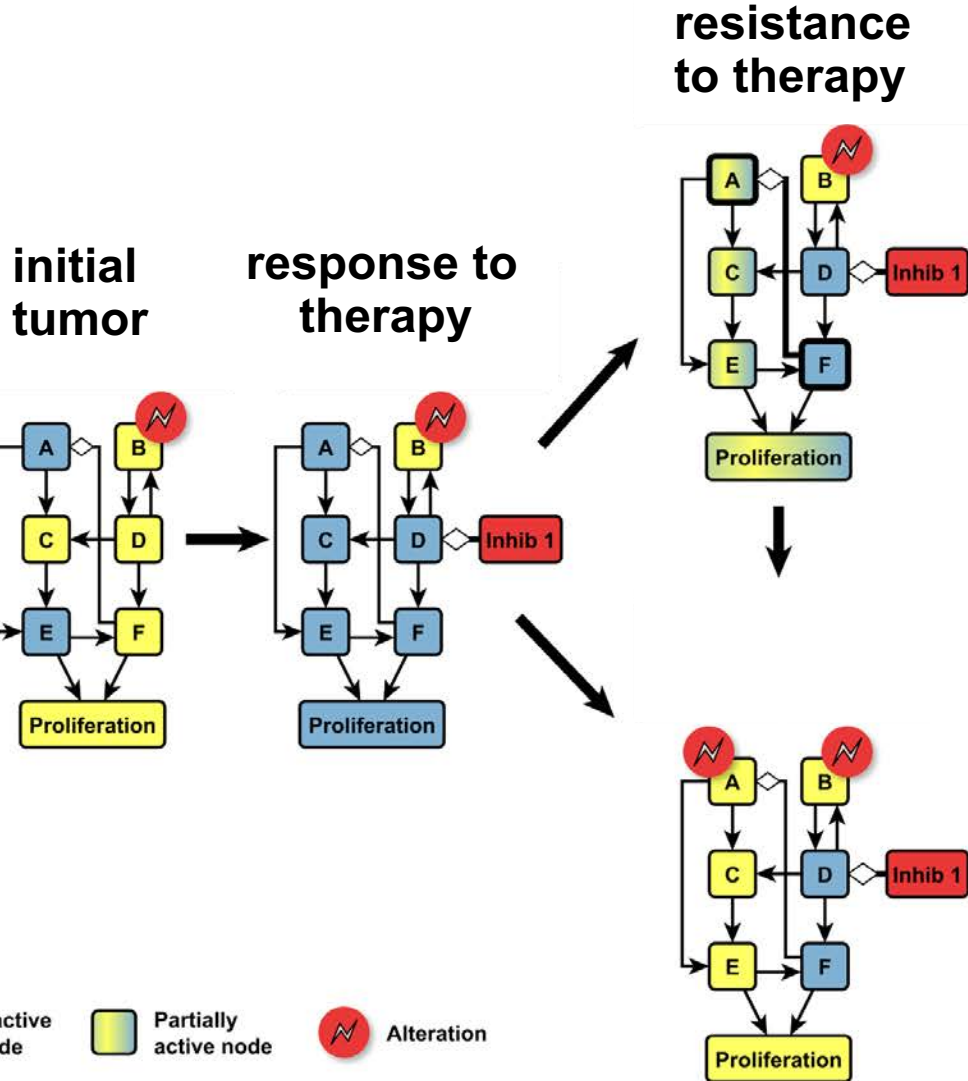


Hanahan, Weinberg
(2000)

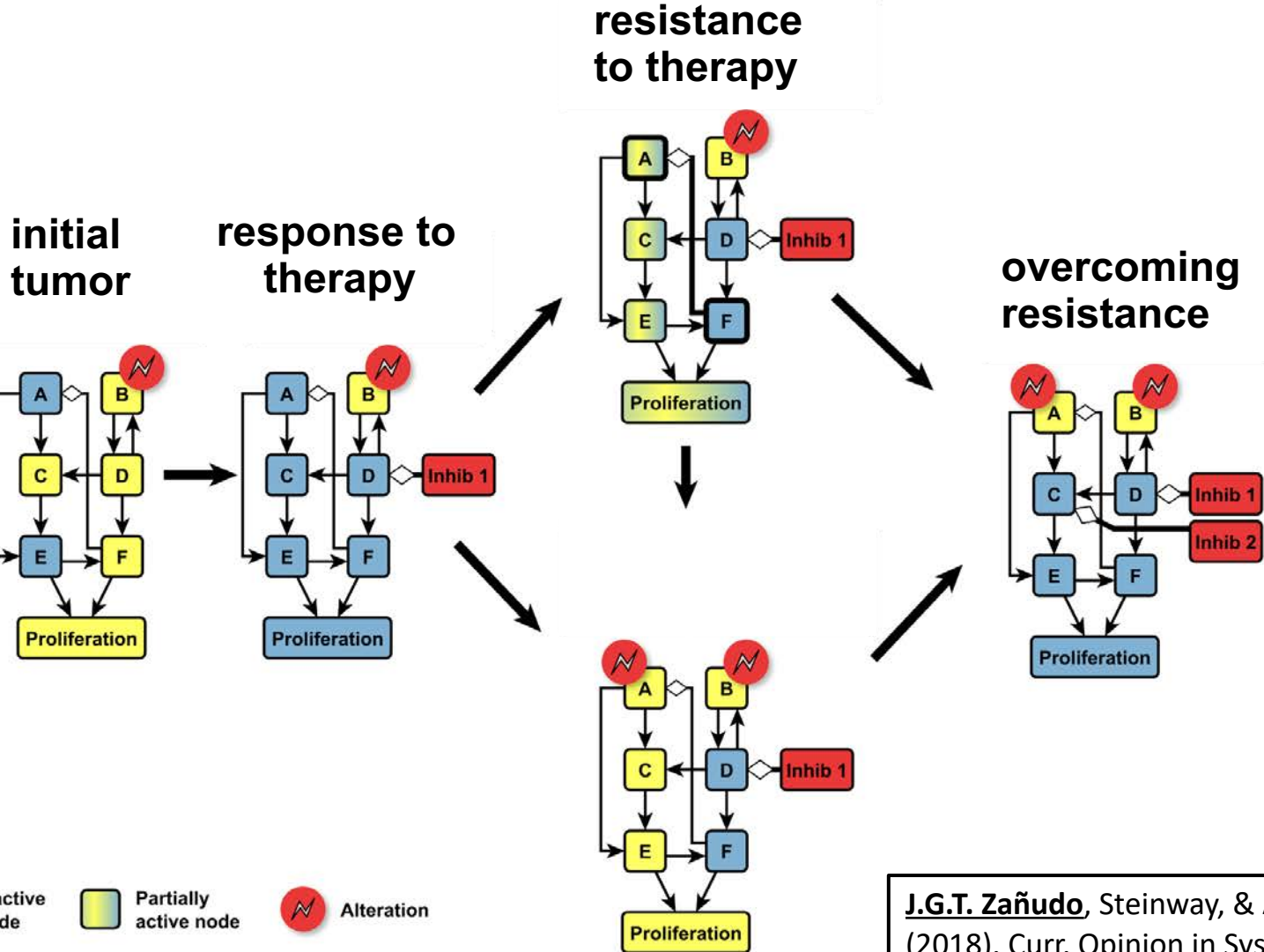
Many current challenges in cancer (drug resistance, combination treatments) can be tackled through mechanistic network modeling



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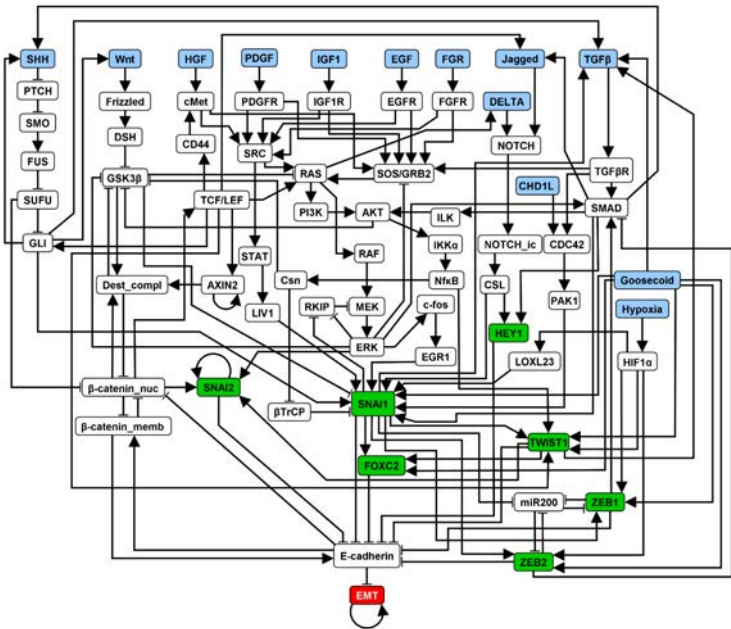
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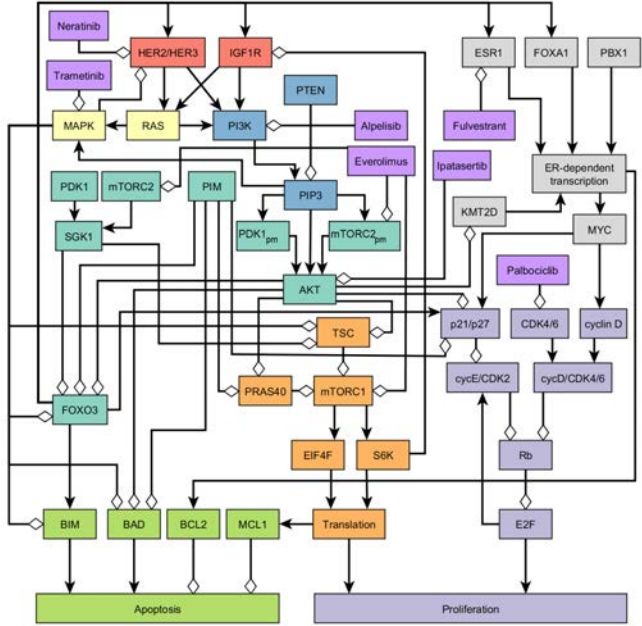
Objective of my research

Use network models and control methods to predict

Nodes that block metastatic reprogramming
(EMT in liver cancer)



Resistance mechanisms and drug combinations
(PI3K inhibition in ER+ MBC)



SN Steinway, **JGT Zañudo**, et al. Cancer Res. (2014).
SN Steinway*, **JGT Zañudo***, et al. npj Syst. Biol. & Appl. (2015).

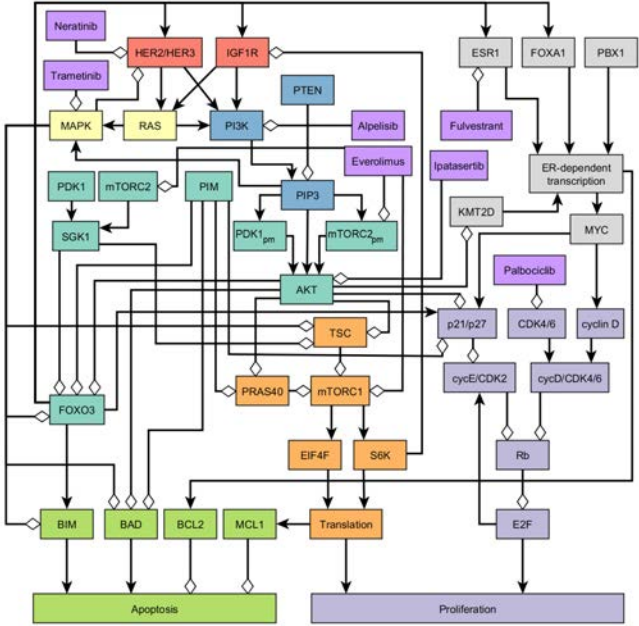
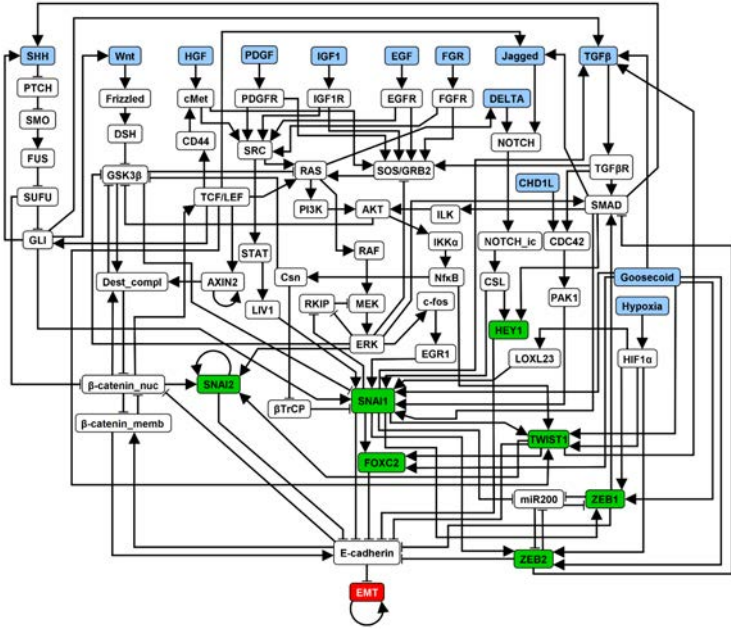
JGT Zañudo, et al. Cancer Convergence. (2017).
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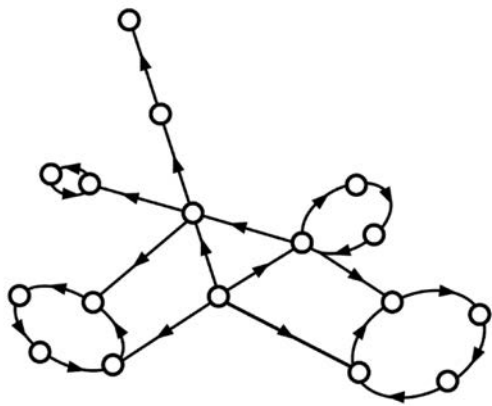
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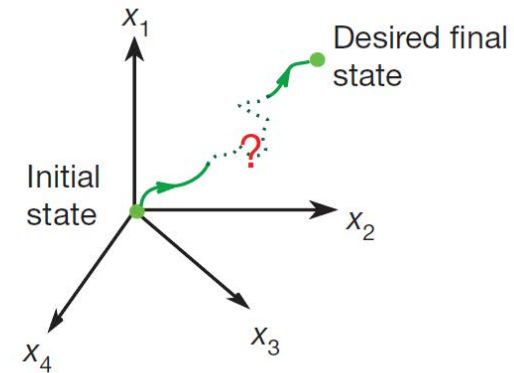
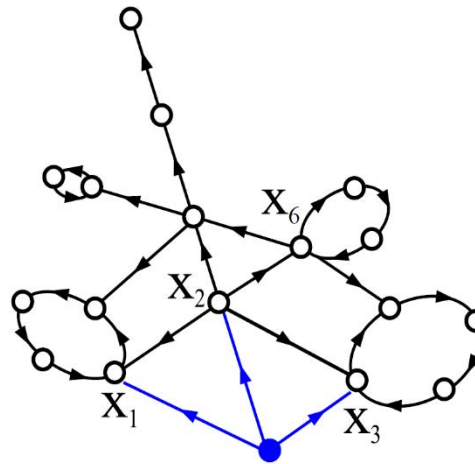
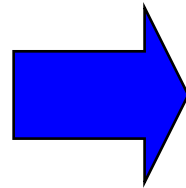
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SN Steinway*, **JGT Zañudo***, et al. npj Syst. Biol. & Appl. (2015).

JGT Zañudo, et al. Cancer Convergence. (2017).
JGT Zañudo, et al. bioRxiv. (2020).

Network control: Control the internal state of a network and drive it towards a desired state.



**Network
control**



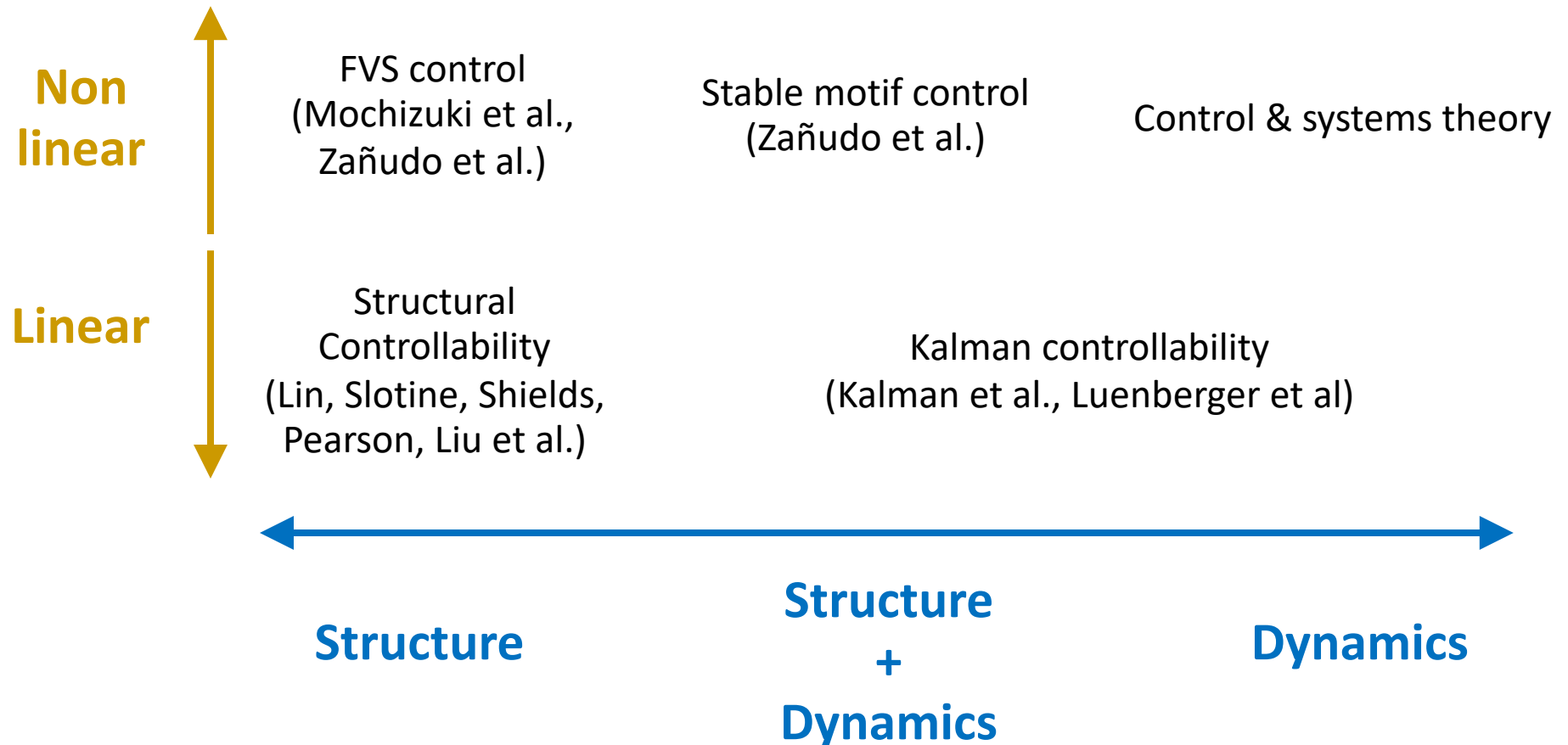
YY Liu et al. Nature **473**,
167-173 (2011)

Network control:

- Network + dynamic model
- Intervention + state $X \rightarrow$ state Y

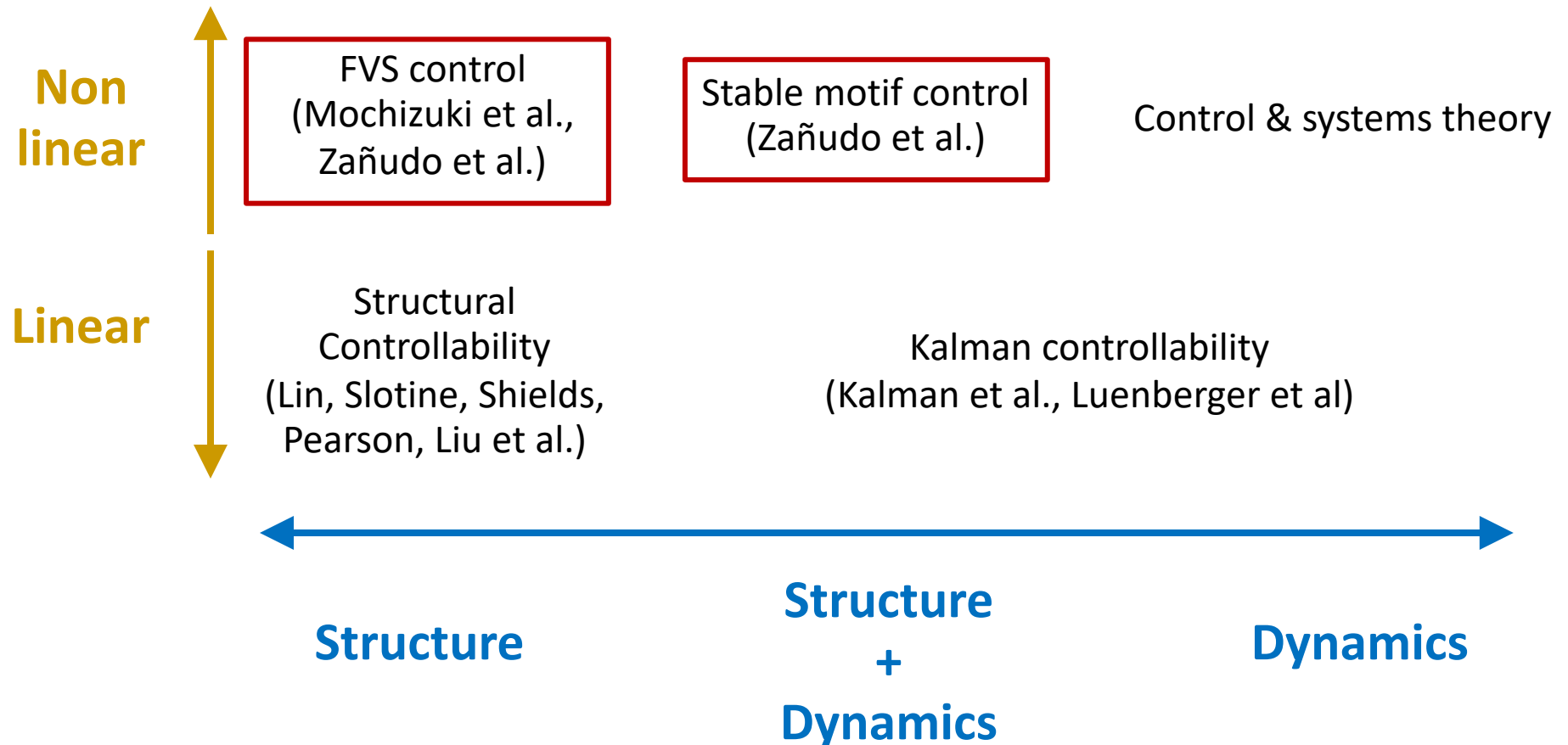
Network control:

- Network + dynamic model
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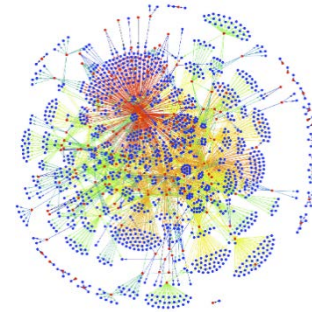
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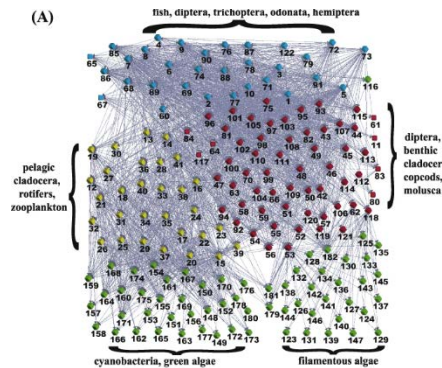
Realistic dynamics are **nonlinear** and have **dynamical attractors** (e.g. steady states) that correspond to stable patterns of activity:

$$\frac{dx_i}{dt} = -Bx_i + \sum_{j=1}^N A_{ij} R \frac{x_j^h}{1+x_j^h}$$



Intracellular dynamics
 - cell types or cell states

$$\frac{dx_i}{dt} = -Bx_i^b + \sum_{j=1}^N A_{ij} R x_j^a$$



Population dynamics
 - stable population sizes

Some definitions and references

Fiedler, B., Mochizuki, A., et al. (2013), *J. Dynamics and Differential Equations*.
Mochizuki, A., Fiedler, B., et al. (2013), *J. Theor. Bio.*
Zanudo J.G.T. & Albert R. et al. (2015), *PLoS Comp. Bio.*
Zanudo J.G.T., Yang G., & Albert R. (2017), *PNAS*.

Dynamics

$x(t)$ is a trajectory in:

- An ODE system: $\dot{x} = F(x)$, $x \in \mathbb{R}^n$, $x_i \geq 0$, F is dissipative,
- A Boolean system: $x(t + 1) = B(x(t))$, $x \in \{0,1\}^n$, $t \in \{0,1,2, \dots\}$

G is the graph induced by the dynamics.

- ODE system: $i \rightarrow j$ if $\partial F_j / \partial x_i \neq 0$, $i \rightarrow i$ only if $\partial F_i / \partial x_i > 0$
- Boolean system: $i \rightarrow j$ if any prime implicant of B_j depends on x_i

Attractor control

Let $x_{\mathcal{A}}$ be a fixed point (or the trajectory of a limit cycle) of the system

Control approach: we clamp the variables x_I , $I \subseteq \{1,2, \dots, n\}$ so that $x_k(t) = g_k(t)$ if $k \in I$, otherwise they follow their uncontrolled dynamic equation. The controlled system is denoted $x^*(t)$

Attractor control: $\|x^*(t) - x_{\mathcal{A}}\| \rightarrow 0$, $\forall x^*(0)$, as $t \rightarrow \infty$

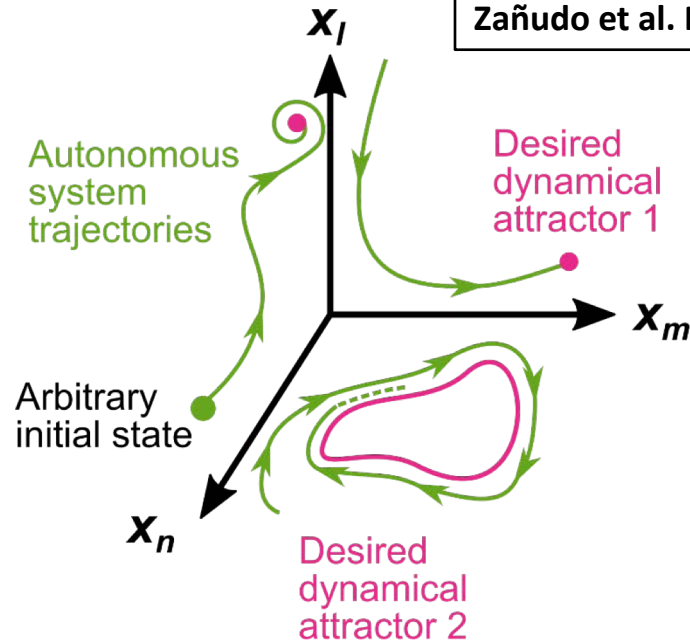
Feedback vertex set control (FC)

- Dynamics:

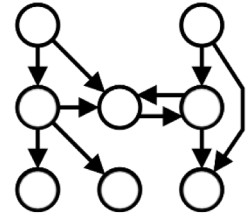
$$\frac{dX_i}{dt} = F_i(X_i, X_{I_i}, t),$$



Mass-action kin.
Michaelis-Menten



Mochizuki et al. J. Theor. Biol. 335 (2013)
Zañudo et al. PNAS 114 (2017)



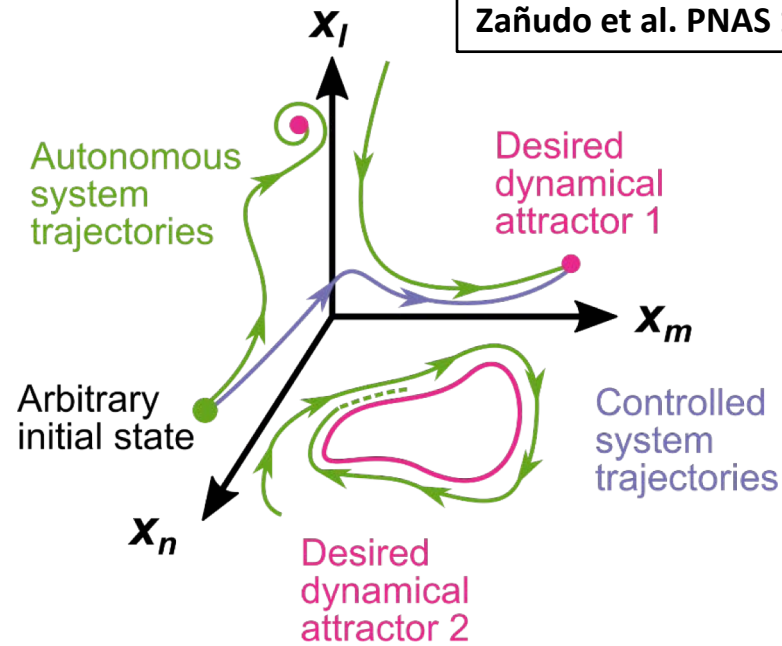
Feedback vertex set control (FC)

- Dynamics:

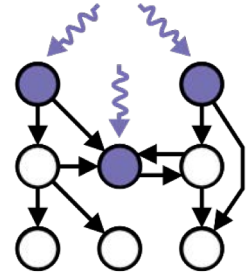
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**Mass-action kin.
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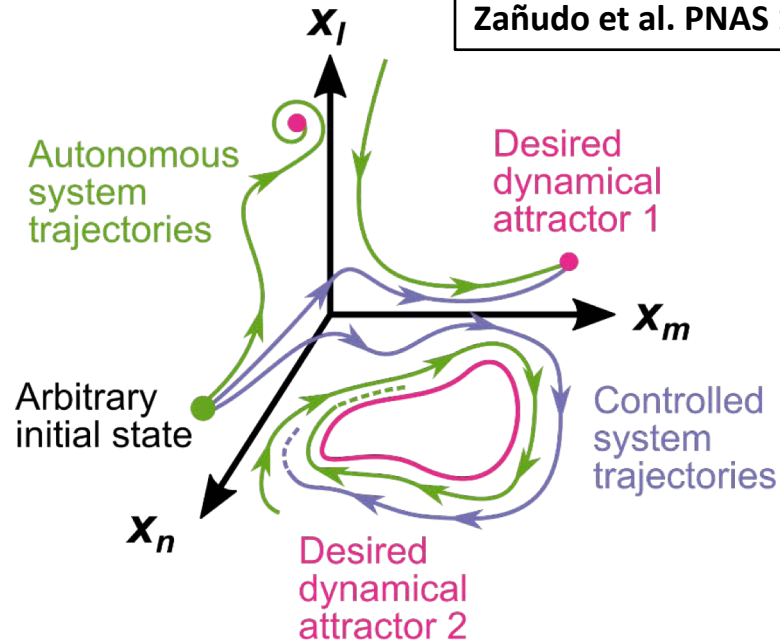
Feedback vertex set control (FC)

- Dynamics:

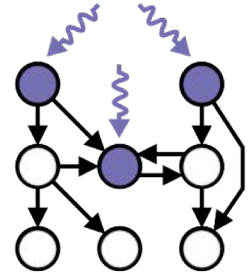
$$\frac{dX_i}{dt} = F_i(X_i, X_{I_i}, t),$$



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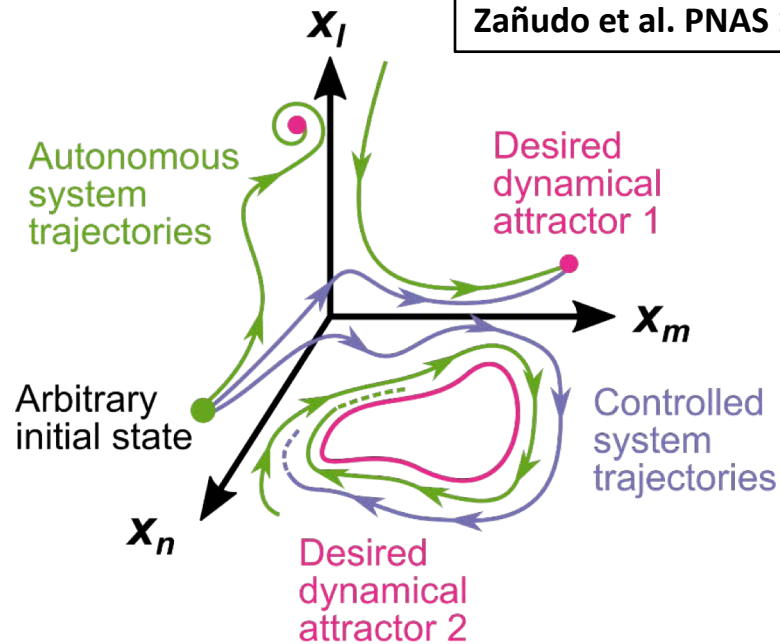
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- Dynamics:

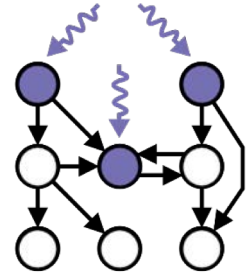
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Mass-action kin.
Michaelis-Menten



Mochizuki et al. J. Theor. Biol. 335 (2013)
Zañudo et al. PNAS 114 (2017)



- Feedback Vertex Set Control node set:

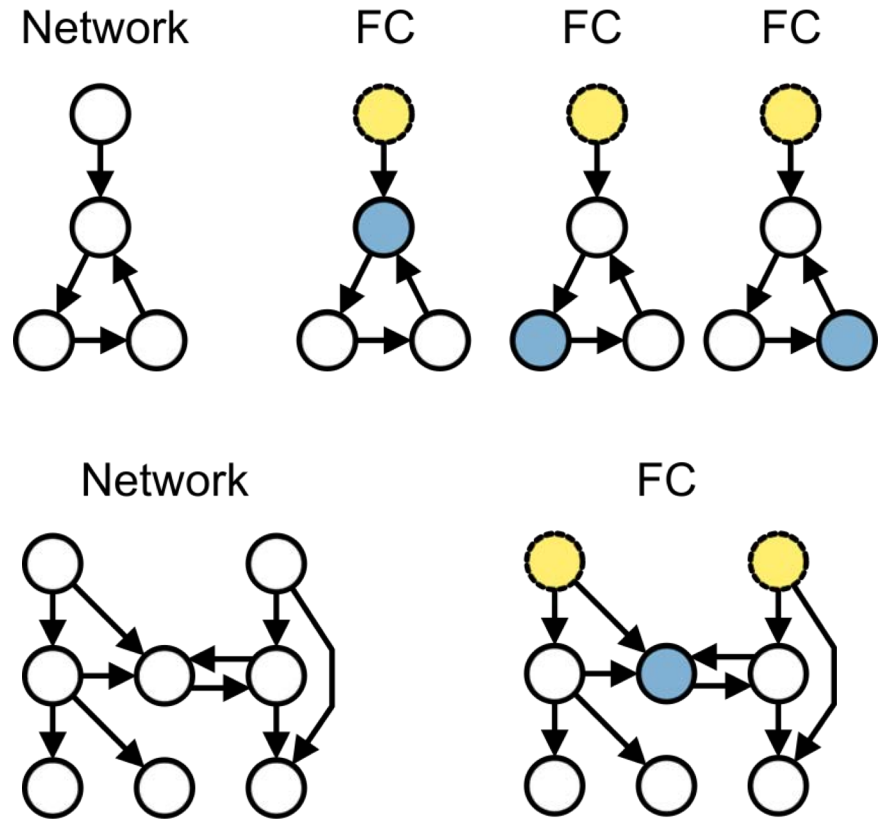
- **Given a network, sufficient for control in each model (F_i)**
- **Only control set that works for every model (F_i) on the network**

- What do we need to control?

 Source nodes

+

 A node in every cycle (FVS)



- What do we need to control?

 Source nodes

+

 A node in every cycle

- Finding exact minimal FVS is NP-hard
- Good heuristics to find near-minimal FVS

Topological ordering + simulated annealing
(Galnier et al., J. of Heuristics 19, 2013):

https://github.com/yanggangthu/FVS_python

https://github.com/yanggangthu/FVS_cython

GRASP (Pardalos et al. J. Comb. Optim. 2,
1999)

<http://calgo.acm.org/> (Algorithm 815)

- What is the control action?

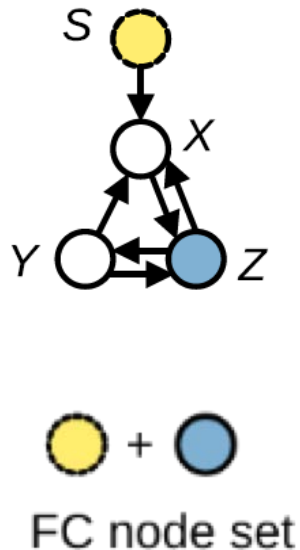
Mochizuki et al. *J. Theor. Biol.* 335 (2013)
Zañudo et al. *PNAS* 114 (2017)

Node state clamping (fix state into attractor trajectory, no “controller”)

- What is the control action?

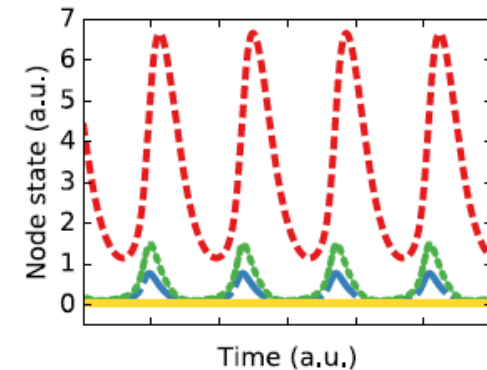
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Node state clamping (fix state into attractor trajectory, no “controller”)

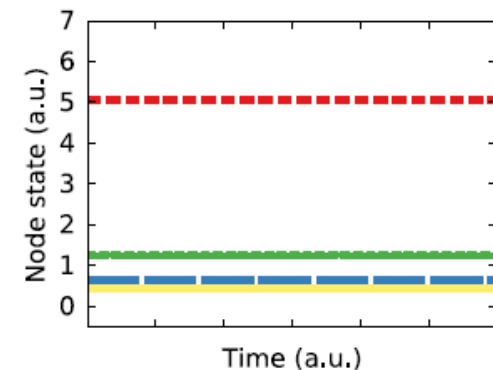


System attractors

Attractor 1



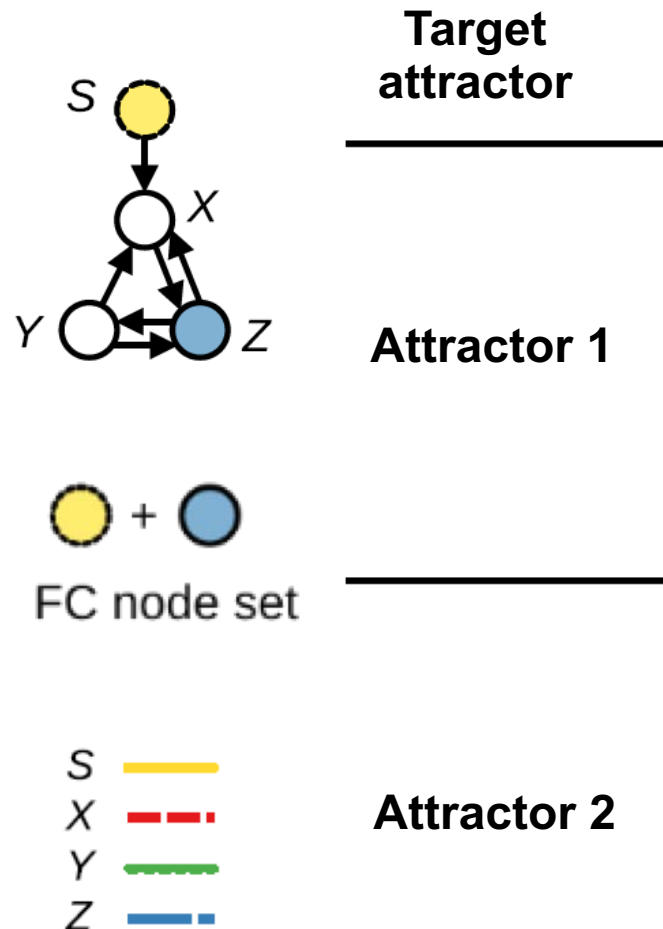
Attractor 2



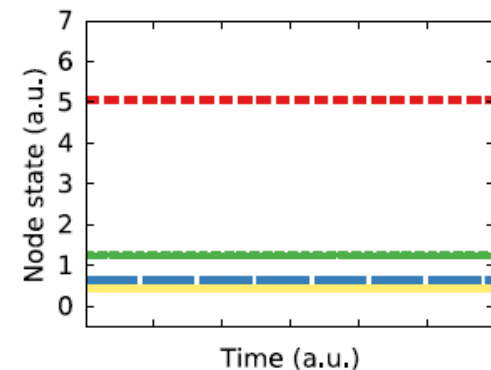
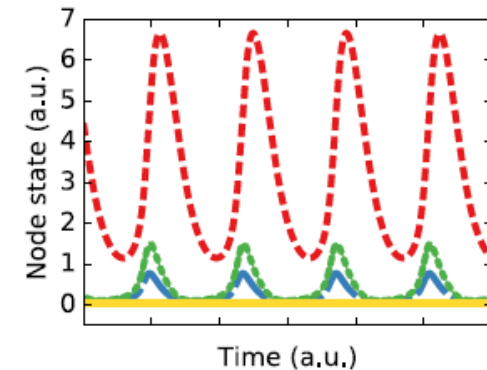
- What is the control action?

Mochizuki et al. J. Theor. Biol. 335 (2013)
Zañudo et al. PNAS 114 (2017)

Node state clamping (fix state into attractor trajectory, no “controller”)



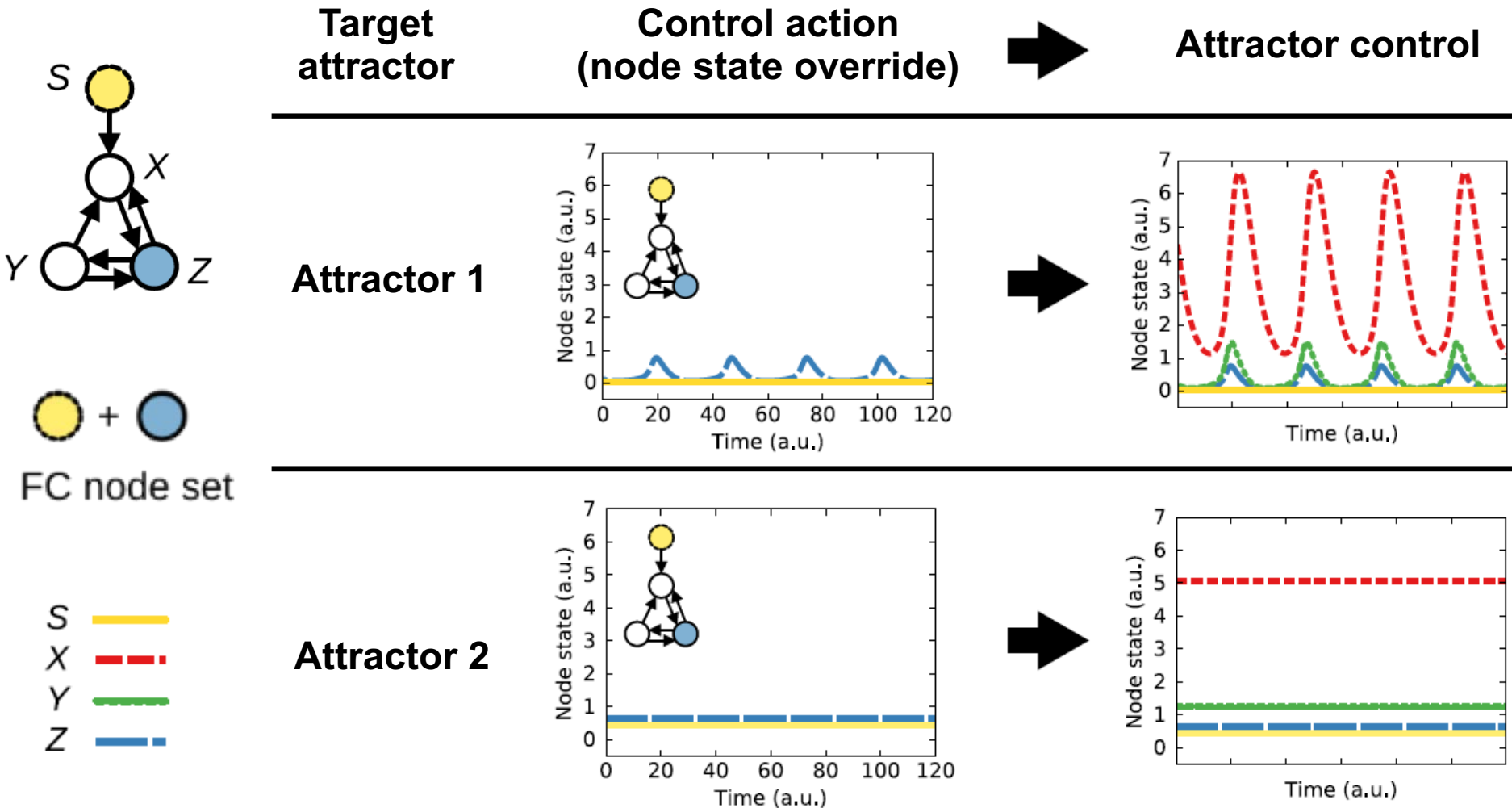
Attractor control



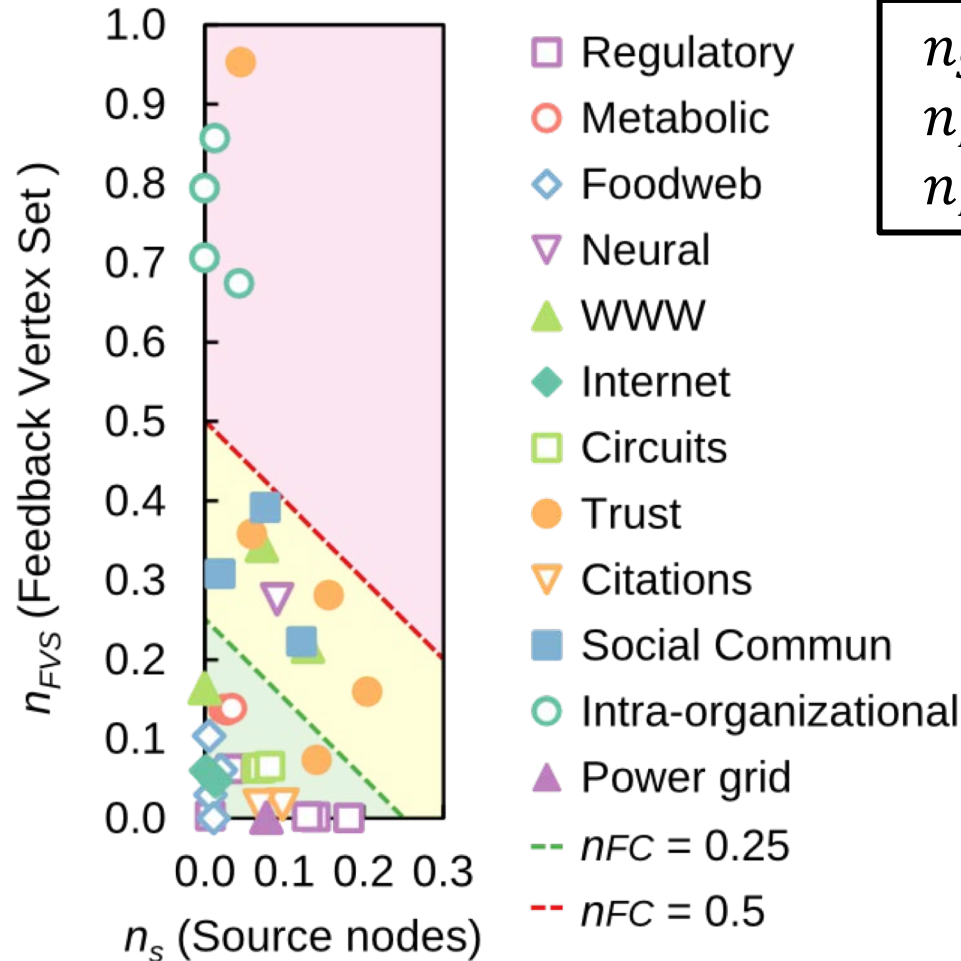
- What is the control action?

Mochizuki et al. J. Theor. Biol. 335 (2013)
 Zañudo et al. PNAS 114 (2017)

Node state clamping (fix state into attractor trajectory, no “controller”)

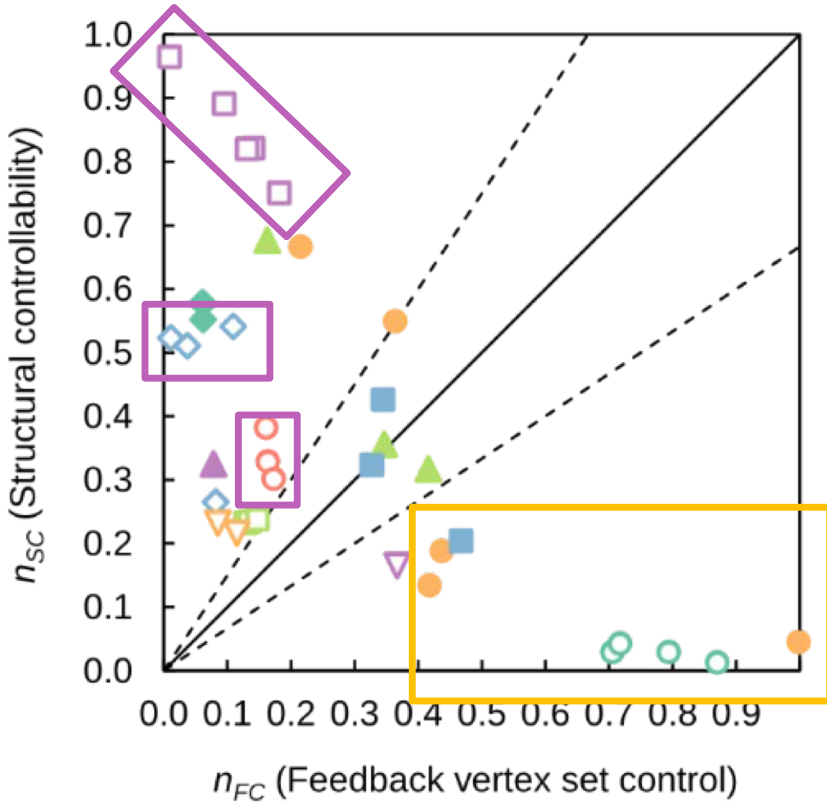


Real networks require varying fraction of nodes for FVS control

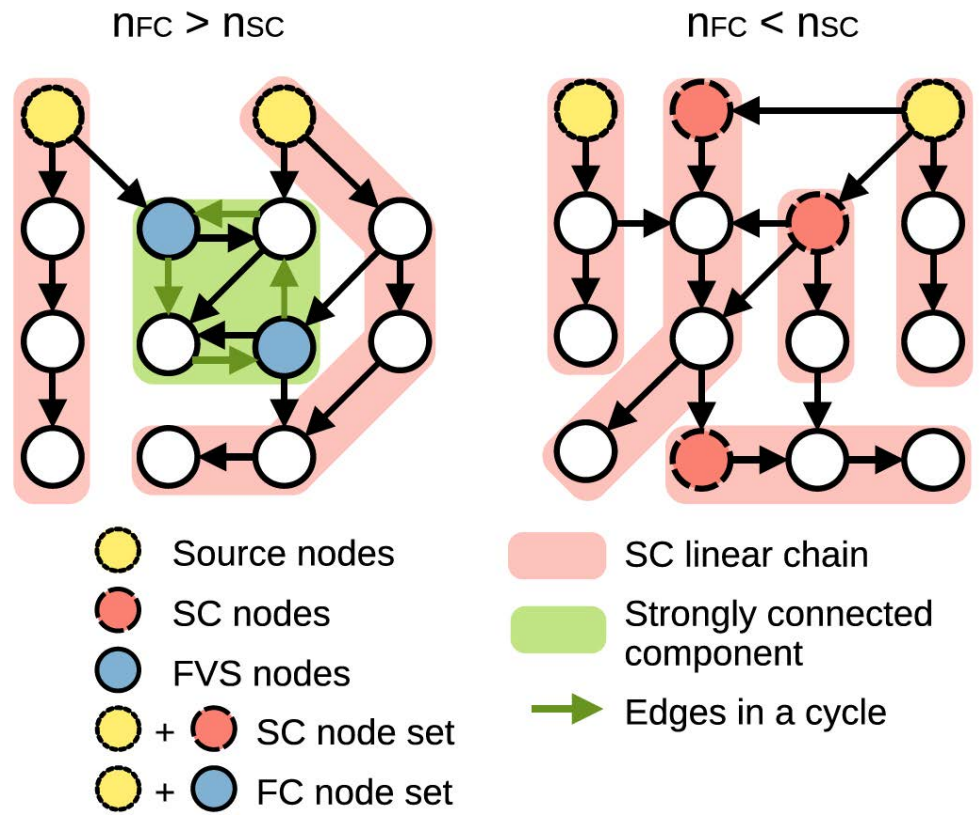


n_S	Sources
n_{FVS}	Feedback vertex set
$n_{FC} = n_S + n_{FVS}$	FVS control

Control fractions n_{FC} and n_{SC} are quite different for many networks



- Regulatory
- ◇ Foodweb
- ▽ Neural
- ▲ WWW
- ◆ Internet
- ◻ Circuits
- Trust
- ▽ Citations
- Social Commun
- Intra-organizational
- ▲ Power grid

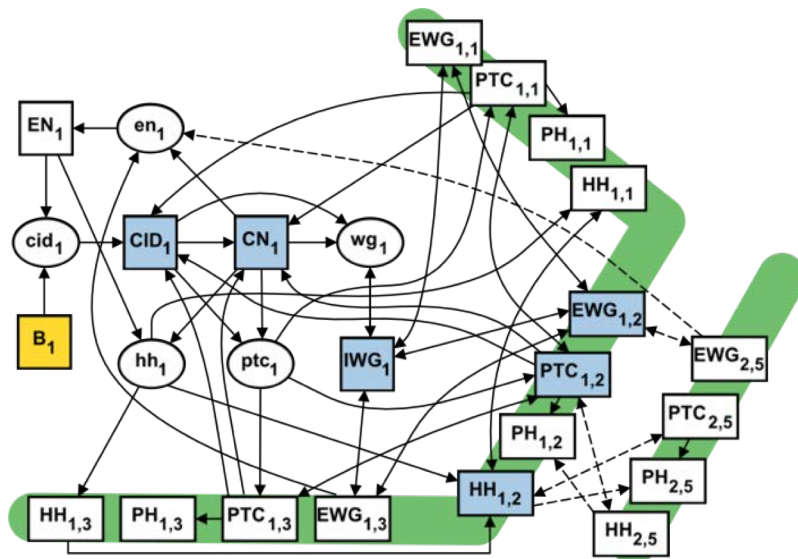


FC: FVS control
SC: Structural controllability

What happens when using FVS control on a real biological network model?

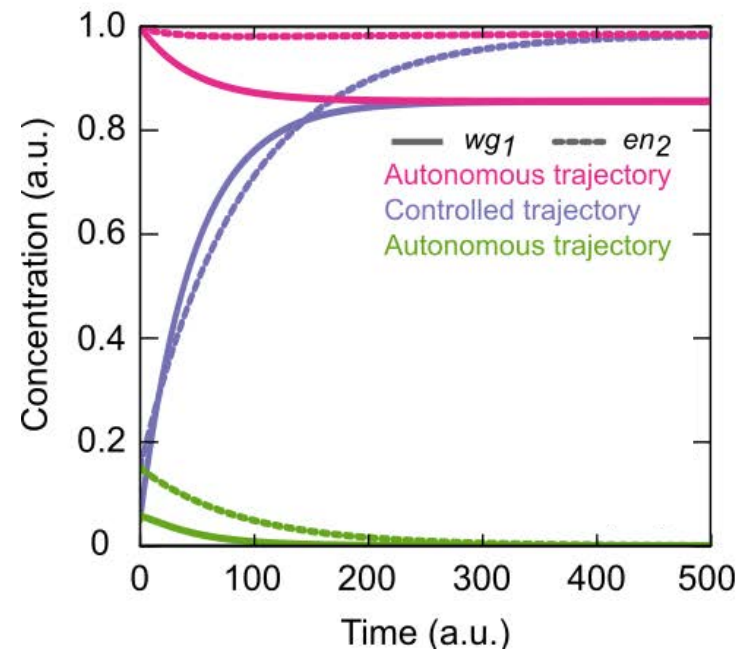
FC makes **model-independent** predictions (valid for all parameters)

Fruit fly segmentation network model



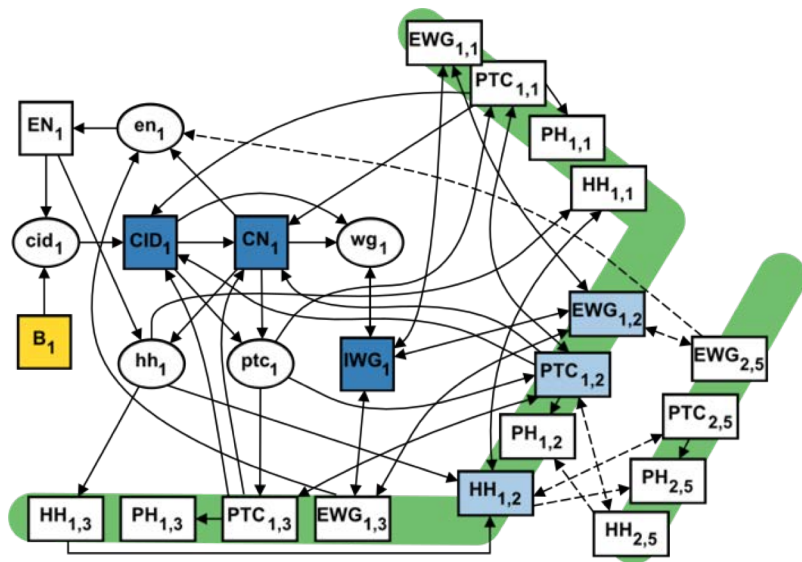
 +  FC node set

FVS control trajectories

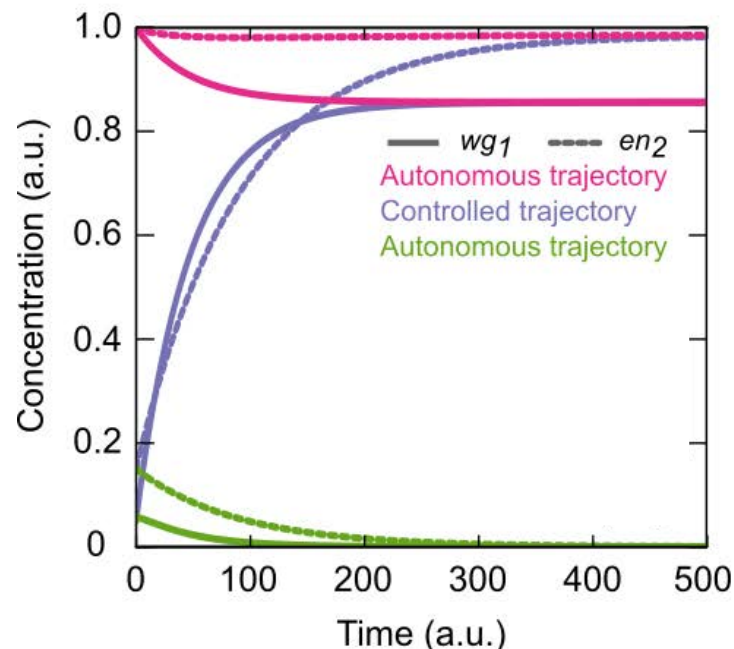





FC makes **model-independent** predictions (valid for all parameters)
 Starting from FC, we can find **model-dependent** predictions



Fruit fly segmentation network model



FVS control trajectories



 +  +  FC node set (model-independent)

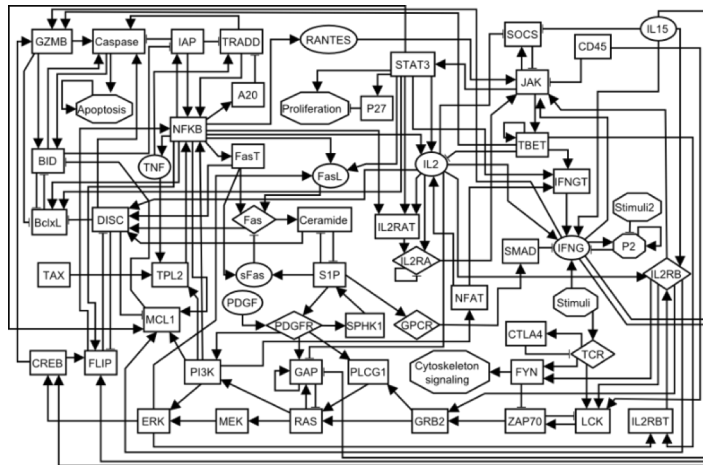
 +  Reduced FC node set (model-dependent)

Can we find a more principled way to do model-dependent attractor control?

Can we find a more principled way to do model-dependent attractor control?

Start with simplest nonlinear dynamics:
Boolean systems

Note: the method I will describe is very similar to the one described earlier by Jun Pang

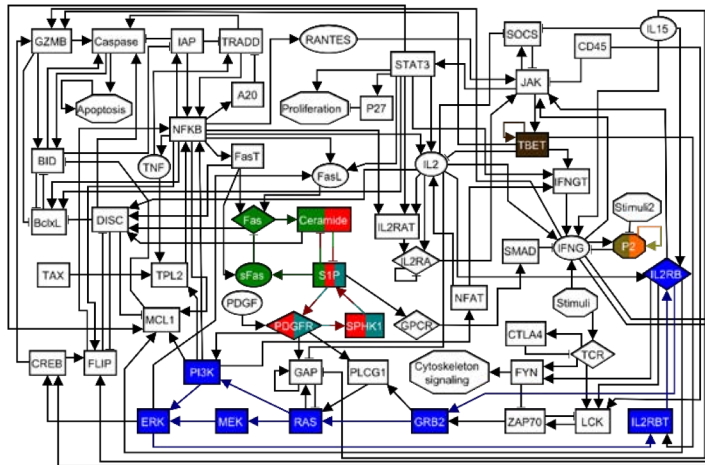


Cell fate A

Cell fate B

Zañudo and Albert
PLoS Comp. Biol.
11(4): e1004193
(2015).

Attractor control: Find subnetworks that stabilize in a fixed state

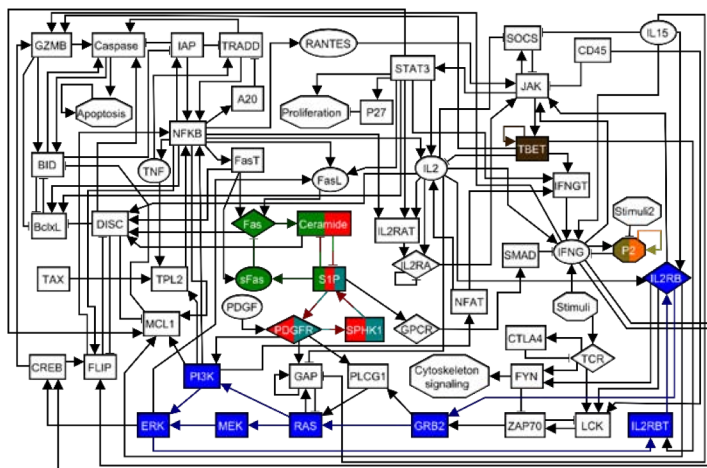


Cell fate A

Cell fate B

Zañudo and Albert
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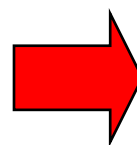
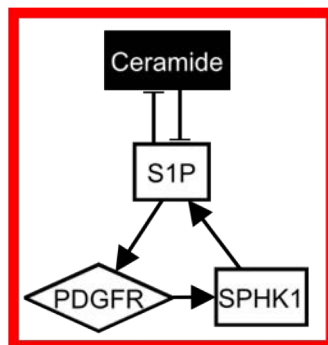
Attractor control: Find subnetworks that stabilize in a fixed state



Cell fate A

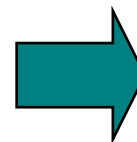
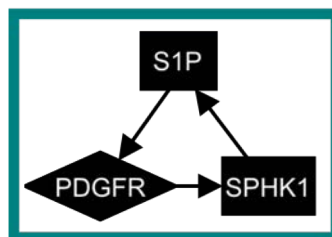
Cell fate B

Zañudo and Albert
 PLoS Comp. Biol.
 11(4): e1004193
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Cell fate A

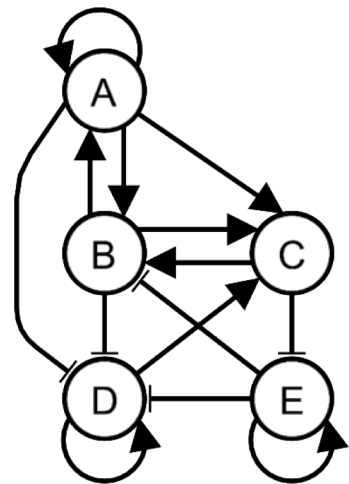
White: ON
 Black: OFF



Cell fate B

Subnetworks that stabilize in a fixed state: stable motifs

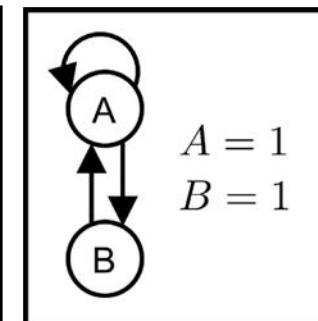
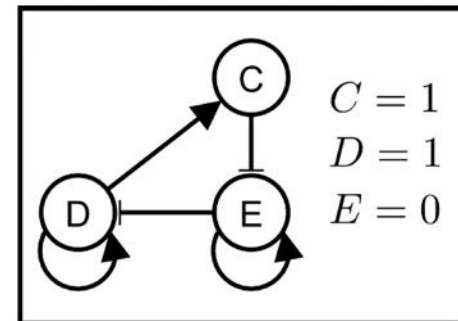
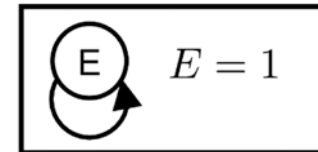
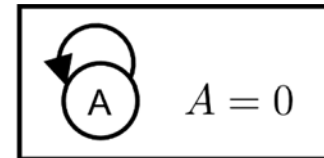
Logical model



$$\begin{aligned}
 f_A &= A \text{ AND } B \\
 f_B &= A \text{ OR } C \text{ OR NOT } E \\
 f_C &= (A \text{ AND } B) \text{ OR } D \\
 f_D &= (\text{NOT } B \text{ AND NOT } A) \\
 &\quad \text{OR } (D \text{ AND NOT } A) \\
 &\quad \text{OR } (D \text{ AND NOT } B) \\
 &\quad \text{OR NOT } E \\
 f_E &= E \text{ OR NOT } C
 \end{aligned}$$



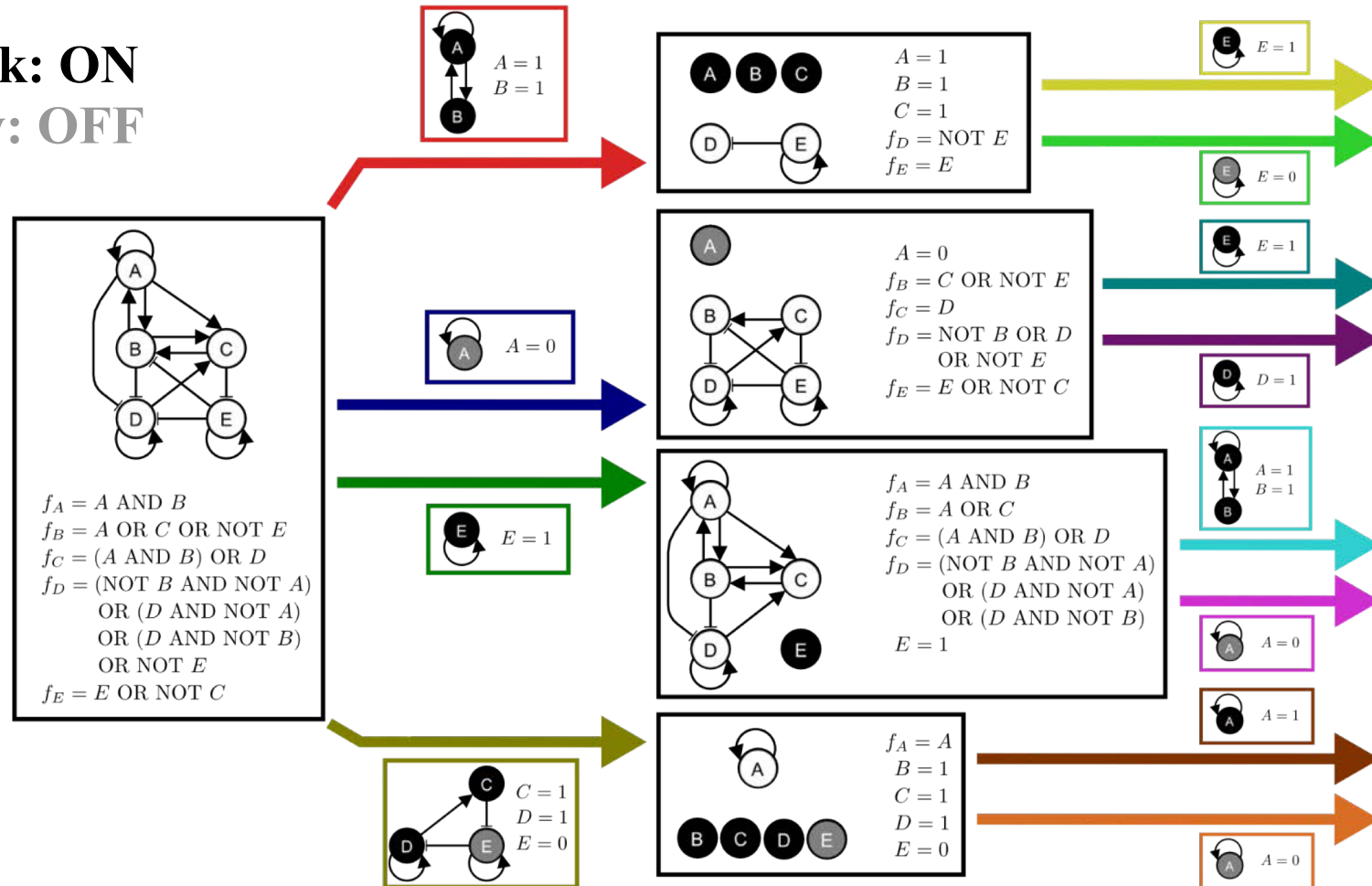
Stable motifs



- Stable motifs

- Identified on a logic-expanded network representation
- Network property: Intersecting positive feedback loops
- Dynamical property: Trap subspaces

Black: ON
Grey: OFF



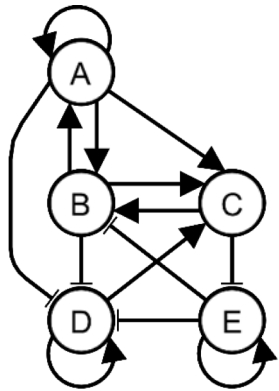
Original logical network model

Stable motifs of the original network model

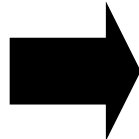
Reduced logical network models

Stable motifs of the reduced network models

Black: ON
Grey: OFF

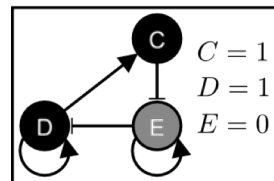
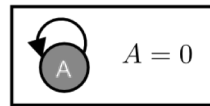
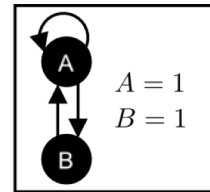


+



Stable motifs

Attractors



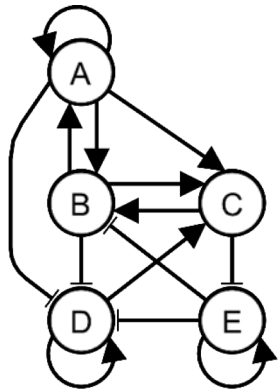
$f_A = A \text{ AND } B$
 $f_B = A \text{ OR } C \text{ OR NOT } E$
 $f_C = (A \text{ AND } B) \text{ OR } D$
 $f_D = (\text{NOT } B \text{ AND NOT } A) \text{ OR } (D \text{ AND NOT } A) \text{ OR } (D \text{ AND NOT } B) \text{ OR NOT } E$
 $f_E = E \text{ OR NOT } C$

J.G.T. Zañudo and R. Albert.
 PLoS Comp. Biol. 11(4):
 e1004193 (2015).

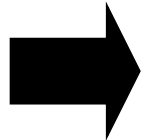
Dynamics →

- Attractor control: Sequence of stable motifs → Attractor

Black: ON
Grey: OFF

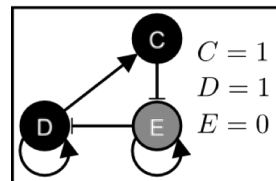
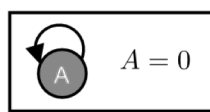
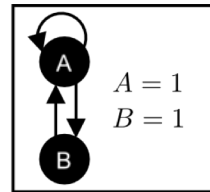


+



Stable motifs

Attractors



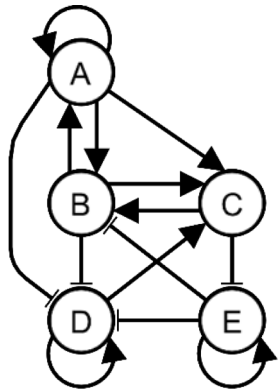
$f_A = A \text{ AND } B$
 $f_B = A \text{ OR } C \text{ OR NOT } E$
 $f_C = (A \text{ AND } B) \text{ OR } D$
 $f_D = (\text{NOT } B \text{ AND NOT } A)$
 OR $(D \text{ AND NOT } A)$
 OR $(D \text{ AND NOT } B)$
 OR NOT E
 $f_E = E \text{ OR NOT } C$

J.G.T. Zañudo and R. Albert.
 PLoS Comp. Biol. 11(4):
 e1004193 (2015).

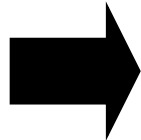
Dynamics →

- Attractor control: Sequence of stable motifs → Attractor

Black: ON
Grey: OFF

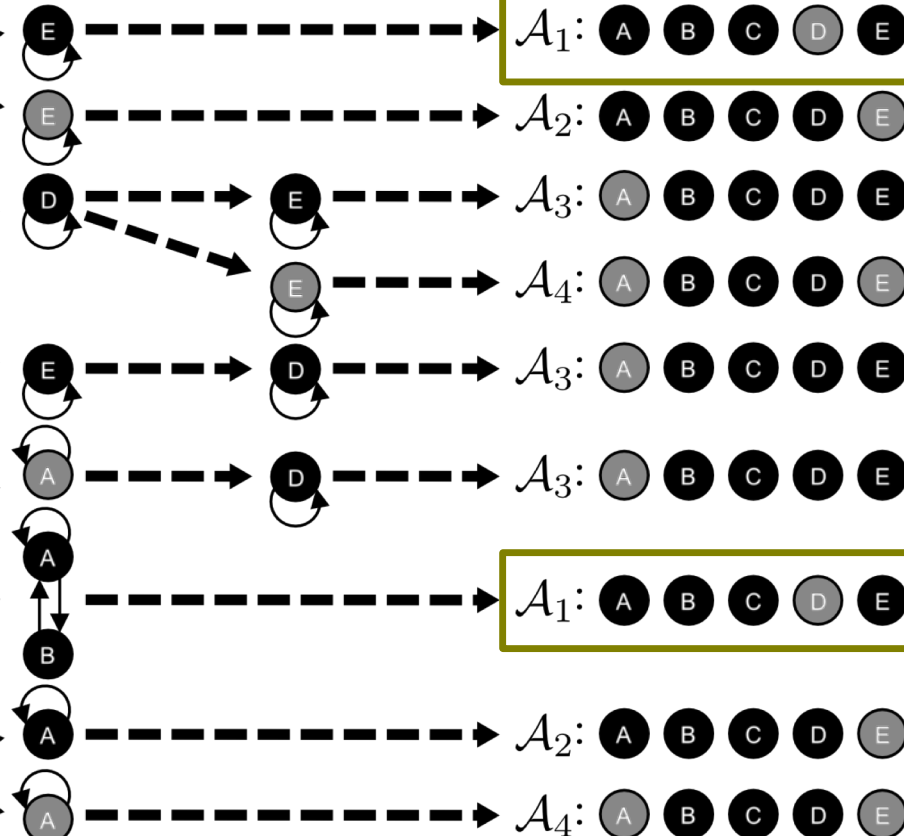
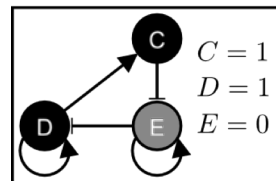
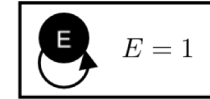
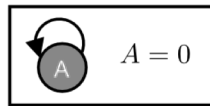
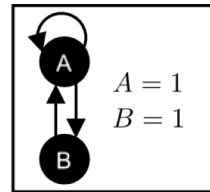


+



Stable motifs

Attractors



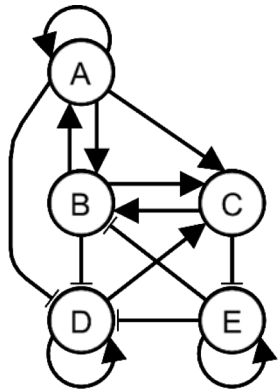
$f_A = A \text{ AND } B$
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 $f_D = (\text{NOT } B \text{ AND NOT } A) \text{ OR } (D \text{ AND NOT } A) \text{ OR } (D \text{ AND NOT } B) \text{ OR NOT } E$
 $f_E = E \text{ OR NOT } C$

J.G.T. Zañudo and R. Albert.
PLOS Comp. Biol. 11(4):
e1004193 (2015).

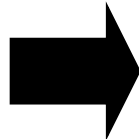
Dynamics →

- Attractor control: Sequence of stable motifs → Attractor

Black: ON
Grey: OFF

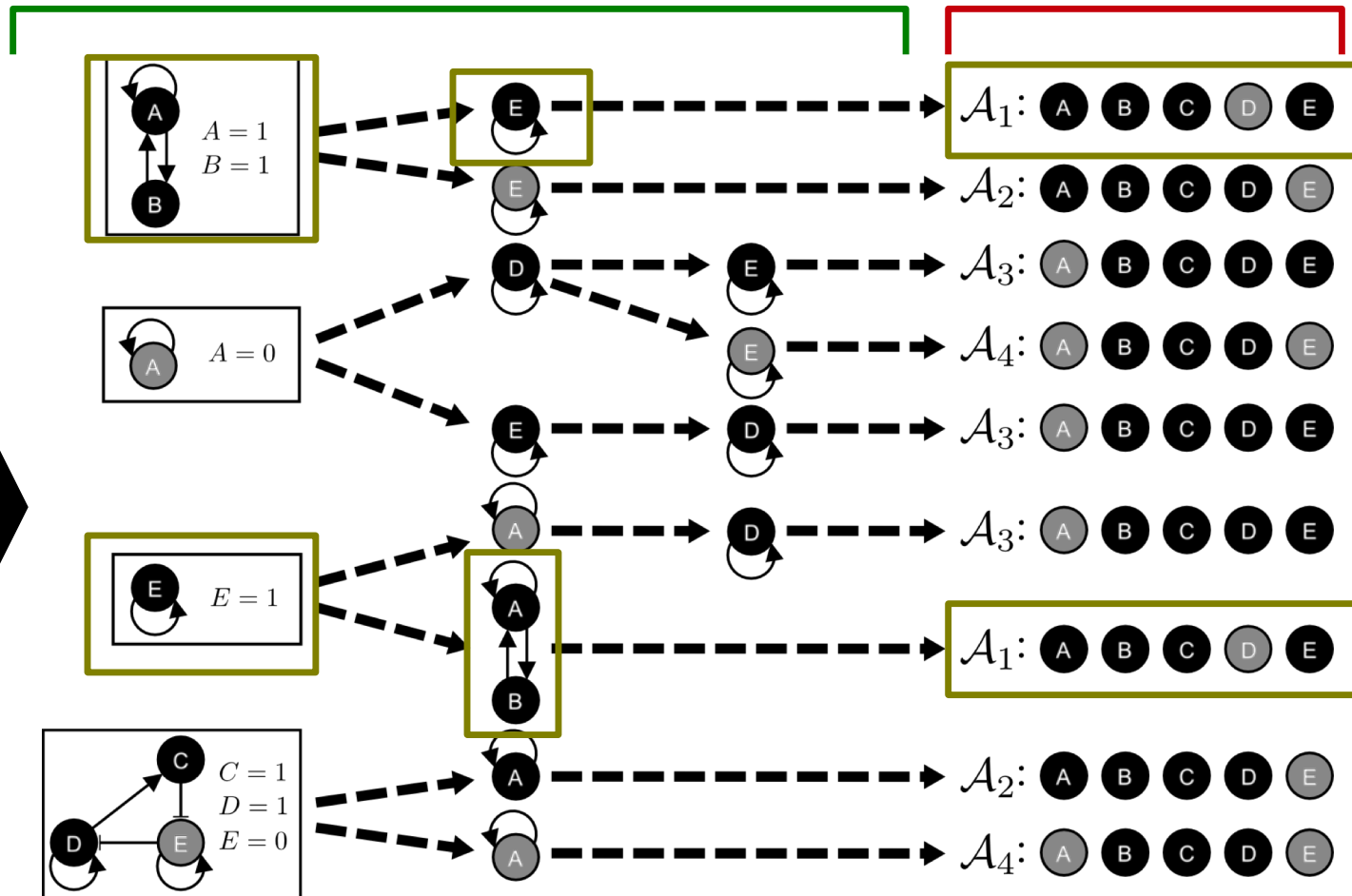


+



Stable motifs

Attractors



$f_A = A \text{ AND } B$
 $f_B = A \text{ OR } C \text{ OR NOT } E$
 $f_C = (A \text{ AND } B) \text{ OR } D$
 $f_D = (\text{NOT } B \text{ AND NOT } A) \text{ OR } (D \text{ AND NOT } A) \text{ OR } (D \text{ AND NOT } B) \text{ OR NOT } E$
 $f_E = E \text{ OR NOT } C$

J.G.T. Zañudo and R. Albert.
 PLoS Comp. Biol. 11(4):
 e1004193 (2015).

Dynamics →

What is the connection between stable motif control and FVS control?

Model-dependent
 (model-specific cycles)

VS

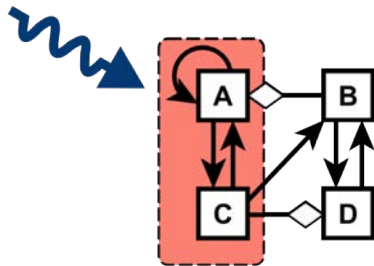
Model-independent
 (all cycles)

Control method

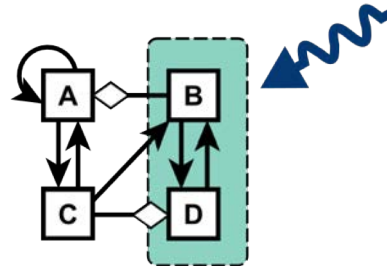
Stable motif (SM) control
 (model-dependent)

Stable motif (SM) control
 (model-dependent)

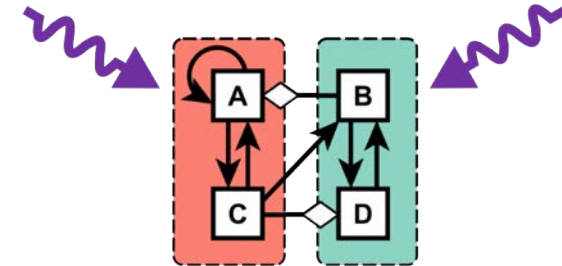
Feedback vertex set (FVS)
 control (model-independent)



Model 1
 (Parameters = P1)



Model 2
 (Parameters = P2)

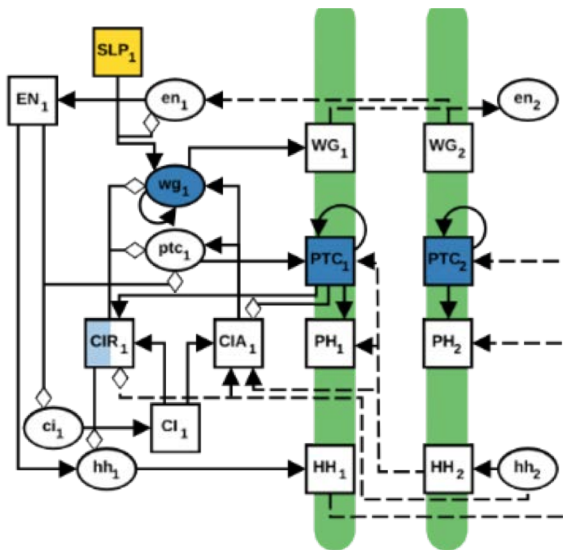


Model unknown
 (Parameters = arbitrary)

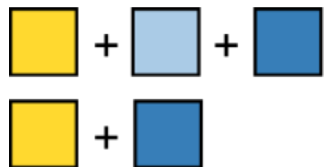
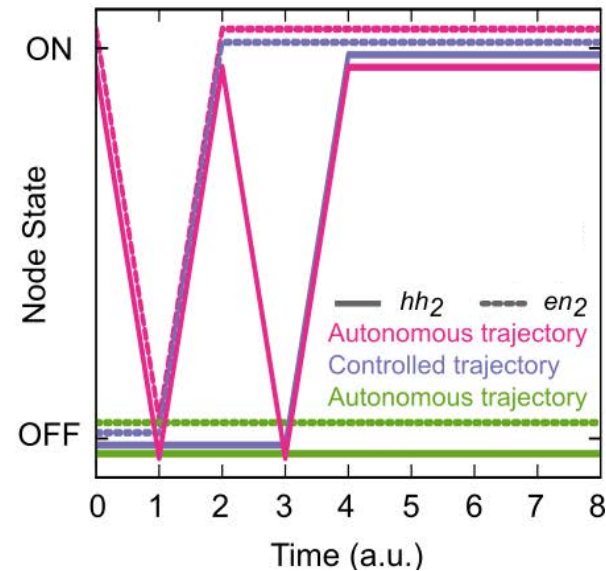
Model
 (parameters)

Stable motif control (model-dependent) vs FVS control (model-independent)

Fruit fly Boolean network model



Controlled trajectories



FVS control (model-independent)

Stable motif control (model-dependent)

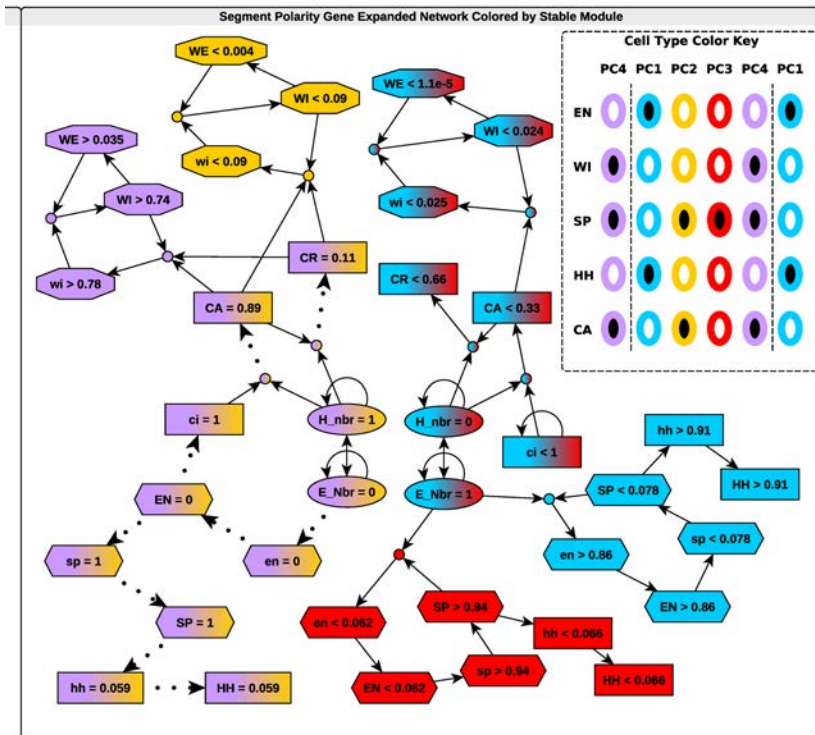
Stable motifs in continuous models might allow model-dependent attractor control predictions for continuous systems



Identifying (un)controllable dynamical behavior in complex networks

Jordan C. Rozum^{1*}, Réka Albert^{1,2}

PLoS Comput Biol 14(12): e1006630



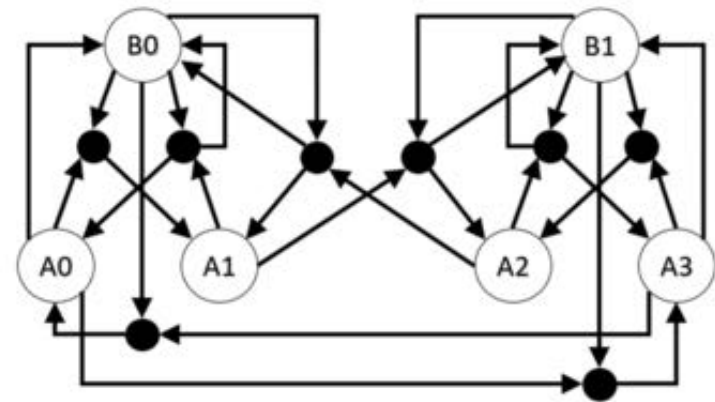
PHYSICAL REVIEW E

covering statistical, nonlinear, biological, and soft matter physics

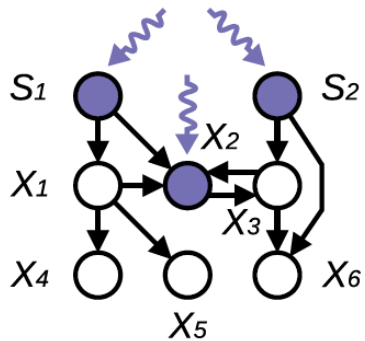
General method to find the attractors of discrete dynamic models of biological systems

Xiao Gan and Réka Albert

Phys. Rev. E **97**, 042308



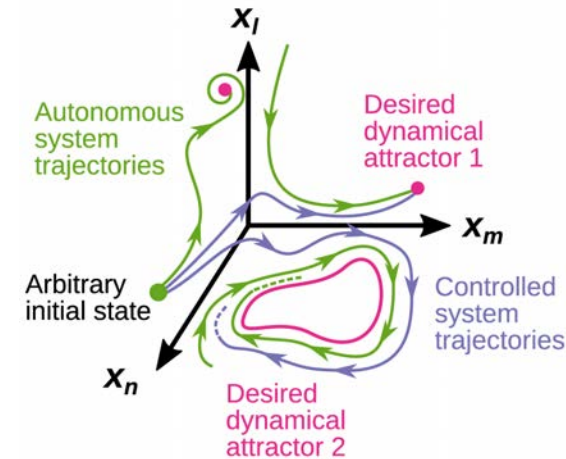
- Structure-based control approach for networks with nonlinear dynamics:



Feedback Vertex Set control



Attractor-based network control

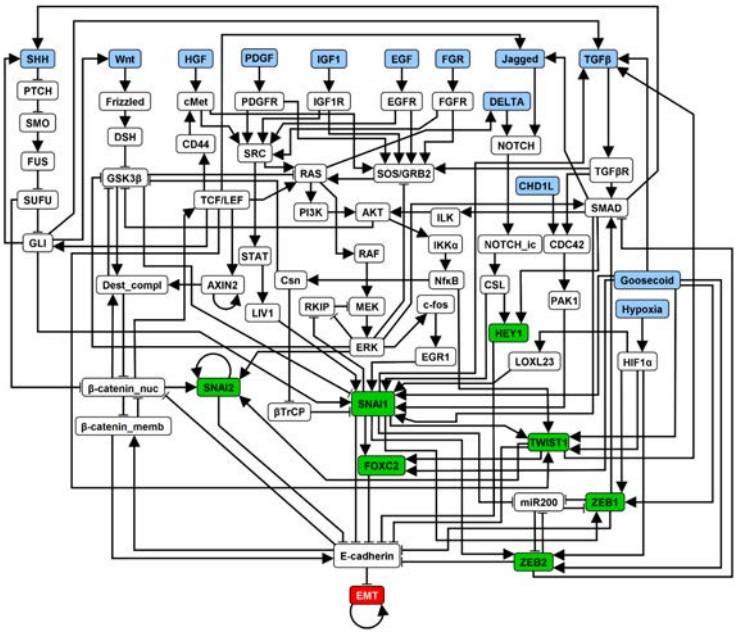


- Stable motif control allows control when the model dynamics are specified
- Cycles in the network are crucial for nonlinear attractor control
- FVS control (model-independent) and stable motif control (model-dependent); complementary control approaches

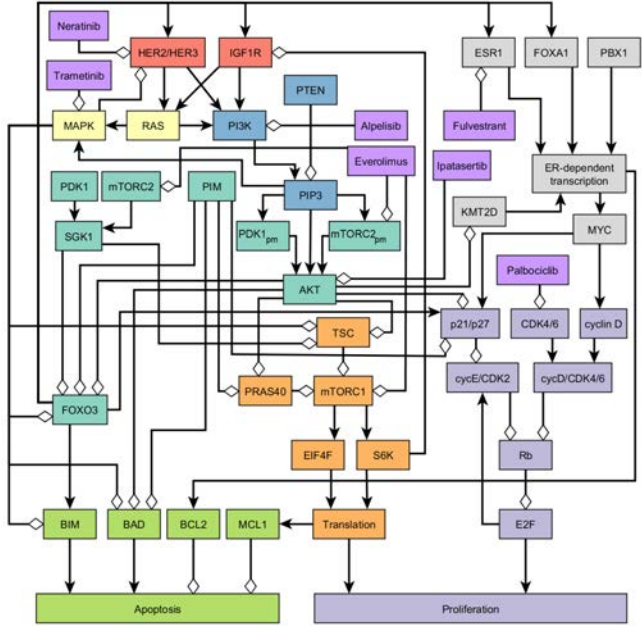
Objective of my research

Use mathematical models and control methods to predict

Nodes that block metastatic reprogramming
(EMT in liver cancer)



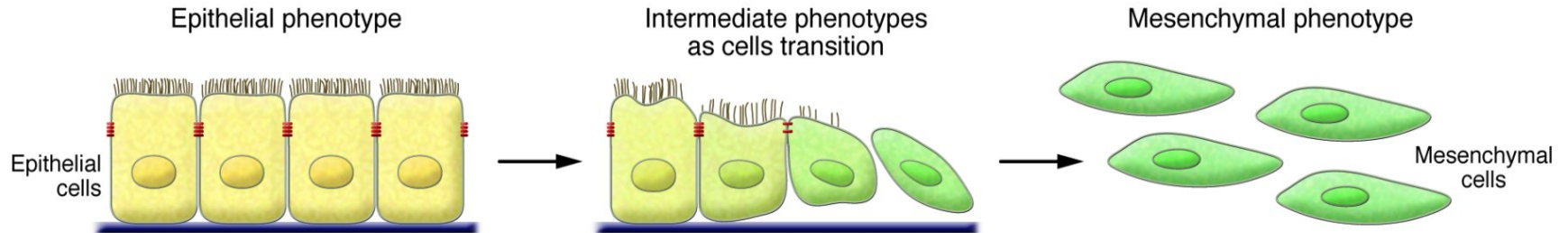
Resistance mechanisms and drug combinations
(PI3K inhibition in ER+ MBC)



SN Steinway, **JGT Zañudo**, et al. Cancer Res. (2014).
SN Steinway*, **JGT Zañudo***, et al. npj Syst. Biol. & Appl. (2015).

JGT Zañudo, et al. Cancer Convergence. (2017).
JGT Zañudo, et al. bioRxiv. (2020).

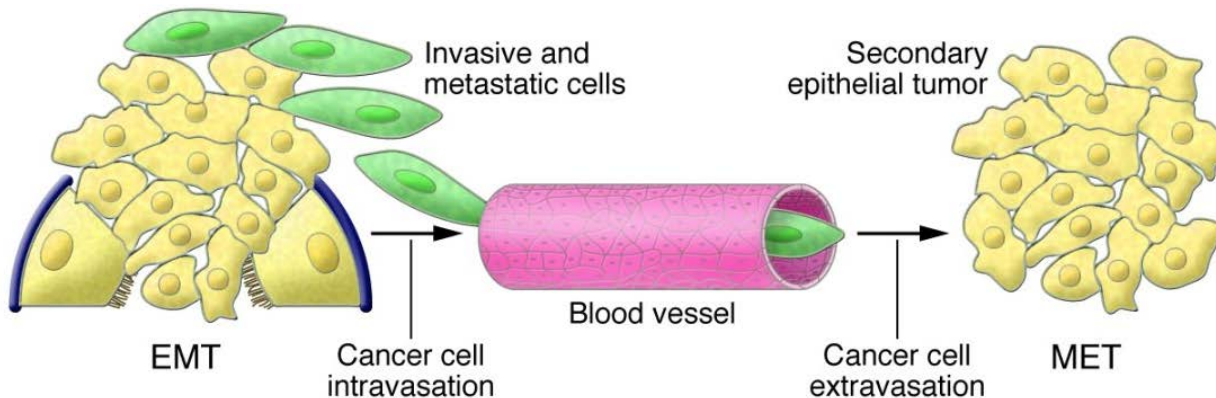
- Epithelial-to-mesenchymal transition (EMT) is a natural developmental and wound-healing cellular process.



High E-cadherin expression
Strong Adhesion

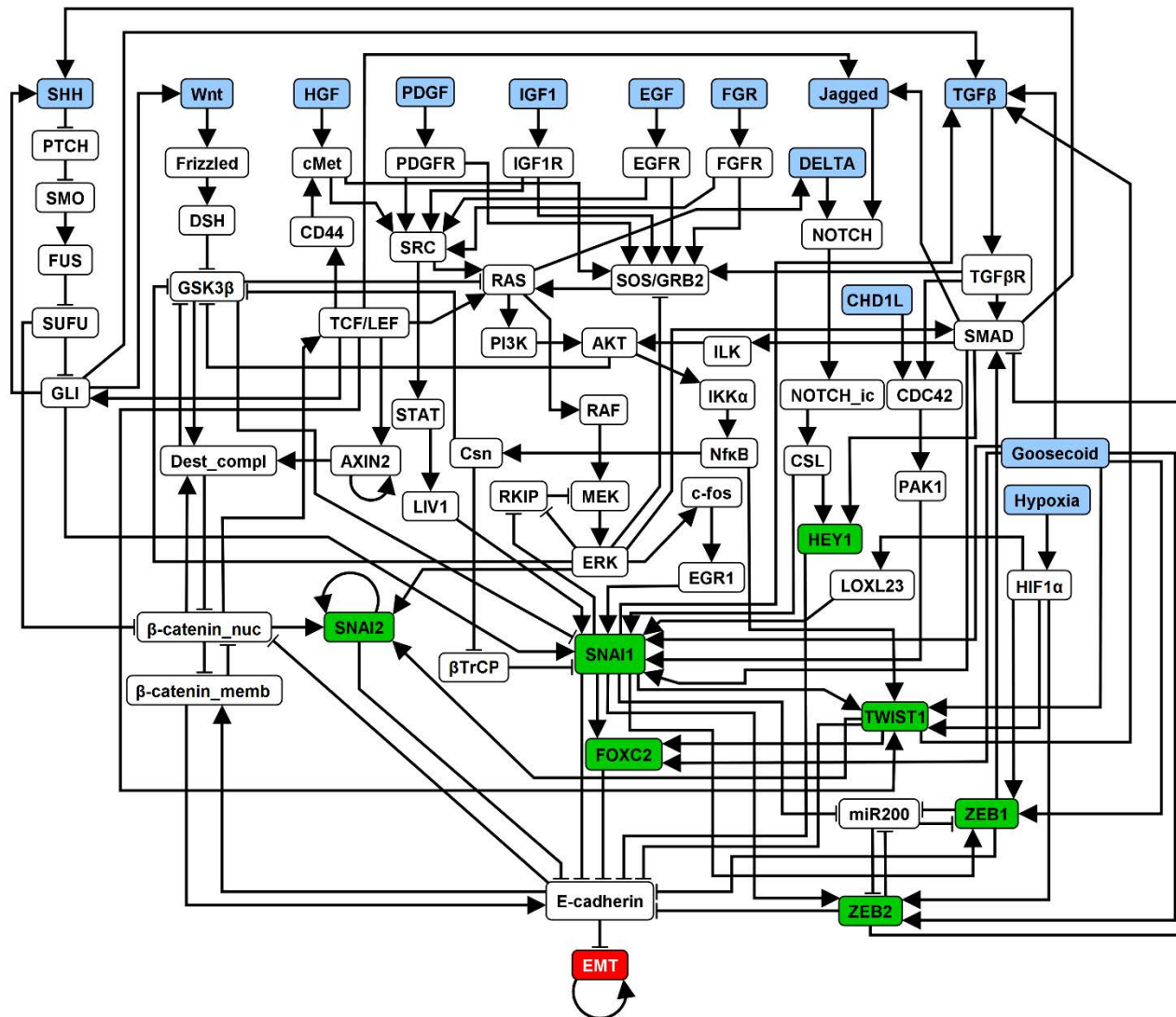
Loss of E-cadherin expression
Weak adhesion

- EMT process is hijacked by cancer cells (initiation of invasion and metastasis).



Kalluri and Weinberg.
J Clin Invest **119** (6)
(2009).

Network representing the known regulation of EMT was curated from the literature.



69 nodes and
 135 interactions

BLUE:
 External signals

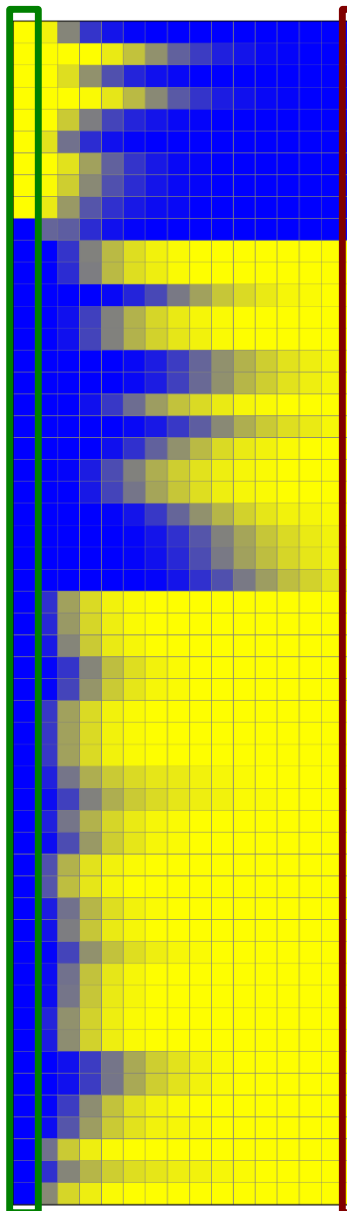
GREEN:
 Transcription factors

RED:
 Hallmark node

SN Steinway, JGT Zañudo, W Ding, CB Rountree, D Feith, TP Loughran, R Albert. *Cancer Res* 74 (21) (2014).



Color coded node activity



- Dest_compl
- β-catenin_memb
- βtrep
- E-cadherin
- SUFU
- GSK3β
- RKIP
- miR200
- PTCH
- SOS/GRB2 ←
- c-fos
- Csn
- EMT
- EGR1
- GLI ←
- AXIN2 ←
- CD44
- DSH
- eMet
- β-catenin_nuc
- Wnt ←
- Frizzled
- TCF/LEF
- SRC
- STAT
- LIV1
- AKT
- NOTCH ←
- NOTCH_ic
- FOXC2
- TWIST1
- DELTA
- PI3K
- RAF
- ILK
- Jagged
- SHH ←
- HEY1
- RAS ←
- PAK1
- SNAI1
- ERK
- FUS ←
- Csl ←
- NfkB
- MEK
- IKKα
- ZEB1
- ZEB2
- SNAI2
- SMO
- CDC42
- SMAD ←
- TGFβR

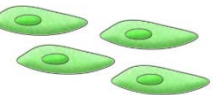
Model we built has two steady states (without external signals):

- Epithelial state (E)
- Mesenchymal state (M)

Epithelial + TGFβ → Mesenchymal

Predicts activation of multiple signaling pathways during TGFβ induction

We experimentally test activation of certain pathways

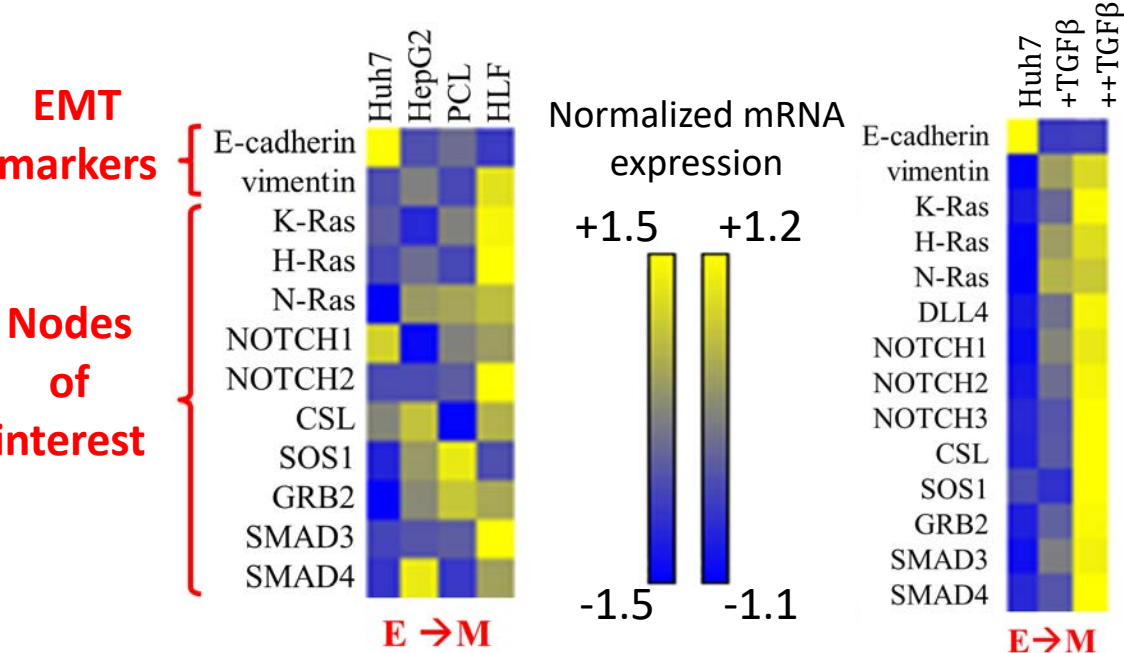


+TGFβ Time steps Mesenchymal

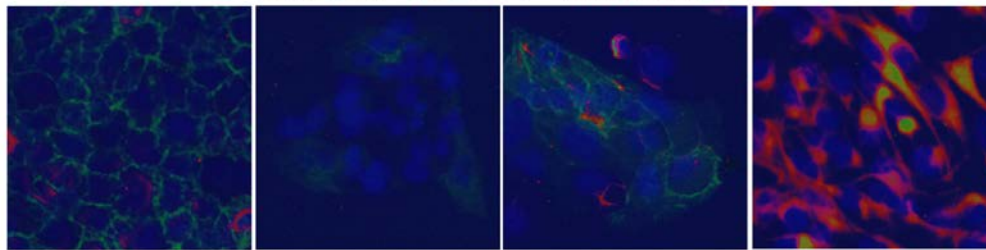
SN Steinway, JGT Zañudo, W Ding, CB Rountree, D Feith, TP Loughran, R Albert. Cancer Res 74 (21) (2014).

We validated model-directed activation of several signaling pathways and genes during TGFβ-driven EMT

CELL LINES



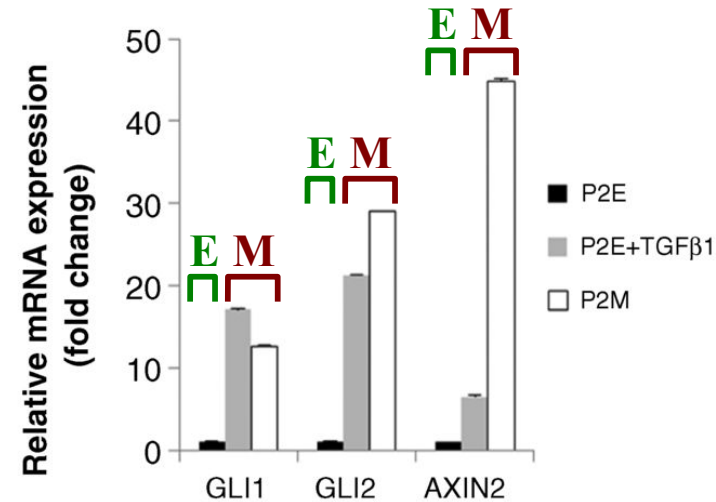
E-cadherin: GREEN vimentin: RED



Huh7 HepG2 PLC/PRF/5 HLF

E → M

MICE

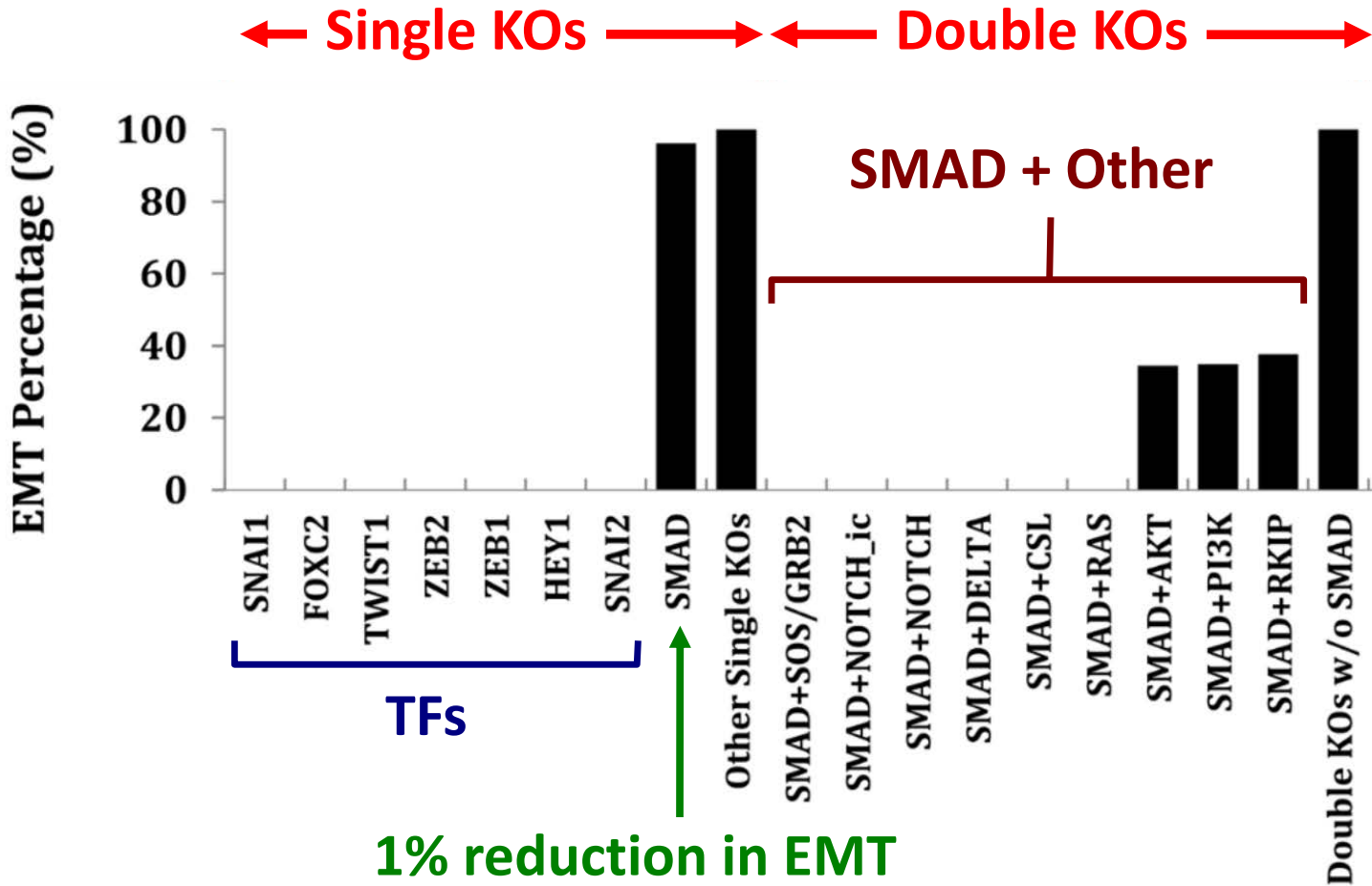


SN Steinway*, **JGT Zañudo***, PJ Michel, D Feith, TP Loughran, R Albert. npj Syst. Biol. and Applic. 15014 (2015).

SN Steinway, **JGT Zañudo**, W Ding, CB Rountree, D Feith, TP Loughran, R Albert. Cancer Res 74 (21) (2014).

How do we disrupt the network to suppress EMT and tumor invasion?

Computational interventions

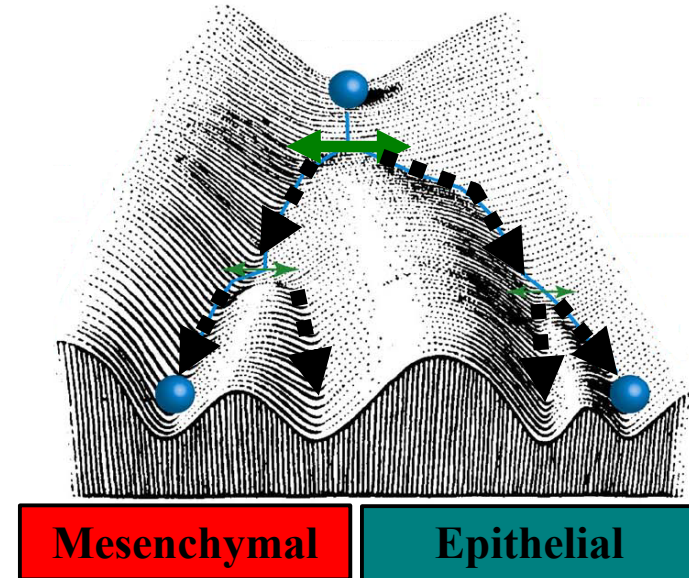


SN Steinway*, **JGT Zañudo***, PJ Michel, D Feith, TP Loughran, R Albert. npj Syst. Biol. and Applic. 15014 (2015).

So what?

Stable motifs help explain the
interventions

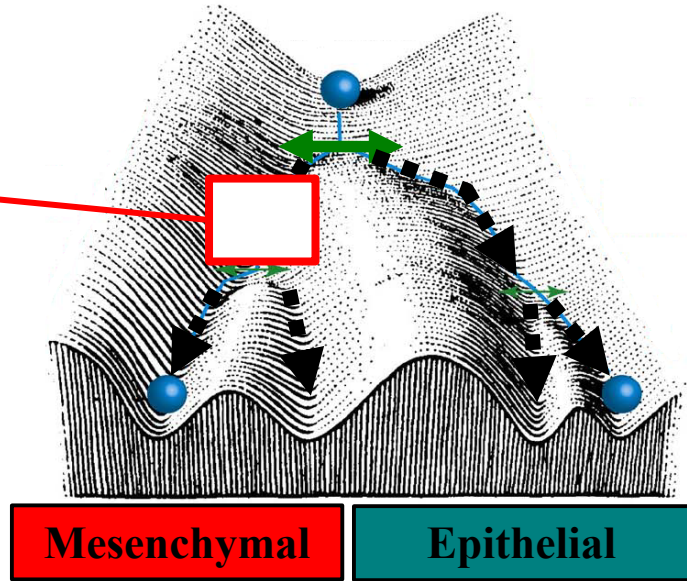
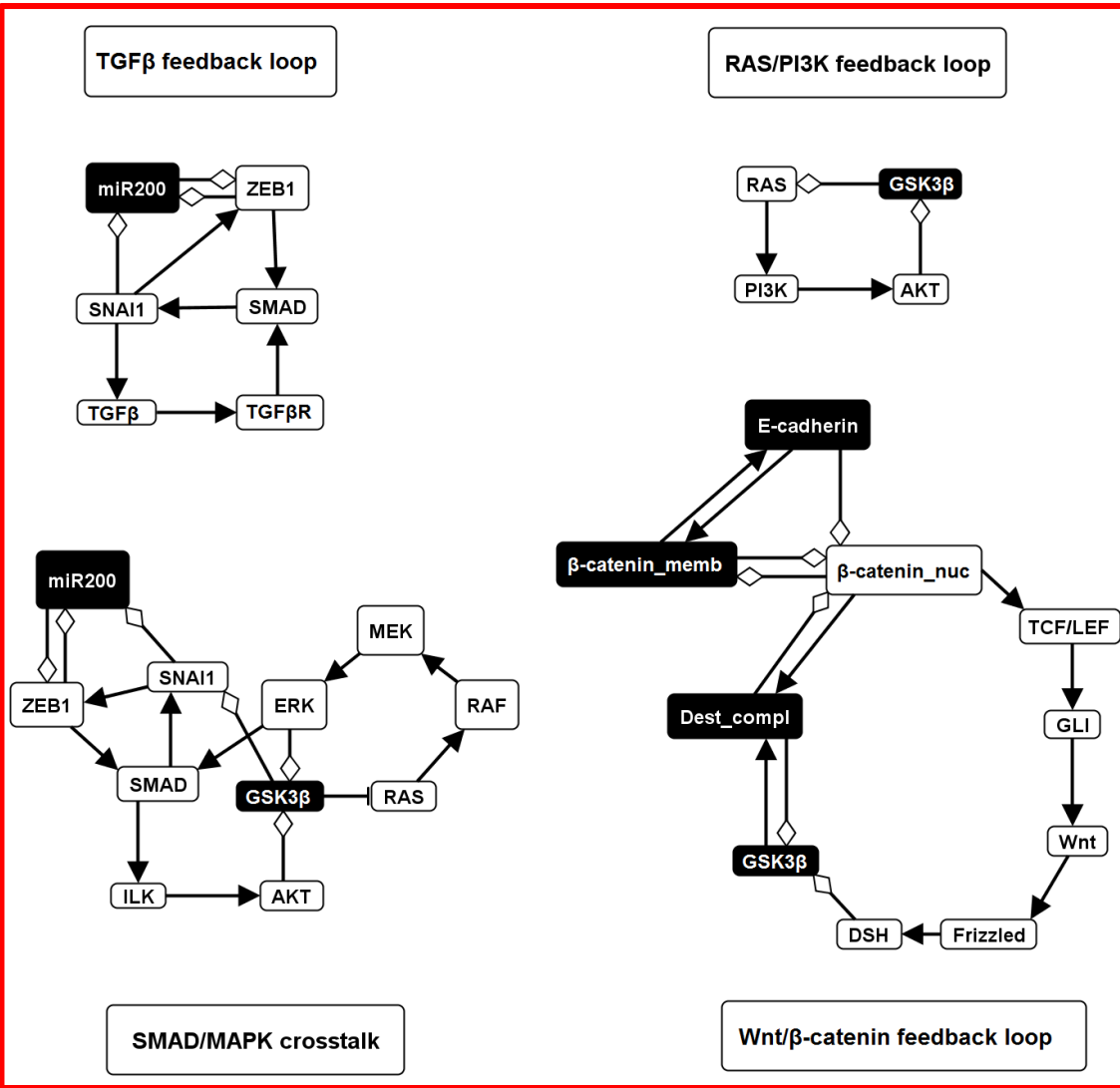
We used network control theory to identify that $TGF\beta$ drives EMT through the activation of intersecting feedback loops (stable motifs)



White: ON
Black: OFF

SN Steinway, JGT Zañudo, W Ding, CB Rountree, D Feith, TP Loughran, R Albert. Cancer Res 74 (21) (2014).

We used network control theory to identify that **TGF β** drives EMT through the activation of intersecting feedback loops (stable motifs)

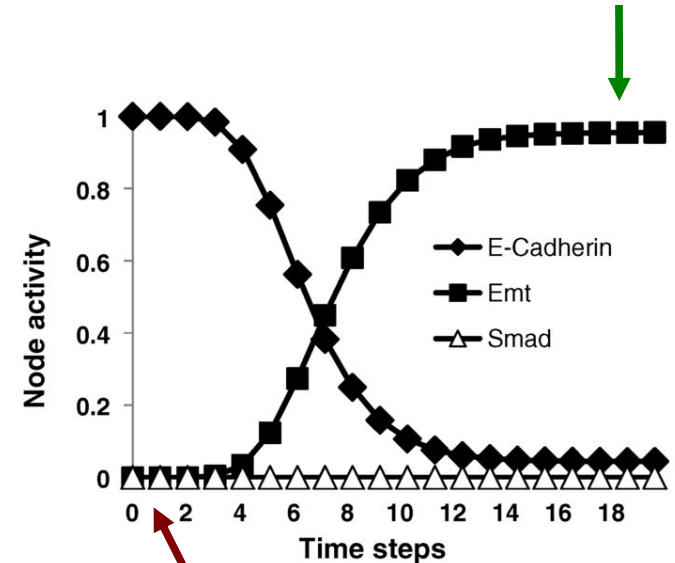


White: ON
 Black: OFF

SN Steinway, **JGT Zañudo**, W Ding, CB Rountree, D Feith, TP Loughran, R Albert. Cancer Res 74 (21) (2014).

Stable motifs explain why SMAD KD has minimal effect on EMT induction

1% reduction in EMT



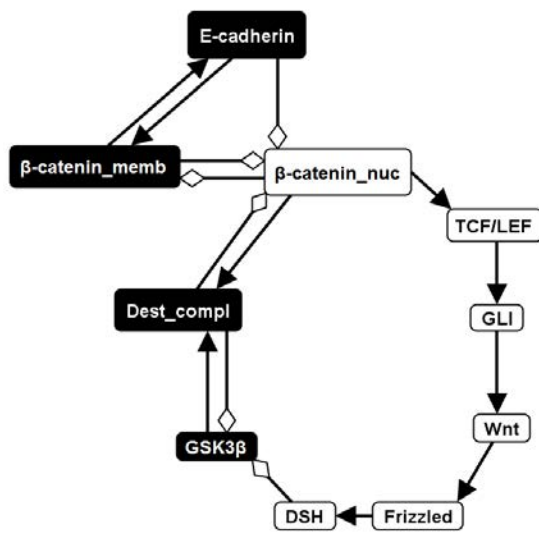
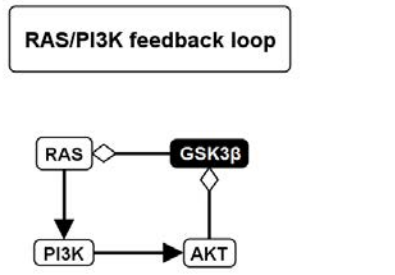
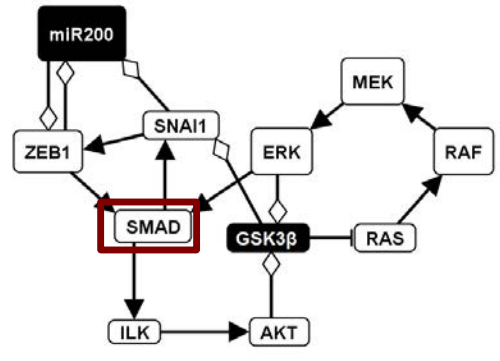
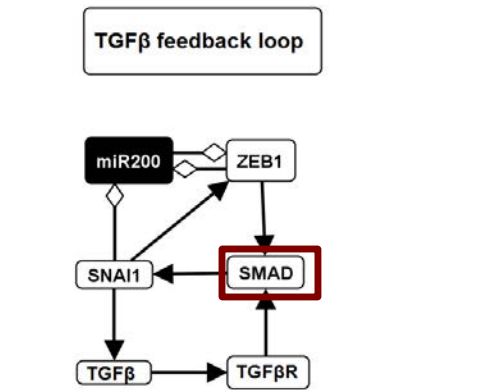
SMAD knock out

White: ON

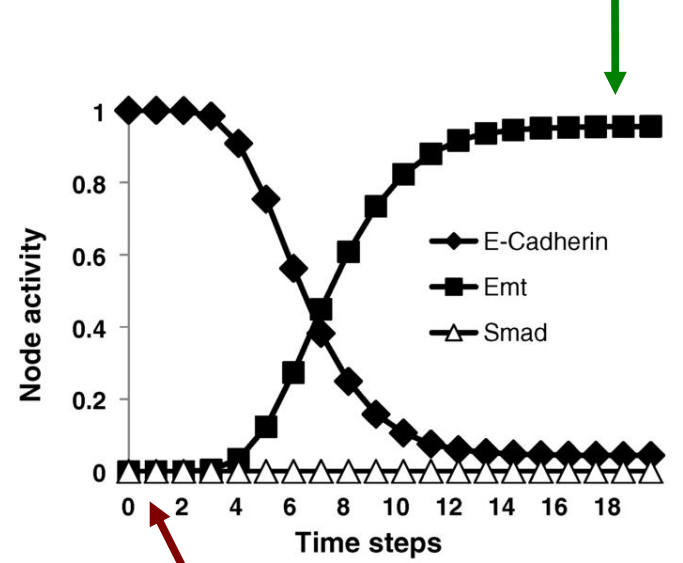
Black: OFF

SN Steinway, JGT Zañudo, W Ding, CB Rountree, D Feith, TP Loughran, R Albert. Cancer Res 74 (21) (2014).

Stable motifs explain why SMAD KD has minimal effect on EMT induction



1% reduction in EMT

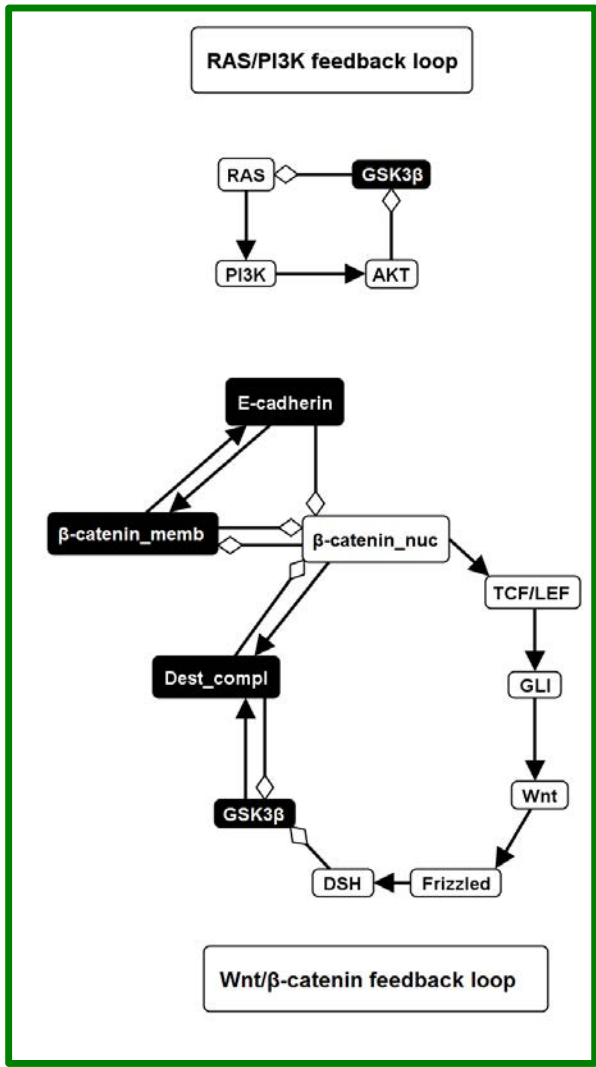
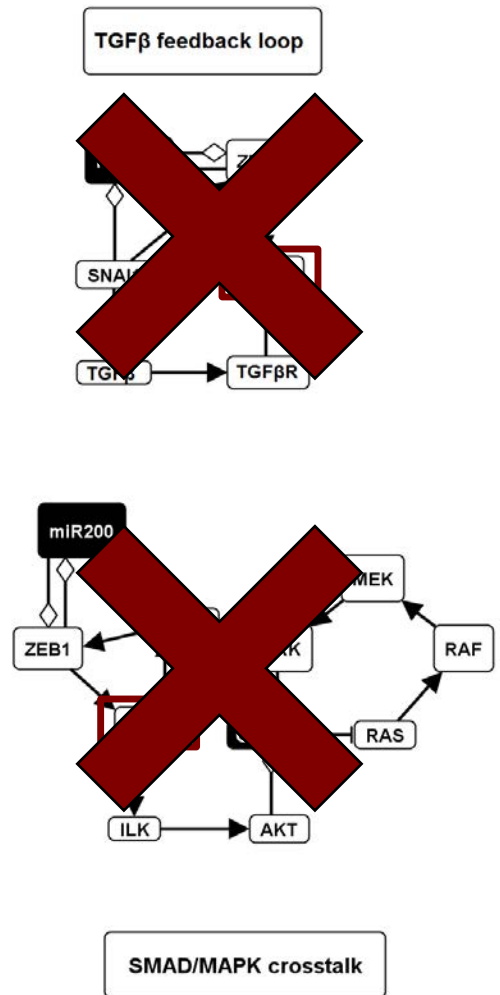


SMAD knock out

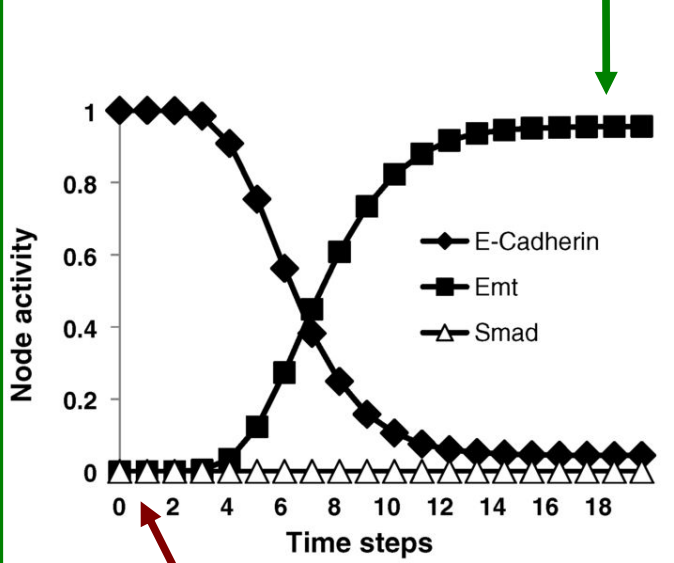
White: ON
 Black: OFF

SN Steinway, JGT Zañudo, W Ding, CB Rountree, D Feith, TP Loughran, R Albert. Cancer Res 74 (21) (2014).

Stable motifs explain why SMAD KD has minimal effect on EMT induction



1% reduction in EMT



SMAD knock out

White: ON
 Black: OFF

SN Steinway, JGT Zañudo, W Ding, CB Rountree, D Feith, TP Loughran, R Albert. Cancer Res 74 (21) (2014).

CONCLUSIONS

- Model recapitulates known EMT dynamics and predicts novel pathway cross activation.
- Model predicts KO combinations that suppress TGF β -driven EMT.
- Wet-lab experiments confirm many combinations suppress EMT.
- Stable motif analysis and control provides the motifs that drive EMT and the mechanism through which the KO combinations act.

Acknowledgements

J.G.T. Zañudo
Model-dependent and model-independent control of biological network models



ALBERT GROUP (PSU)

PENNSTATE



Réka Albert



Gang Yang

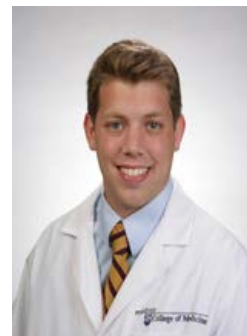
WAGLE LAB (DFCI, Broad)



LOUGHRAN LAB



UNIVERSITY
of VIRGINIA



- Steven N. Steinway
- Thomas P. Loughran
- David Feith

Discussions and data (FVS)

M. Angulo (UNAM)
YY. Liu (BWH, HMS)
A. Mochizuki (RIKEN)
YC. Lai (ASU)

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- Current funding from The V foundation /SU2C Convergence Scholar Award.



Jorge Gómez Tejeda Zañudo
Postdoctoral researcher
Broad Institute of MIT and Harvard
Dana-Farber Cancer Institute



Thank you for your time!
Questions, comments, suggestions?
Complaints???

Contact: jgtz@broadinstitute.org
[@jgtzanudo](https://twitter.com/jgtzanudo) (Twitter)

References:

Fiedler, B., Mochizuki, A., et al. (2013), *J. Dynamics and Differential Equations*.
Mochizuki, A., Fiedler, B., et al. (2013), *J. Theor. Bio.*
Zanudo J.G.T. & Albert R. et al. (2015), *PLoS Comp. Bio.*
Zanudo J.G.T., Yang G., & Albert R. (2017), *PNAS*.

Feedback vertex set control (FC)

Mochizuki et al. J. Theor. Biol. 335 (2013)
Zañudo et al. PNAS 114 (2017)

- **Structural:**

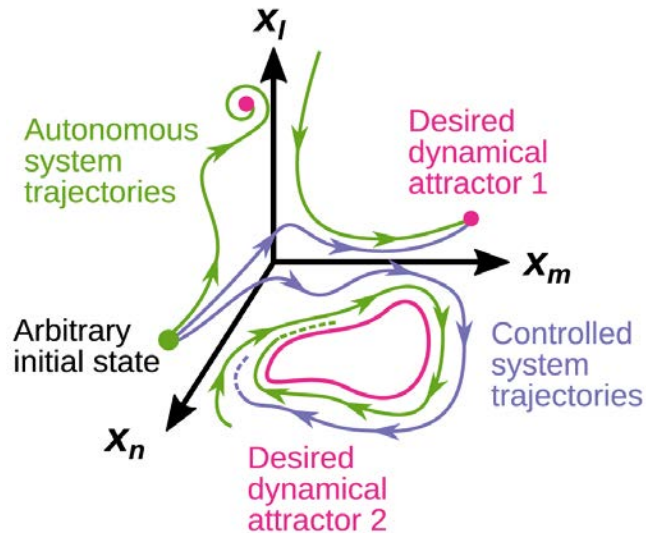
- Control nodes based solely on structure
- Guarantees control for the ensemble of networks with a given structure

- **Dynamics:**

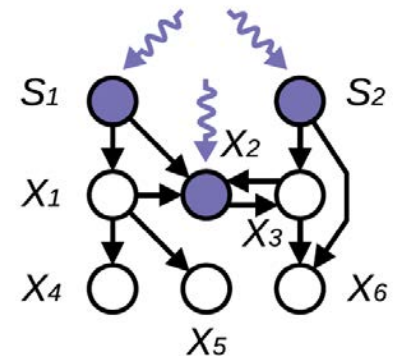
- Nonlinear with decay
- System attractors

- **Control actions:**

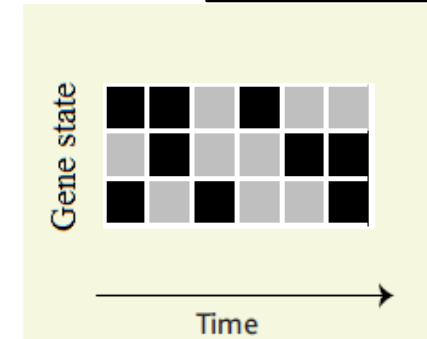
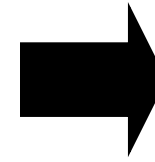
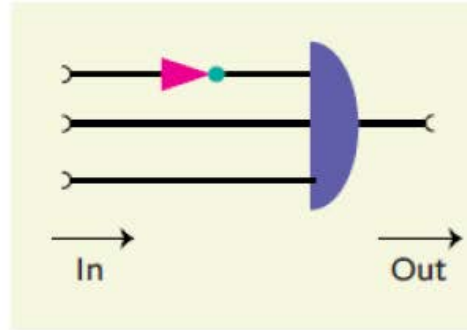
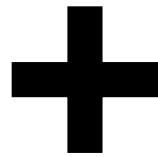
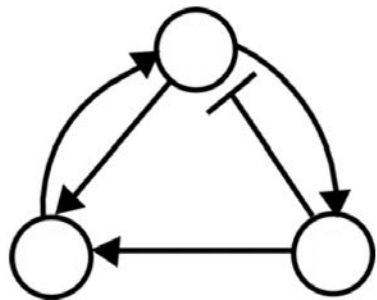
- Any IC to a target system attractor
- Fix state variable of FVS & sources into their state in the target attractor



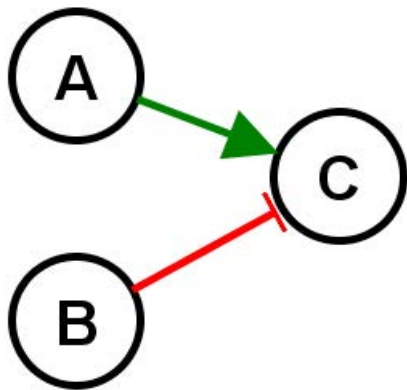
$$\frac{dX_i}{dt} = F_i(X_i, X_{I_i}, t),$$
$$\frac{dS_j}{dt} = G_j(t),$$



- Boolean models: ON (active) or OFF (inactive)



Bornholdt. Science
310, 5747 (2005).



Boolean variables

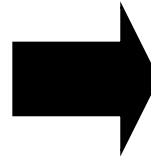
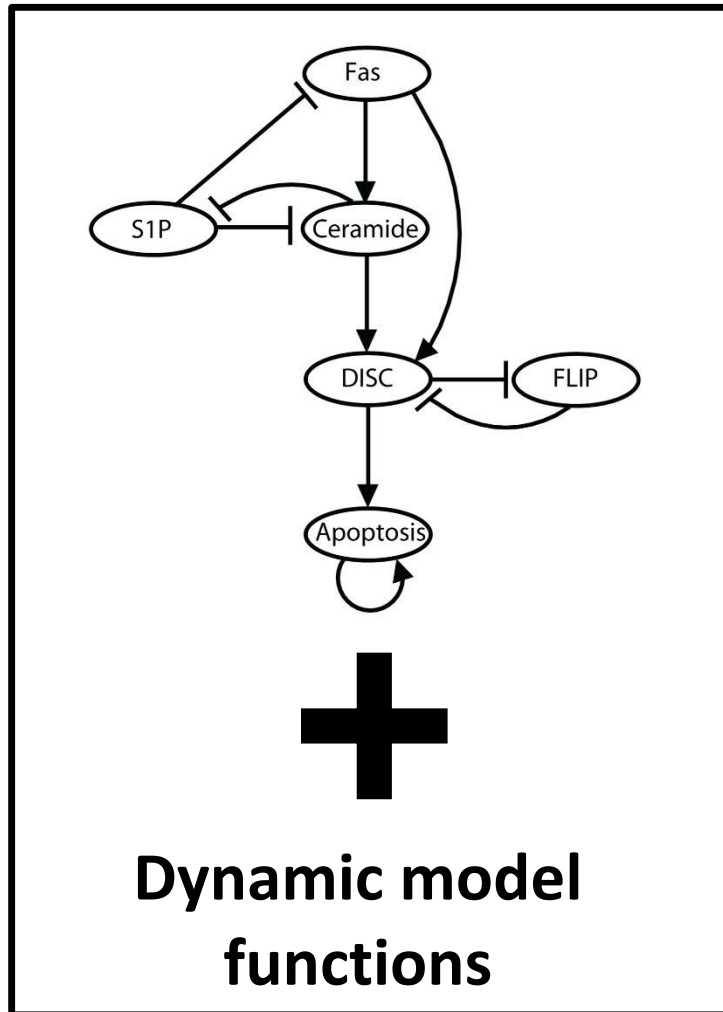
$$C(t + \tau) = \underline{A(t) \text{ and } (\text{not } B(t))}$$

Updating scheme dependent

Logical function

- Updating scheme: stochastic asynchronous (samples all timescales)

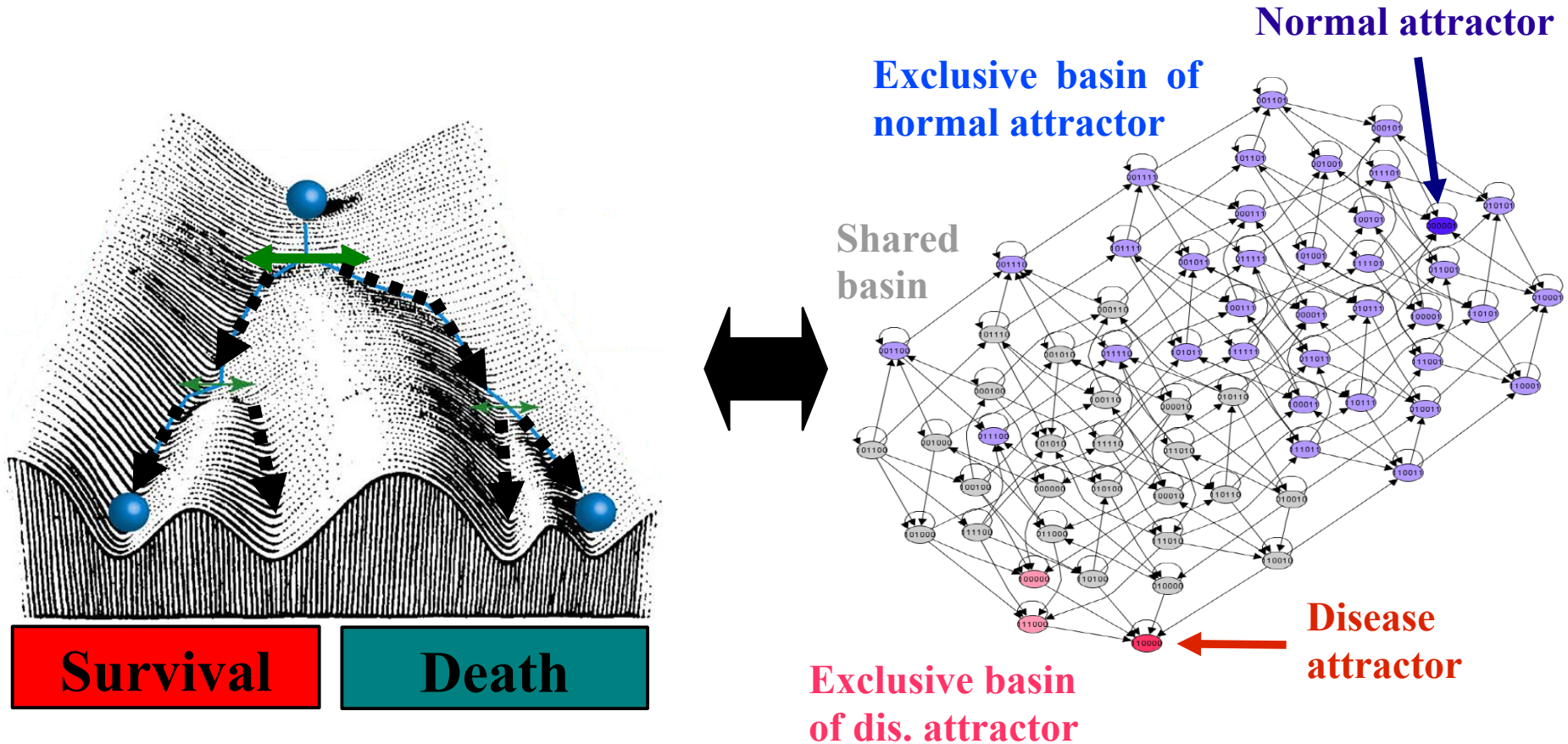
Attractors of models of intracellular networks: **stable cell states**
 (e.g. healthy state, disease states, etc)



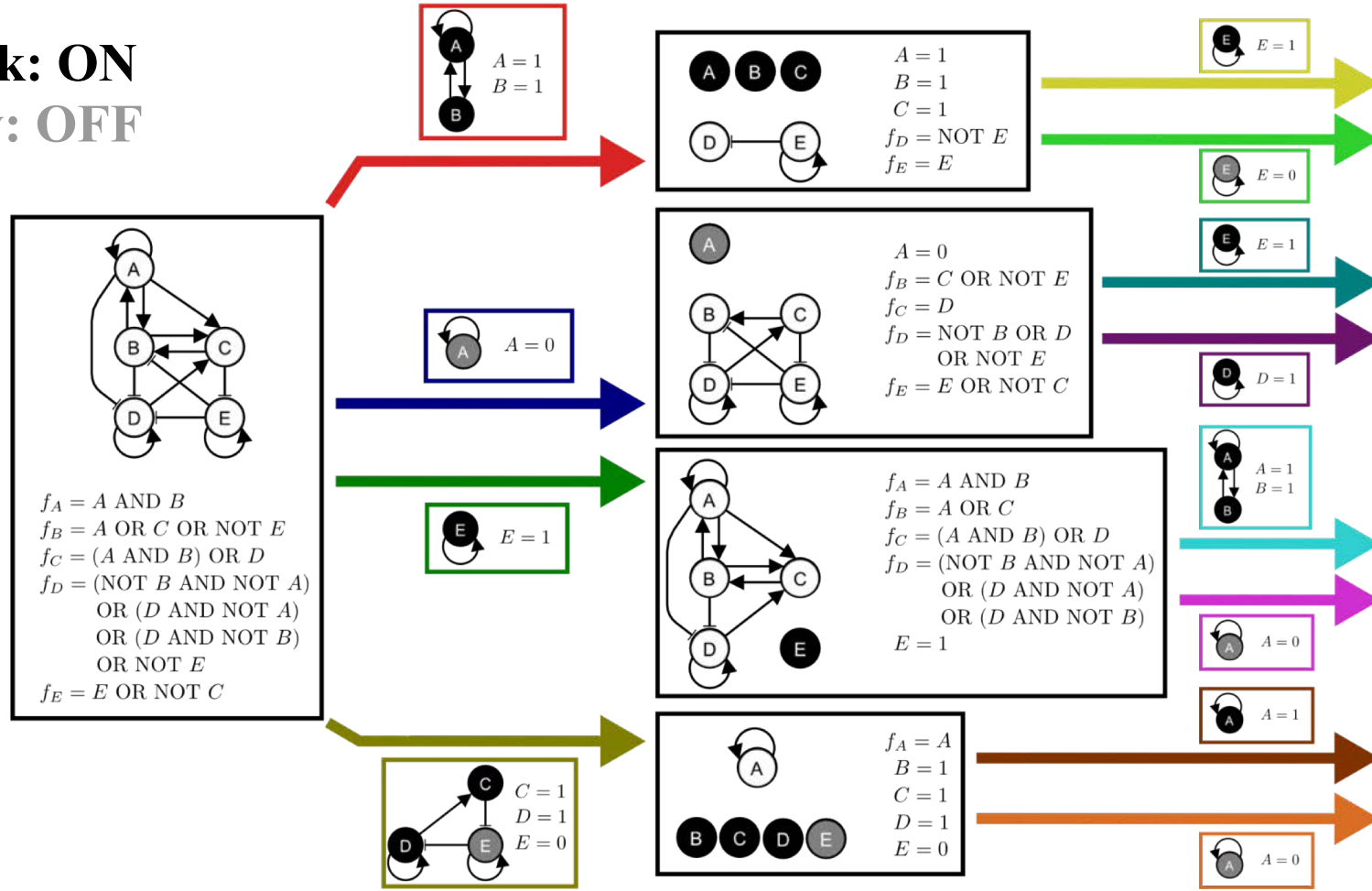
$t = 0$
 $t = 1$
 $t = 2$
 $t = 3$
 $t = 4$
 $t = 5$
 $t = 6$
 $t = 7$

	Fas	S1P	Ceramide	DISC	FLIP	Apoptosis
$t = 0$	Grey	Grey	Grey	Grey	Black	Black
$t = 1$	Grey	Grey	Black	Grey	Black	Black
$t = 2$	Black	Grey	Black	Grey	Black	Black
$t = 3$	Black	Grey	Black	Black	Grey	Black
$t = 4$	Black	Grey	Black	Black	Grey	Black
$t = 5$	Black	Grey	Black	Black	Grey	Black
$t = 6$	Black	Grey	Black	Black	Grey	Black
$t = 7$	Black	Grey	Black	Black	Grey	Black

Attractors of models of intracellular networks: stable cell states (e.g. healthy state, disease states, etc)



Black: ON
Grey: OFF



Original logical network model

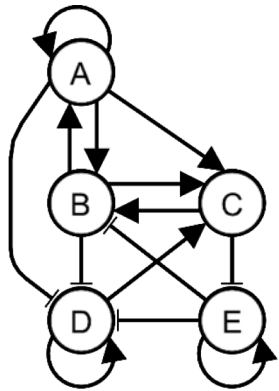
Stable motifs of the original network model

Reduced logical network models

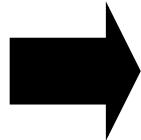
Stable motifs of the reduced network models

- Attractor control: Sequence of stable motifs → Attractor

Black: ON
Grey: OFF

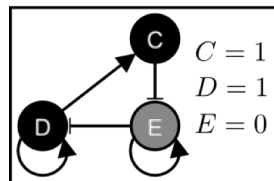
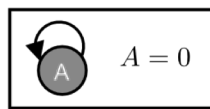
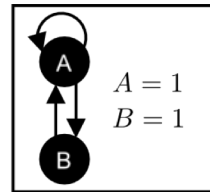


+



Stable motifs

Attractors



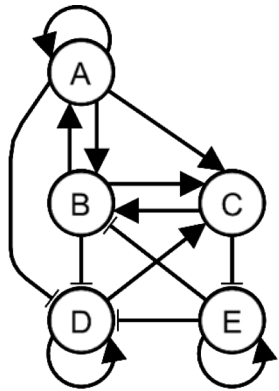
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 $f_C = (A \text{ AND } B) \text{ OR } D$
 $f_D = (\text{NOT } B \text{ AND NOT } A)$
 OR $(D \text{ AND NOT } A)$
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 $f_E = E \text{ OR NOT } C$

J.G.T. Zañudo and R. Albert.
 PLoS Comp. Biol. 11(4):
 e1004193 (2015).

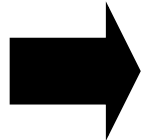
Dynamics →

- Attractor control: Sequence of stable motifs → Attractor

Black: ON
Grey: OFF

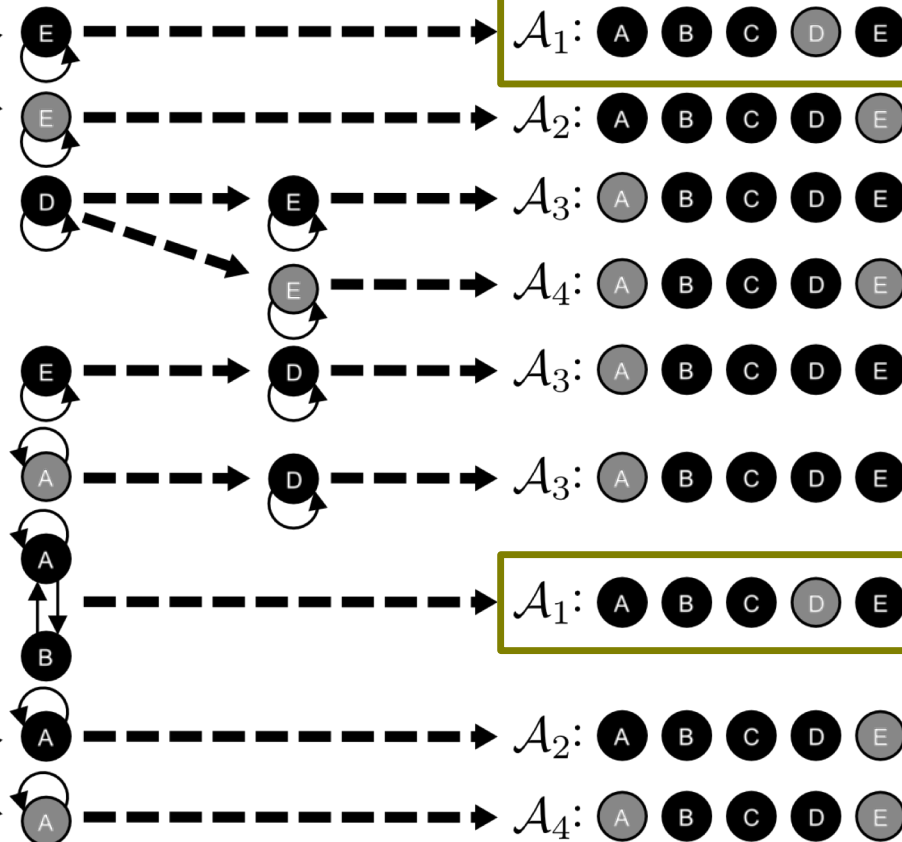
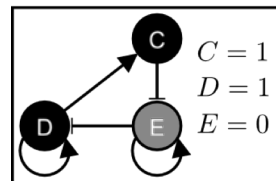
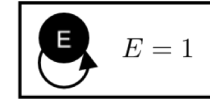
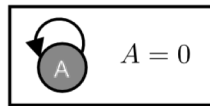
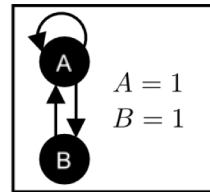


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Stable motifs

Attractors



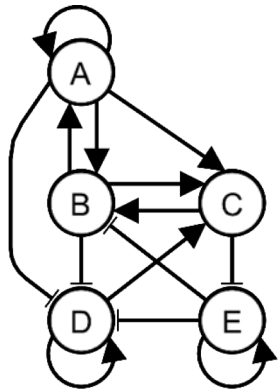
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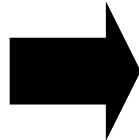
Dynamics →

- Attractor control: Sequence of stable motifs → Attractor

Black: ON
Grey: OFF

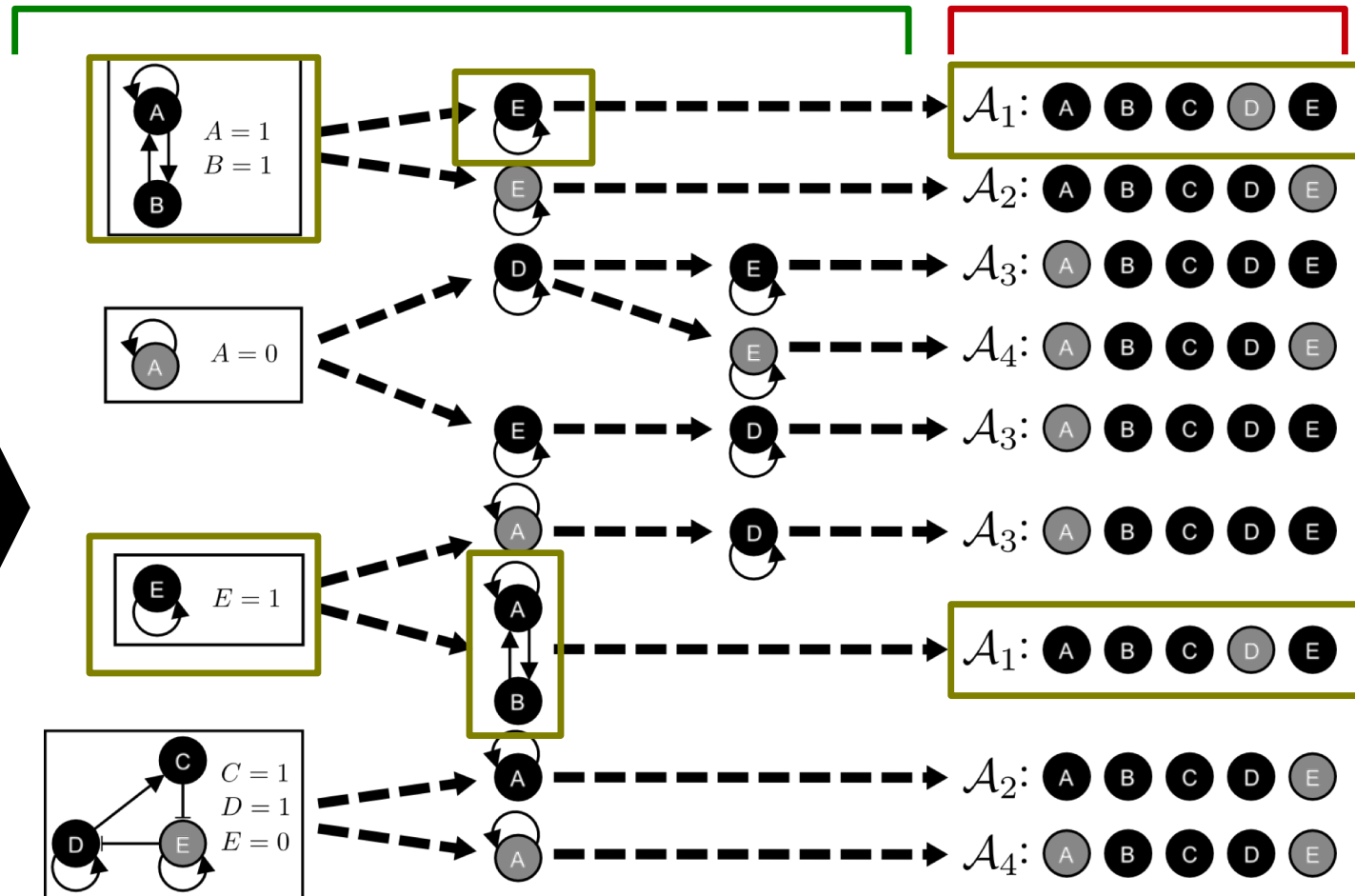


+



Stable motifs

Attractors



$f_A = A \text{ AND } B$
 $f_B = A \text{ OR } C \text{ OR NOT } E$
 $f_C = (A \text{ AND } B) \text{ OR } D$
 $f_D = (\text{NOT } B \text{ AND NOT } A) \text{ OR } (D \text{ AND NOT } A) \text{ OR } (D \text{ AND NOT } B) \text{ OR NOT } E$
 $f_E = E \text{ OR NOT } C$

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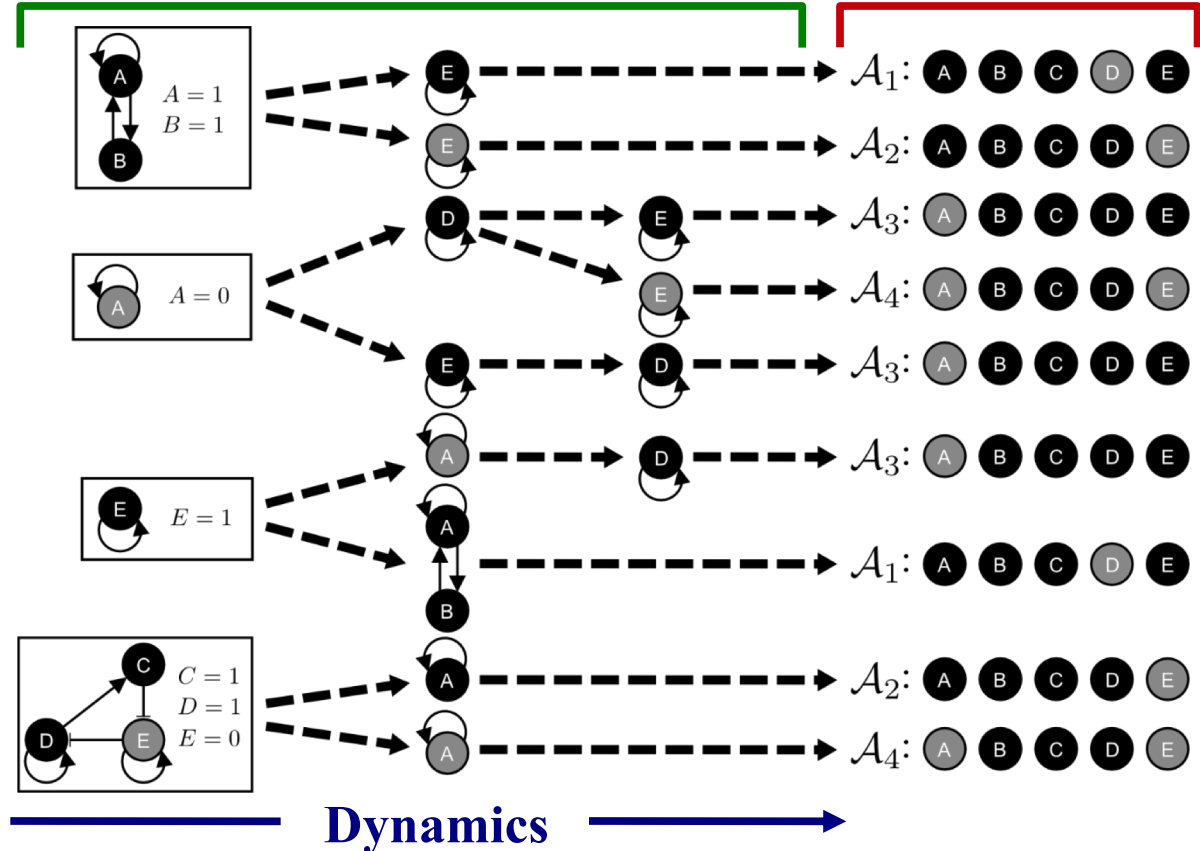
Dynamics →

Stable motif succession diagram

Black: ON
Grey: OFF

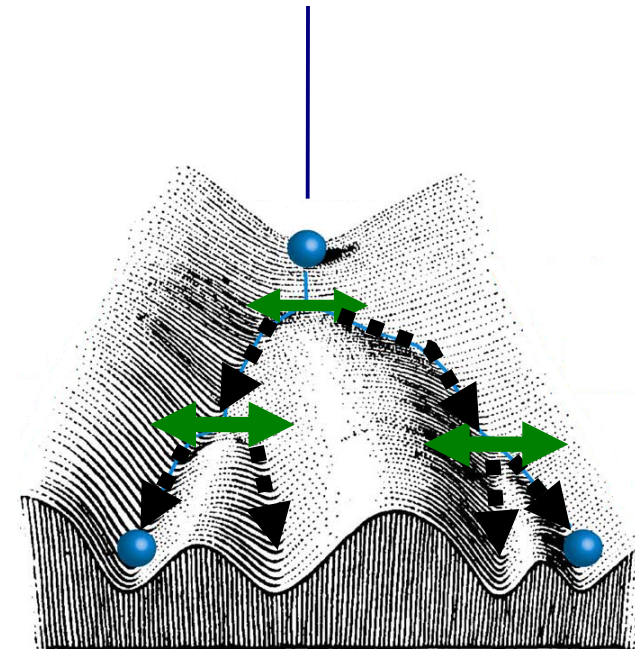
Stable motifs

Attractors



Waddington's epigenetic landscape

Marble rolling down



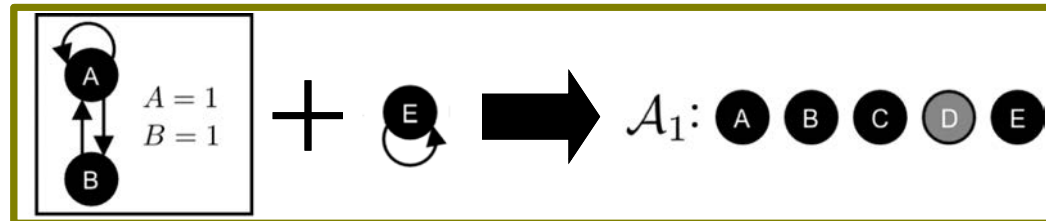
A B C D

Stable cell states

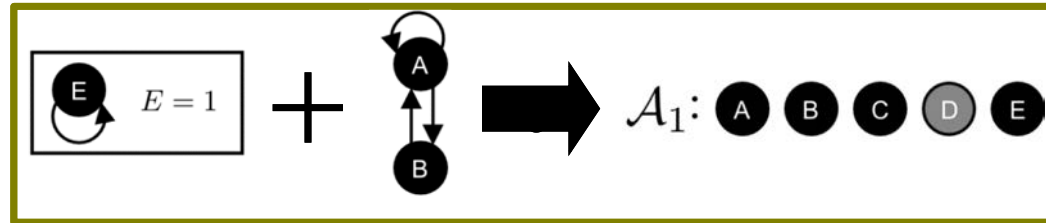
- Stable motif control:

- Fix stable motif states \rightarrow all initial conditions go to target attractor
- Includes steps to reduce number of motifs and states

Motif sequence 1

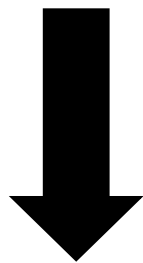


Motif sequence 2



Black: ON
Grey: OFF

Sequences
that lead
to \mathcal{A}_1

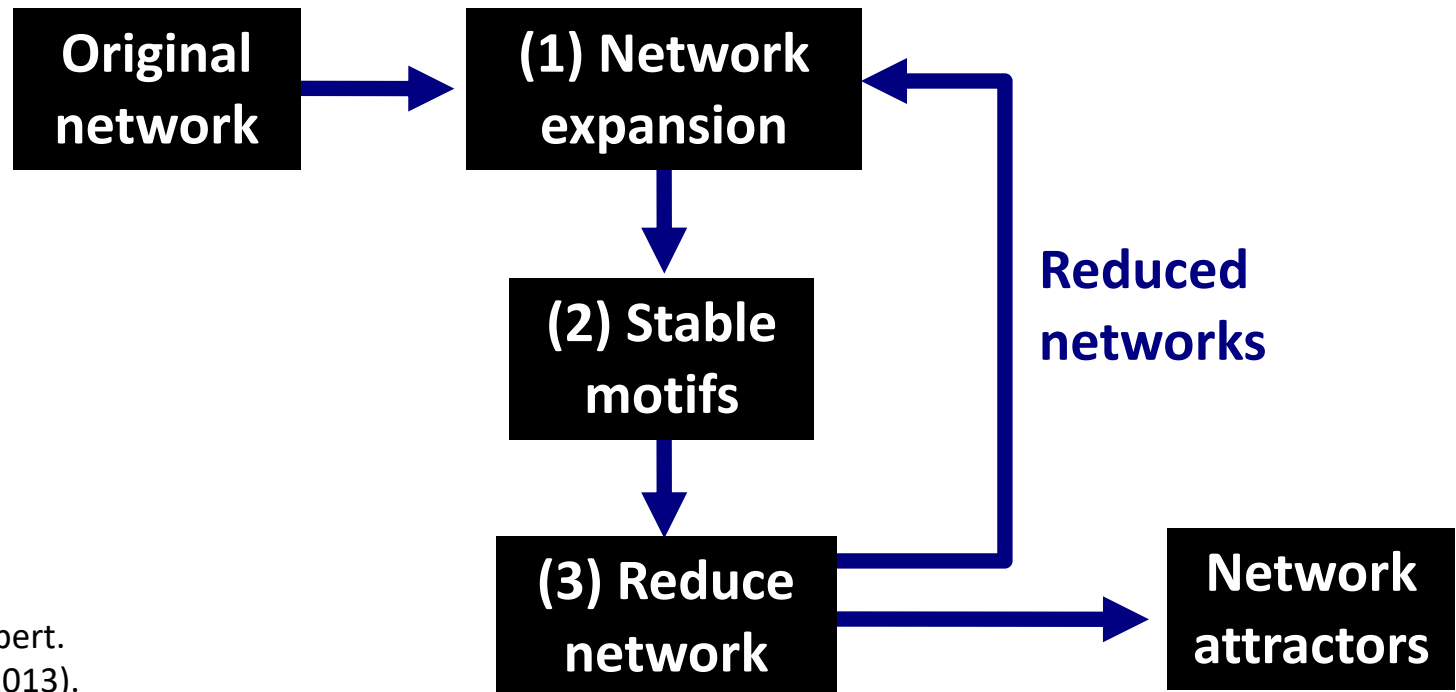


Simplify sequences (remove unnecessary motifs)
Find subset of nodes require to activate motif

Control set for $\mathcal{A}_1: \{A=1, E=1\}$

- Our method:
 - Network topology + function + network reduction.
 - **Finds all attractors*** (formally, quasi-attractors).
 - Tested on small, medium and large networks (~1000 nodes).
- The idea: **Find subnetworks or motifs (stable motifs) that stabilize in a fixed state** (i.e., that are partial fixed points).

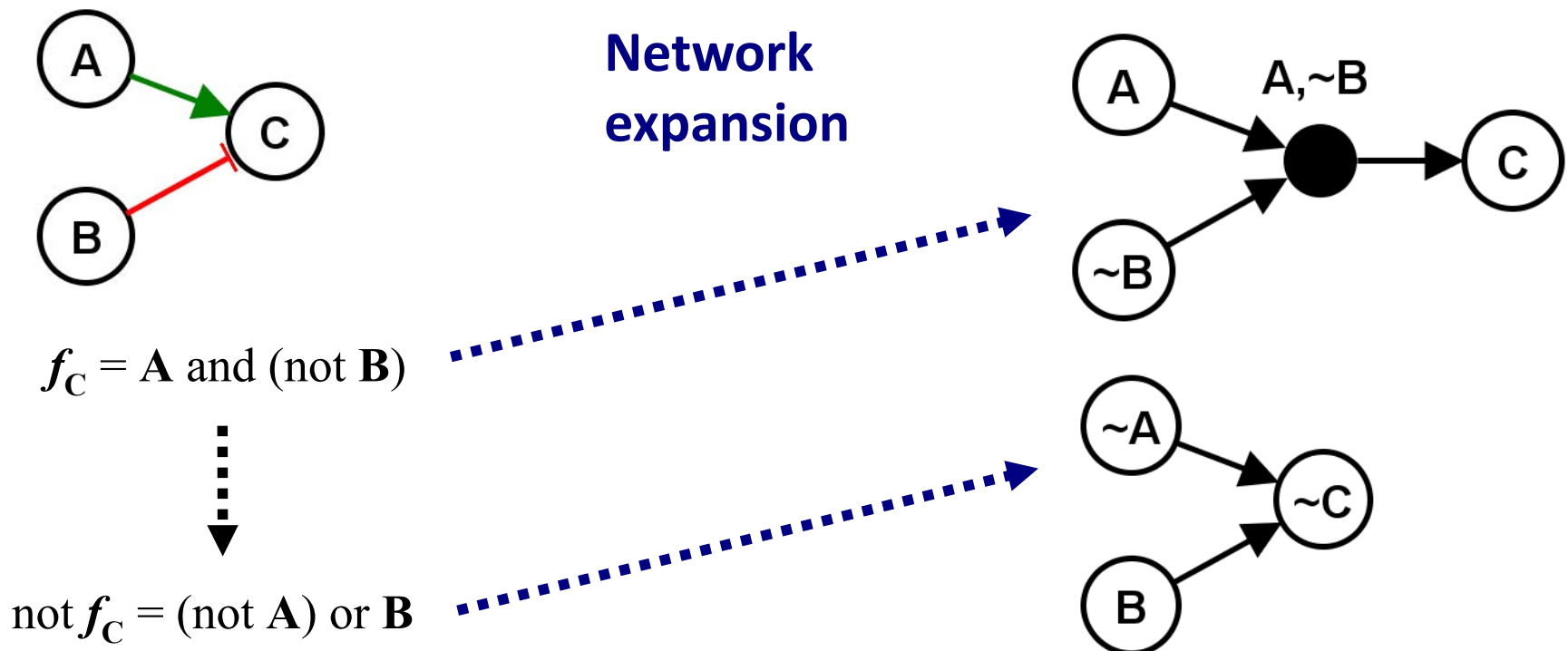
Algorithm:



- Algorithm:

(1) **Network expansion**: Adds information about **combinatorial interactions and their sign** through new nodes.

- Composite nodes: AND relationships (● $A, B = A \text{ and } B$).
- Complementary nodes: NOT relationships ($\sim A = \text{not } A$).



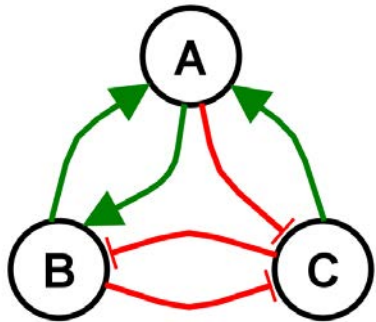
- Algorithm:

(2) Identify stable motifs: Smallest strongly connected components that satisfy two properties.

(i) Contain either a node or its complement.

(ii) Contain all inputs of its composite nodes (if any)

Boolean network



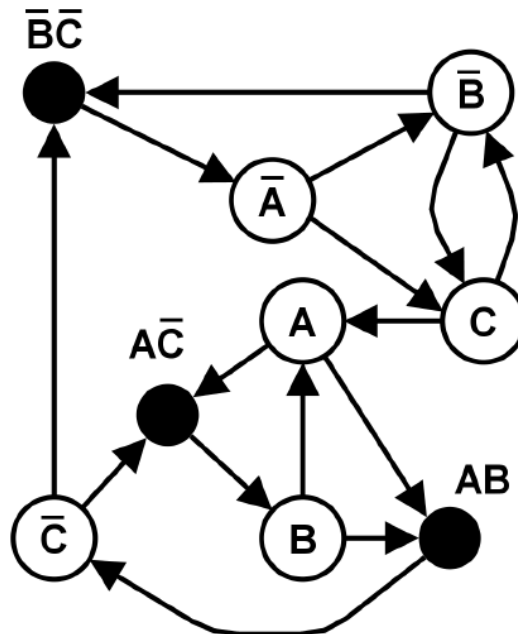
$$f_A = B \text{ or } C$$

$$f_B = A \text{ and (not } C)$$

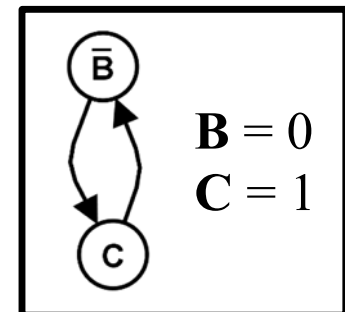
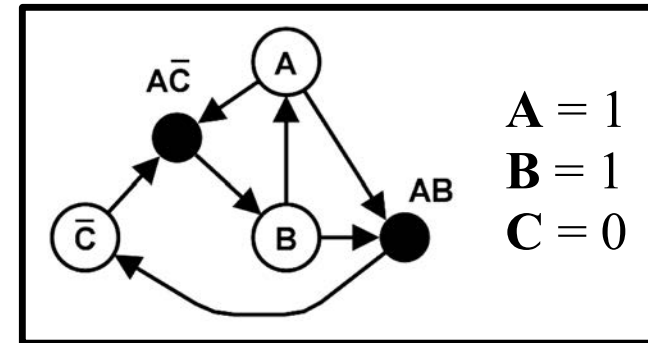
$$f_C = (\text{not } A)$$

or (not **B**)

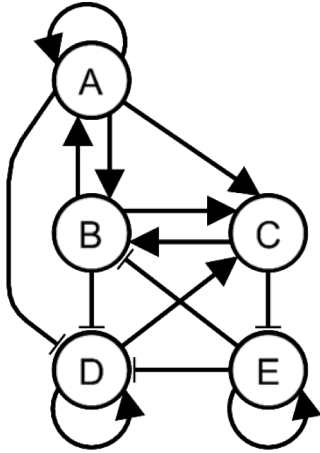
Expanded network



Stable motifs



Boolean network



$$f_A = A \text{ AND } B$$

$$f_B = A \text{ OR } C \text{ OR NOT } E$$

$$f_C = (A \text{ AND } B) \text{ OR } D$$

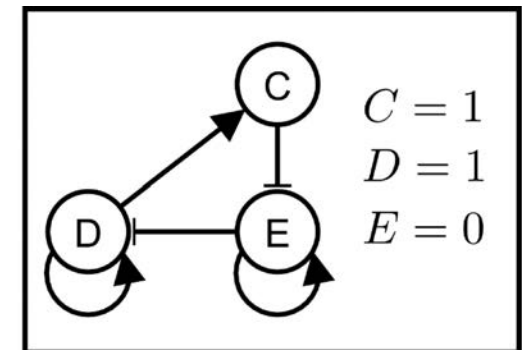
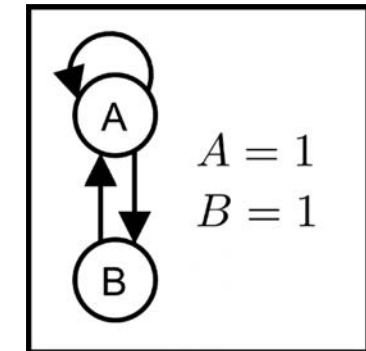
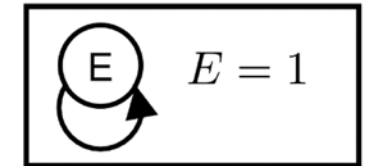
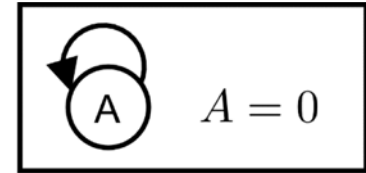
$$f_D = (\text{NOT } B \text{ AND NOT } A) \\ \text{OR } (D \text{ AND NOT } A) \\ \text{OR } (D \text{ AND NOT } B) \\ \text{OR NOT } E$$

$$f_E = E \text{ OR NOT } C$$

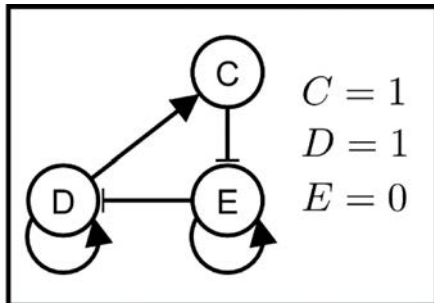
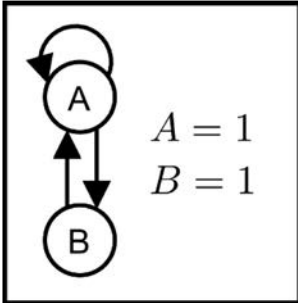
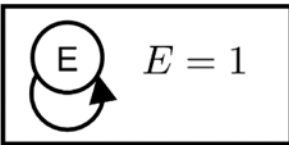
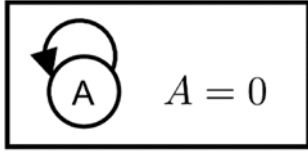


Steps (1) + (2)

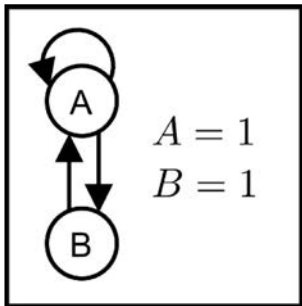
Stable motifs



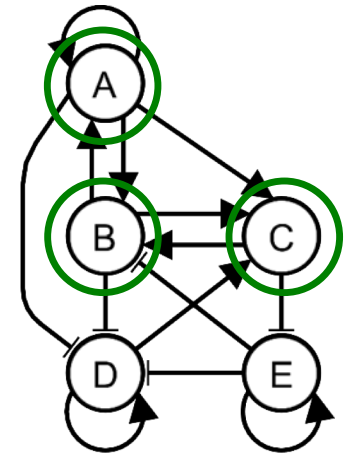
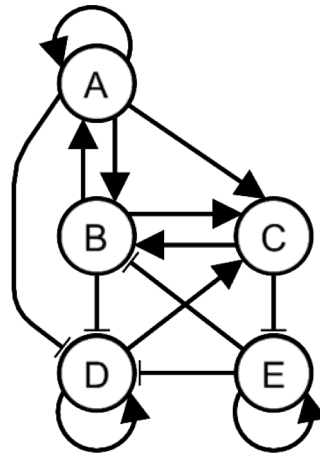
(3) Reduce network using stable motifs.



(3) Reduce network using stable motifs.



Plug in

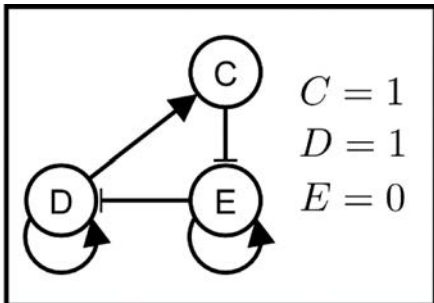
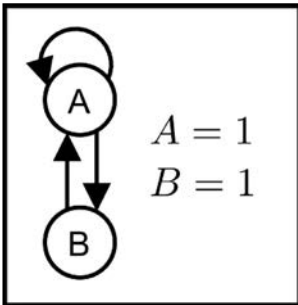
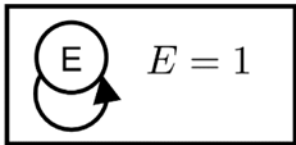
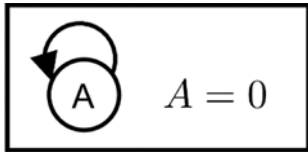


$$\begin{aligned}
 f_A &= A \text{ AND } B \\
 f_B &= A \text{ OR } C \text{ OR NOT } E \\
 f_C &= (A \text{ AND } B) \text{ OR } D \\
 f_D &= (\text{NOT } B \text{ AND NOT } A) \\
 &\quad \text{OR } (D \text{ AND NOT } A) \\
 &\quad \text{OR } (D \text{ AND NOT } B) \\
 &\quad \text{OR NOT } E \\
 f_E &= E \text{ OR NOT } C
 \end{aligned}$$

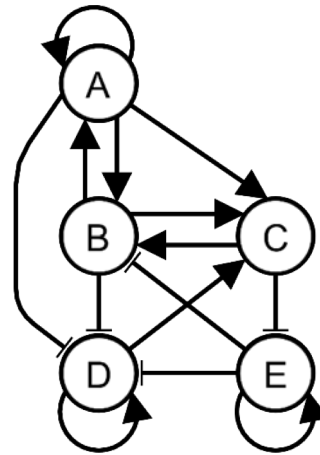
$$\begin{aligned}
 f_D &= \text{not } E \\
 f_E &= E
 \end{aligned}$$

Reduced network

(3) Reduce network using stable motifs.



Plug in



$$\begin{aligned}
 f_A &= A \text{ AND } B \\
 f_B &= A \text{ OR } C \text{ OR NOT } E \\
 f_C &= (A \text{ AND } B) \text{ OR } D \\
 f_D &= (\text{NOT } B \text{ AND NOT } A) \\
 &\quad \text{OR } (D \text{ AND NOT } A) \\
 &\quad \text{OR } (D \text{ AND NOT } B) \\
 &\quad \text{OR NOT } E \\
 f_E &= E \text{ OR NOT } C
 \end{aligned}$$

Reduced network 1

Reduced network 2

Reduced network 3

Reduced network 4