

# Analyzing gene regulatory networks by comparing the dynamics obtained via DSGRN (Dynamic Signatures Generated by Regulatory Networks) and RACIPE (Random Circuit Perturbation)

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## Week Three

# Random Sampling in RACIPE and Rook Fields

$$dA/dt = G_A H^S(B, BA_0, n_{BA}, \lambda_{BA}^-) - k_A A$$

$$dB/dt = G_B H^S(A, AB_0, n_{AB}, \lambda_{AB}^-) - k_B B$$

G : Maximum production rate

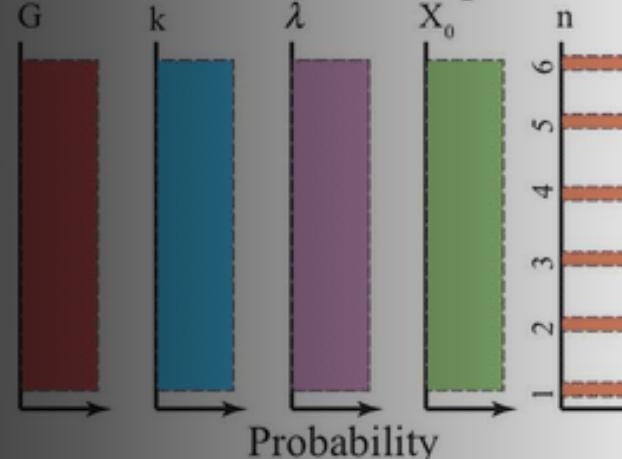
k : Degradation rate

$\lambda$  : Fold change by regulation

$X_0$ : Threshold of regulation

n : Cooperativity of regulation

Randomize the kinetic parameters



$$dA/dt = G_A H^S(B, BA_0, n_{BA}, \lambda_{BA}^-) - k_A A$$

$$dB/dt = G_B H^S(A, AB_0, n_{AB}, \lambda_{AB}^-) - k_B B$$

Update the mathematical model

Protein A  
the stable steady states

Protein B

State I

State II

# Progress

Over the last week, we compiled documents explaining the random sampling of RACIPE and the current literature on the computational cost of RACIPE. We analyzed the half-functional rule using the additional information files and the source code. We then moved to reproduce the results in RACIPE, particularly the ratio between the amount of monostable and bistable steady states. From there, we reproduced the rook fields seen in Konstantin's initial DSGRN presentation. Finally, we have begun working on reproducing the toggle switch results from RACIPE in DSGRN using essential parameters and their neighbors.

```

case 1: // Uniform distribution
for (i = 0; i < num; i++){
    g    = randu(minP, maxP);
    k    = randu(minK, maxK);
    A[i] = g/k;
}

MA = median(A, num);

for (i = 0; i < num; i++){
    g    = randu(minP, maxP);
    k    = randu(minK, maxK);
    B[i] = g/k;

    if (numA != 0){
        for (j = 0; j < numA; j++){
            g      = randu(minP, maxP);
            k      = randu(minK, maxK);
            n      = randd(minN, maxN, dist);
            T      = randu(MA*f1, MA*f2);
            lambda = randu(minF, maxF);

            B[i] = B[i]*Hillshift(g/k, T, n, lambda)/lambda;
        }
    }

    if (numI != 0){
        for (j = 0; j < numI; j++){
            g    = randu(minP, maxP);
            k    = randu(minK, maxK);
            n    = randd(minN, maxN, dist);
            T    = randu(MA*f1, MA*f2);
            lambda = 1.0/randu(minF, maxF);

            B[i] = B[i]*Hillshift(g/k, T, n, lambda);
        }
    }

    MB = median(B, num);
    minT[ID] = MB*f1;
    maxT[ID] = MB*f2;
    free(A);
    free(B);
    break;
}

```

# The Half-Functional Rule

- Isolated gene “num” times
- Isolated genes with inward regulations ”num” times
- Multiply by Hill functions with thresholds from above
- Median outputs

**Toggle-switch circuit (TS):**

$$\begin{aligned}\dot{A} &= G_A H^S(B, BA_0, n_{BA}, \lambda_{BA}^-) - k_A A \\ \dot{B} &= G_B H^S(A, AB_0, n_{AB}, \lambda_{AB}^-) - k_B B,\end{aligned}, \quad (1)$$

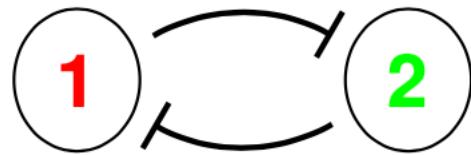
**Toggle-switch circuit with one-sided self-activation (TS1SA):**

$$\begin{aligned}\dot{A} &= G_A H^S(B, BA_0, n_{BA}, \lambda_{BA}^-) H^S(A, AA_0, n_{AA}, \lambda_{AA}^+) / \lambda_{AA}^+ - k_A A \\ \dot{B} &= G_B H^S(A, AB_0, n_{AB}, \lambda_{AB}^-) - k_B B\end{aligned}, \quad , (2)$$

**Toggle-switch circuit with two-sided self-activation (TS2SA):**

$$\begin{aligned}\dot{A} &= G_A H^S(B, BA_0, n_{BA}, \lambda_{BA}^-) H^S(A, AA_0, n_{AA}, \lambda_{AA}^+) / \lambda_{AA}^+ - k_A A \\ \dot{B} &= G_B H^S(A, AB_0, n_{AB}, \lambda_{AB}^-) H^S(B, BB_0, n_{BB}, \lambda_{BB}^+) / \lambda_{BB}^+ - k_B B,\end{aligned}, \quad (3)$$

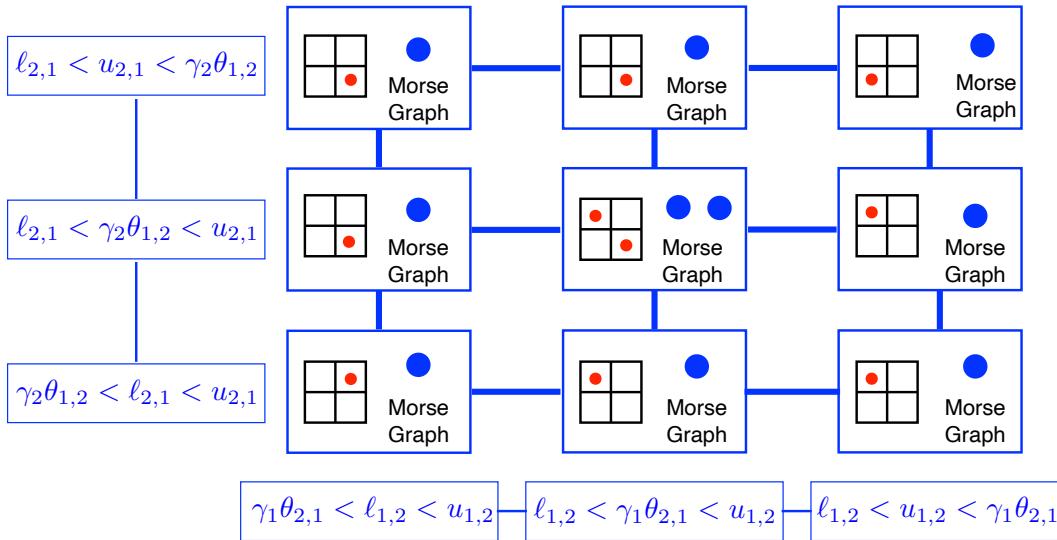
# Toggle Switch Parameter Space in DSGRN



## ORGANIZING THE INFORMATION

DSGRN database

### Parameter Graph: Region of Parameter Space & Dynamics

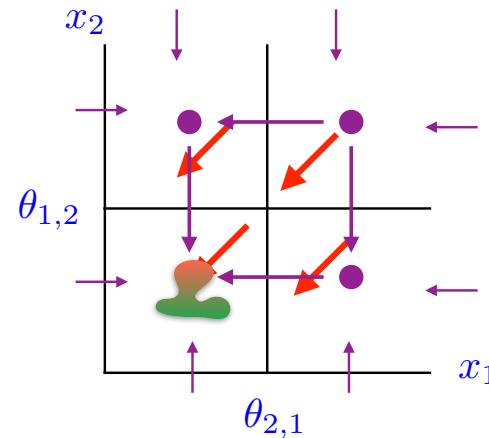


Database provides a complete decomposition of parameter space into explicit regions (semi-algebraic sets) and description of global dynamics over each region. *Purely combinatorial representation.*

$$u = \ell + \delta$$



## REPRESENTING DYNAMICS

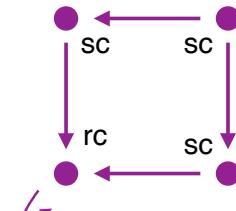


Assume

$$\begin{aligned} \ell_{1,2} < u_{1,2} < \gamma_1 \theta_{2,1} \\ \ell_{2,1} < u_{2,1} < \gamma_2 \theta_{1,2} \end{aligned}$$

Rook Field

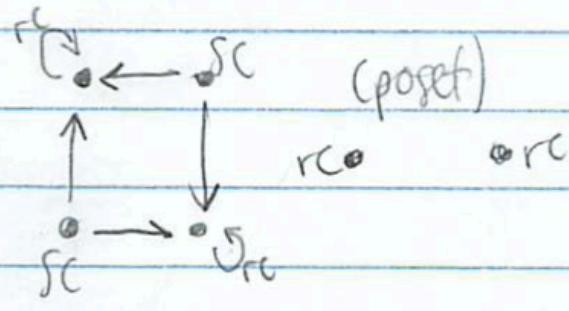
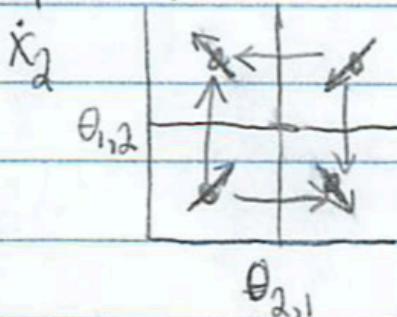
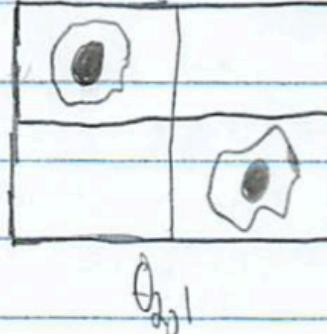
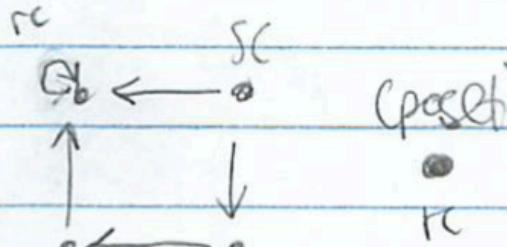
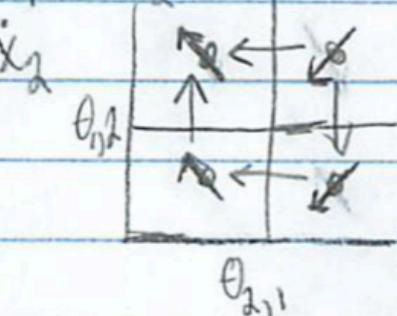
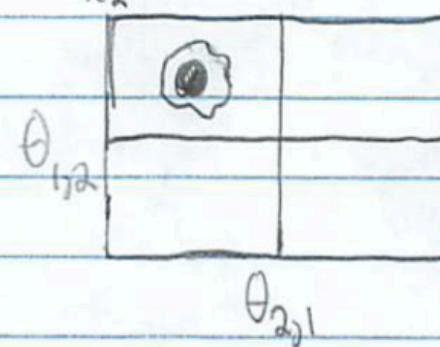
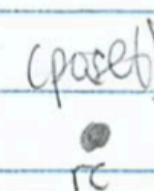
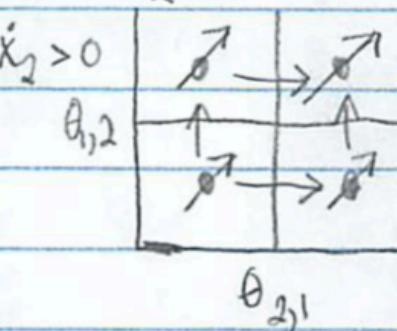
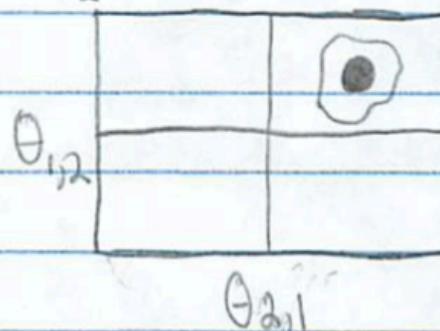
State Transition Graph



Morse Graph  
(poset)

● rc

$$\begin{aligned} -\gamma_1 x_1 + \begin{cases} \ell_{1,2} + \delta_{1,2} & \text{if } x_2 < \theta_{1,2} \\ \ell_{1,2} & \text{if } x_2 > \theta_{1,2} \end{cases} \\ -\gamma_2 x_2 + \begin{cases} \ell_{2,1} + \delta_{2,1} & \text{if } x_1 < \theta_{2,1} \\ \ell_{2,1} & \text{if } x_1 > \theta_{2,1} \end{cases} \end{aligned}$$

5.)  $\dot{x}_1 \quad x_2$  $x_2$ 6.)  $\dot{x}_1 < 0 \quad x_2$  $x_2$ 7.)  $\dot{x}_1 > 0 \quad x_2$  $x_2$ 

# Next Steps

Our next steps include understanding essential parameters, running the RACIPE simulations in DSGRN with the essential parameters, and continuing to study the mathematics that underly both DSGRN and RACIPE.

Thank You for Listening!

and

Thank you to the 2020 David and Dorothy Bernstein  
Endowed Scholarship for Summer Research and  
Aresty Research Center for supporting our research  
this summer!