An approach to infer the gene regulatory network of a stable cell type

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Cellular state

Let x_i = expression level of gene ,
then the cellular state is the vector

$$X = (x_1, x_2, x_3, ..., x_n)$$

How are the levels of expression maintained ?
What are the gene regulatory mechanisms?

Our task is to formulate these questions
mathematically and find a way to solve them

Dynamical system

Assume   varies in time according to

$$\frac{dX(t)}{dt} = A(X(t))$$

The vector field   contains detailed
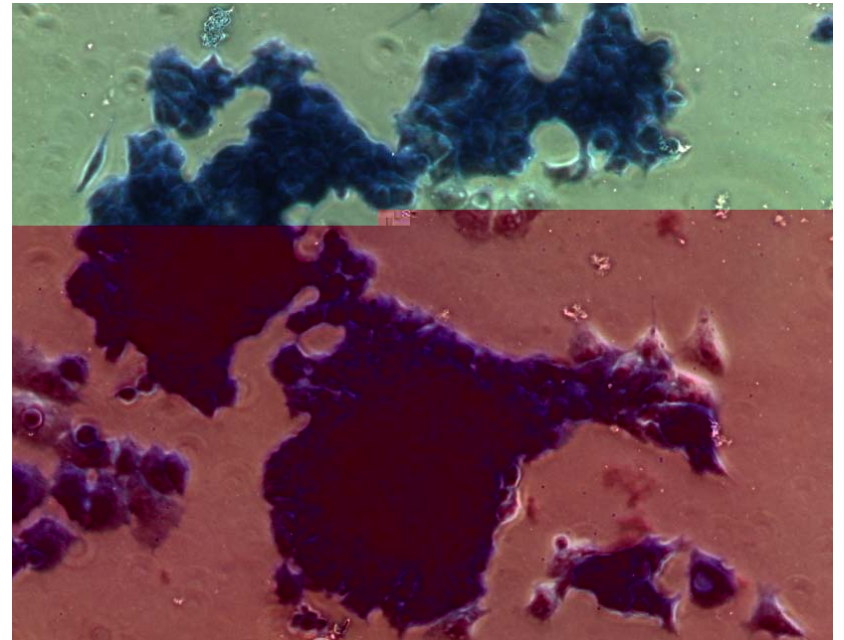information on regulatory information, e.g.

$$A \qquad \uparrow \text{ in}$$

However,   is too complex to reconstruct from
experiments based on current technology.

Stable cell type

A stable cell type can maintain a characteristic pattern of gene expression through a gene regulatory network.

Example:
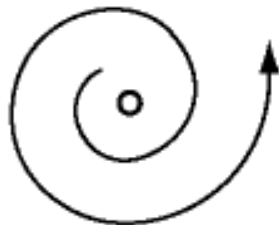 Mouse embryonic stem cells (on 0.1% gelatin, with LIF)

Equilibrium state

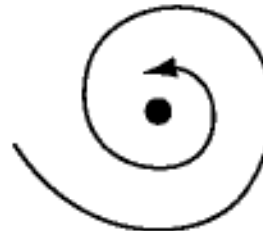A state μ is an <u>equilibrium state</u> if $A(\mu)=0$

The equilibrium is <u>stable</u> if, once the system comes close to μ, it will stay close to μ from then on.

We identify stable cell types with stable equilibrium states of the dynamical system

unstable   stable

Regulatory network

Suppose $X(O) = \mu +$ then for small

$$t \, A(\mu + \quad t \, [A(\mu) + T \quad T$$

where T is the Jacobian matrix: $\quad T \quad A \quad)(\mu)$

We propose to regard T as the regulatory network
that maintains the equilibrium μ

Stability imposes a global constraint on the network:
T must be <u>negative definite</u> to ensure stability

An approach to network reconstruction

- Use RNA-interference to knockdown each regulator in the stable cell type

- Measure gene expression after the perturbation

- Infer network based on a regression model

- Incorporate sparsity & stability into the regression

- Incorporate regulator binding data when available

Regression model

- Response: gene expression changes on I genes

$$Y = \{Y_1, Y_2, \ldots, Y_I\}$$

   where $Y_i = X_i(t) - X_i(0)$

- Predictor: perturbation on   regulators

$$Z = \{Z_1, Z_2, \ldots, Z_J\}$$

   e.g. $Z = ((0.5)\mu_1, 0, 0, \ldots 0)'$

- Model: $E(Y_i) = \sum_{j=1}^{J} T_{ij} Z_j, \text{ for } i = 1, \ldots I$

- Goal: identify non-zero elements in T

Sparsity

- The true network is likely to be sparse
- Lasso-type regularization with L_1 penalty
- Penalized loss function

$$L(T, \lambda_1) = \sum_{per} \sum_{i=1}^{I} \left\| Y_i - \sum_{j=1}^{J} T_{ij} Z_j \right\|_2^2 + \lambda_1 \|T\|_1$$

here the outer sum is over all perturbation experiments

Stability

- Stability imposes useful constraints on T
- Lyapunov stability

$$\left\| X(t) - \mu \right\|^2 = \left\| (I+T)(X(0) - \mu) \right\|^2 \leq \left\| X(0) - \mu \right\|^2$$

choose μ to get an necessary condition

$$T_{jj} \leq 0; \qquad \left\| {}^{(-j)}T_j \right\|_2^2 \leq 1, \text{ for } j = 1,...,J$$

- This leads to the optimization of

$$L(T, \lambda_1, \lambda_2) = \sum_{per} \sum_{i=1}^{I} \left\| Y_i - \sum_{j=1}^{J} T_{ij} Z_j \right\|_2^2 + \lambda_1 \sum_{j=1}^{J} \left\| T_j \right\|_1 + \lambda_2 \sum_{j=1}^{J} \left\| {}^{(-j)}T_j \right\|_2^2$$

- Alternative formulations are possible

Incorporate TF binding location data

- TF association strength (TFAS) integrates the ChIP-seq peak intensities of TF   in the vicinity of gene

$$a_{ij} = \sum_k g_k e^{-d_k / d_0}$$

- Define the TFAS weighting factor

$$c_{ij} = 1 / a_{ij}$$

- Penalized loss function

$$L(T, \lambda_1, \lambda_2, c) = \sum_{per} \sum_{i=1}^{I} \left\| Y_i - \sum_{j=1}^{J} T_{ij} Z_j \right\|_2^2 + \lambda_1 \sum_{j=1}^{J} \left\| c_j \cdot T_j \right\|_1 + \lambda_2 \sum_{j=1}^{J} \left\| c_j \cdot^{(-j)} T_j \right\|_2^2$$

Simulated data:

Manually constructed by Chickarmane et al., (2008) PloS One.
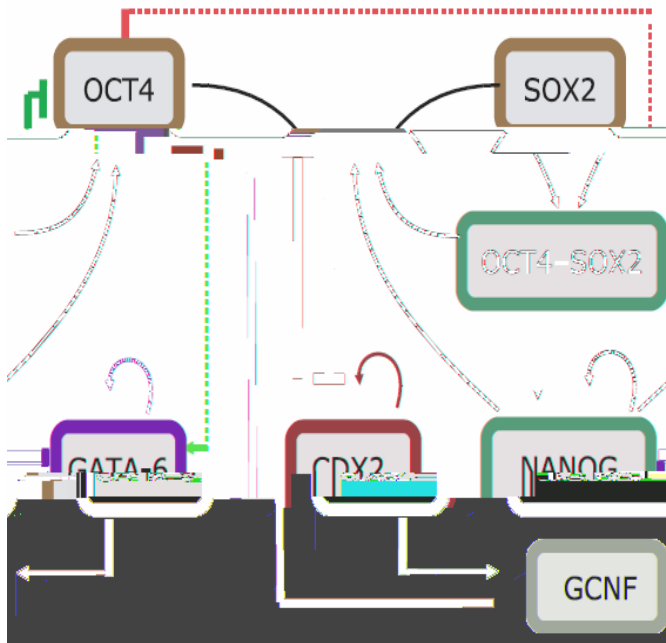
2 stable equilibrium states:
stem cell & endoderm

Use symbolic solver to get the two networks

$$\frac{d[O]}{dt}$$

$$= \frac{a_0 + a_1[A] + a_2[O][S] + a_3[O][S][N]}{1 + b_0[A] + b_1[O] + b_2[O][S] + b_3[O][S][N] + b_4[C][O] + b_5[GC]}$$

$$- \gamma_1[O] \tag{2}$$

$$\frac{d[GC]}{dt} = \frac{i_0 + i_1[C] + i_2[G]}{1 + j_0[C] + j_1[G]} - \gamma_5[GC]$$

$$\frac{d[G]}{dt} = \frac{p_0 + p_1[O] + p_2[G]}{1 + q_0[O] + q_1[G] + q_2[N]} - \gamma_g$$
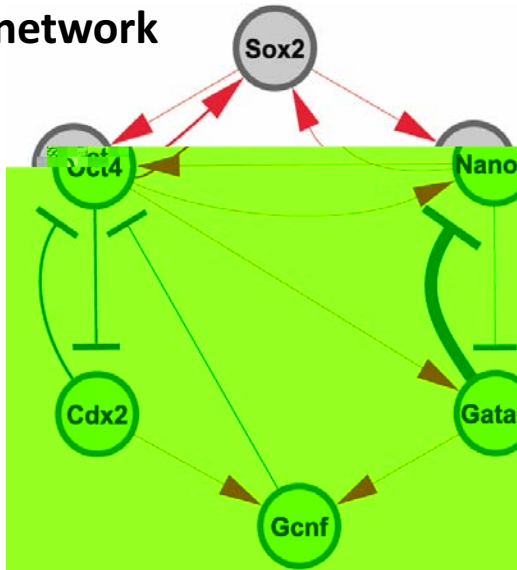
Perturbation of stem cell state
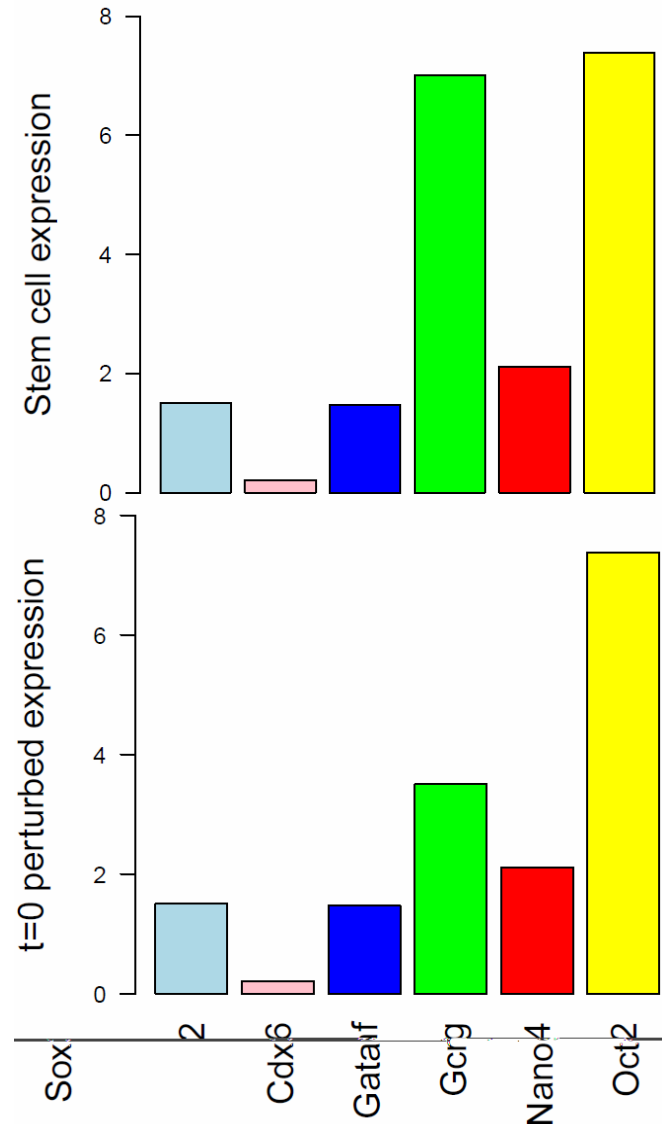
- Knockdown one of the six TFs in each experiment
- The TF expression is reduced by 50% (Nanog) at time =0
- Simulate evolution of expression after perturbation

Time evolution after perturbation
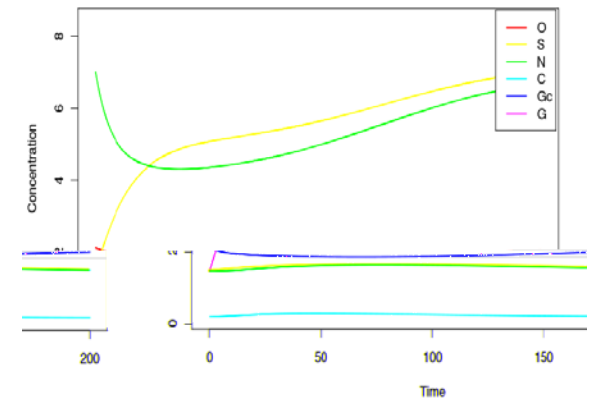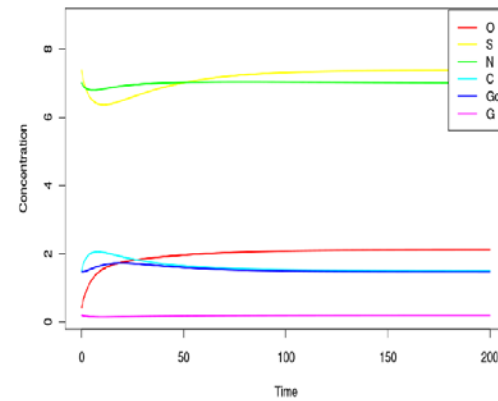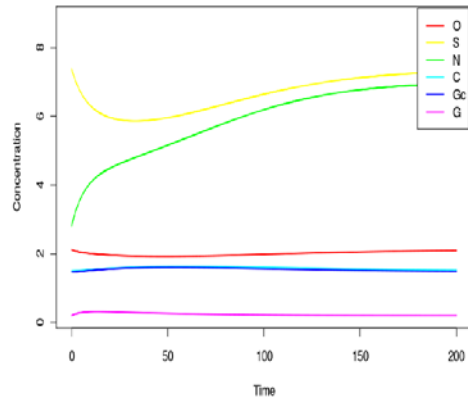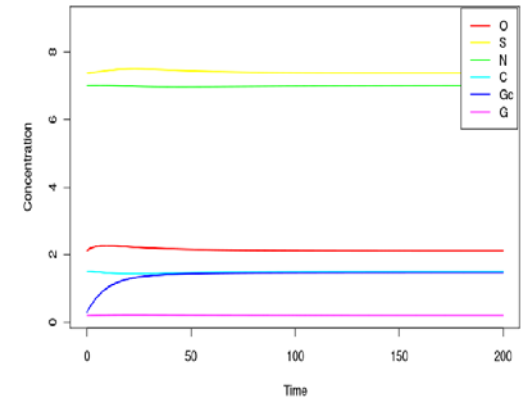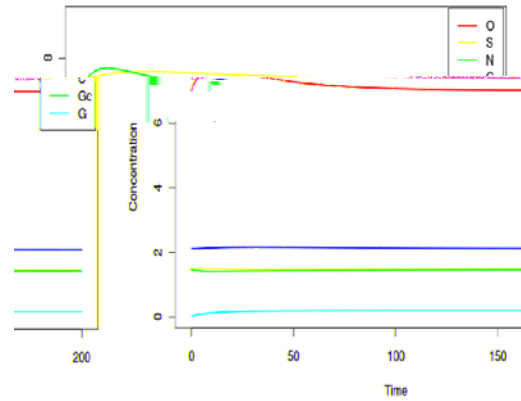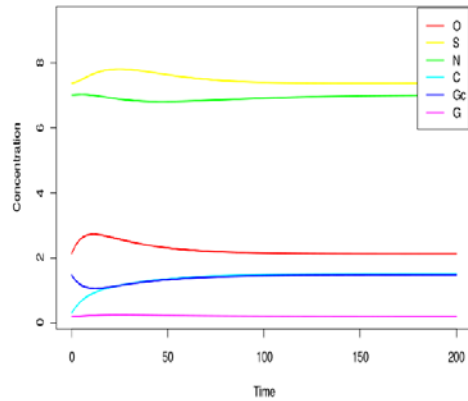
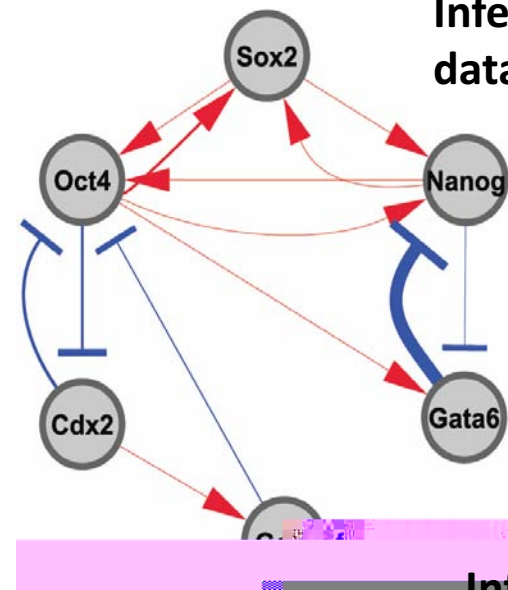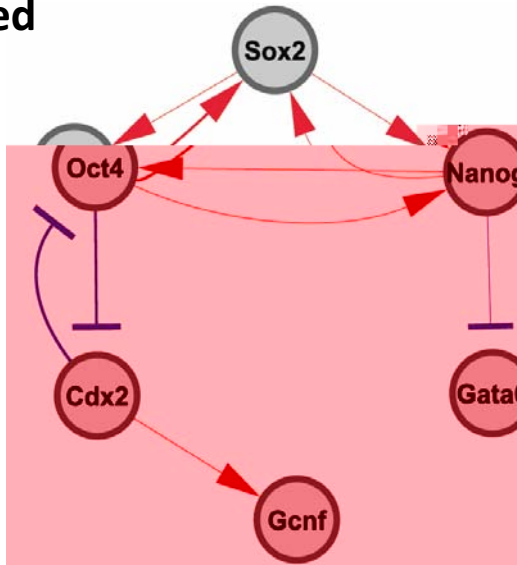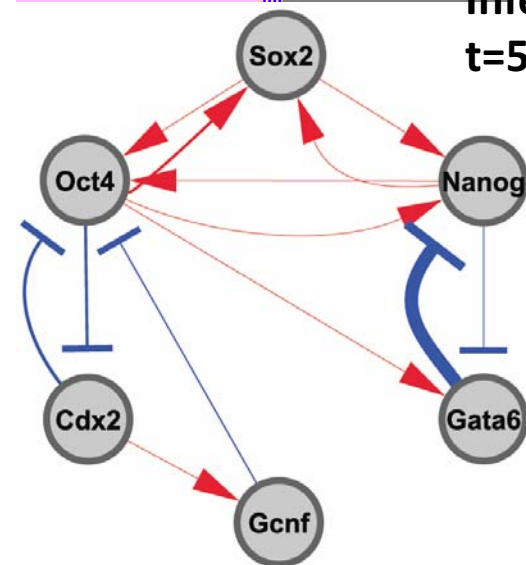# Network reconstruction results

True network

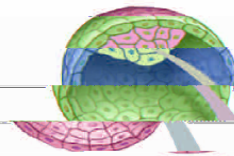Inferred from data at t=1

Inferred t=5

Inferred t=5 + prior

Real data

Embryonic stem cell

1. Origin:
Derived from pre-implantation
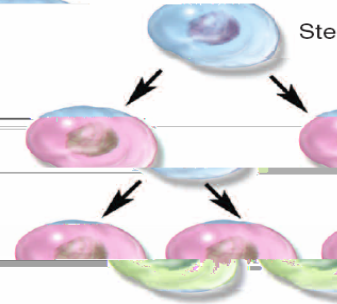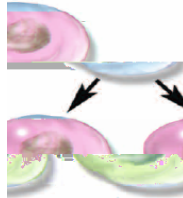or peri-implantation embryo

Blastocyst

n cell

Ster

2. Self-Renewal:
These cells can divide and make
copies of themselves for a
prolonged period of time
without differentiating.

3. Pluripotency:
Embryonic stem cells can give rise to
cells from all three embryonic germ
layers even after being grown

s and one example of a cell type derived from each layer:
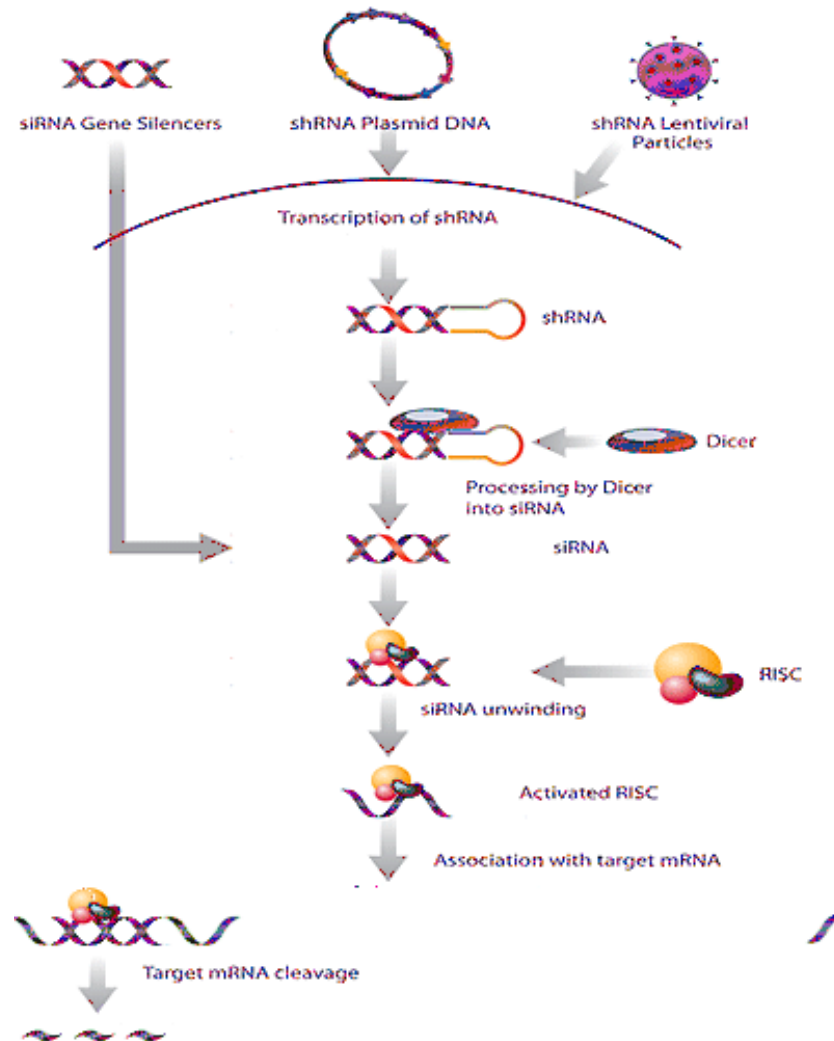
Mesoderm

Endoderm

Ectoderm
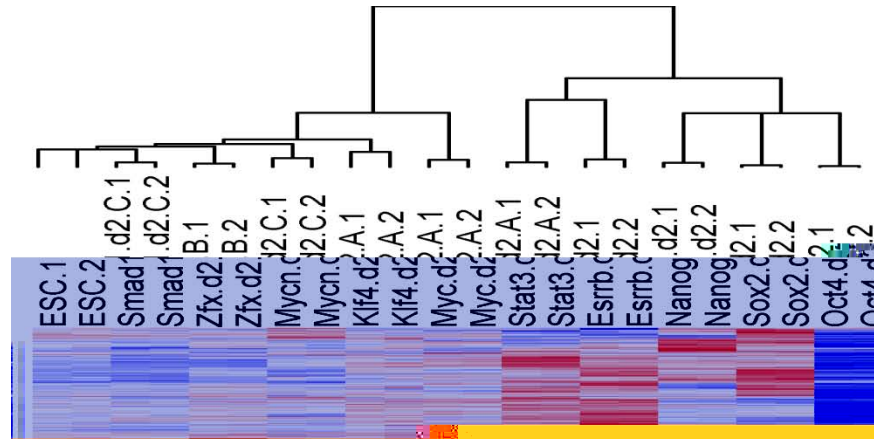
The three germ layer

August 2006.

Gene knockdown by RNA interference

Summary of experiments in our lab

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Sample clustering (after batch effect correction)

some details

- Quantile normalization
- Batch effect modeling
- No gene filtering
  - All 18138 genes entering into the model fitting
  - Perhaps the first attempt on gene regulatory network inference at the whole genome level in a mammalian cell type
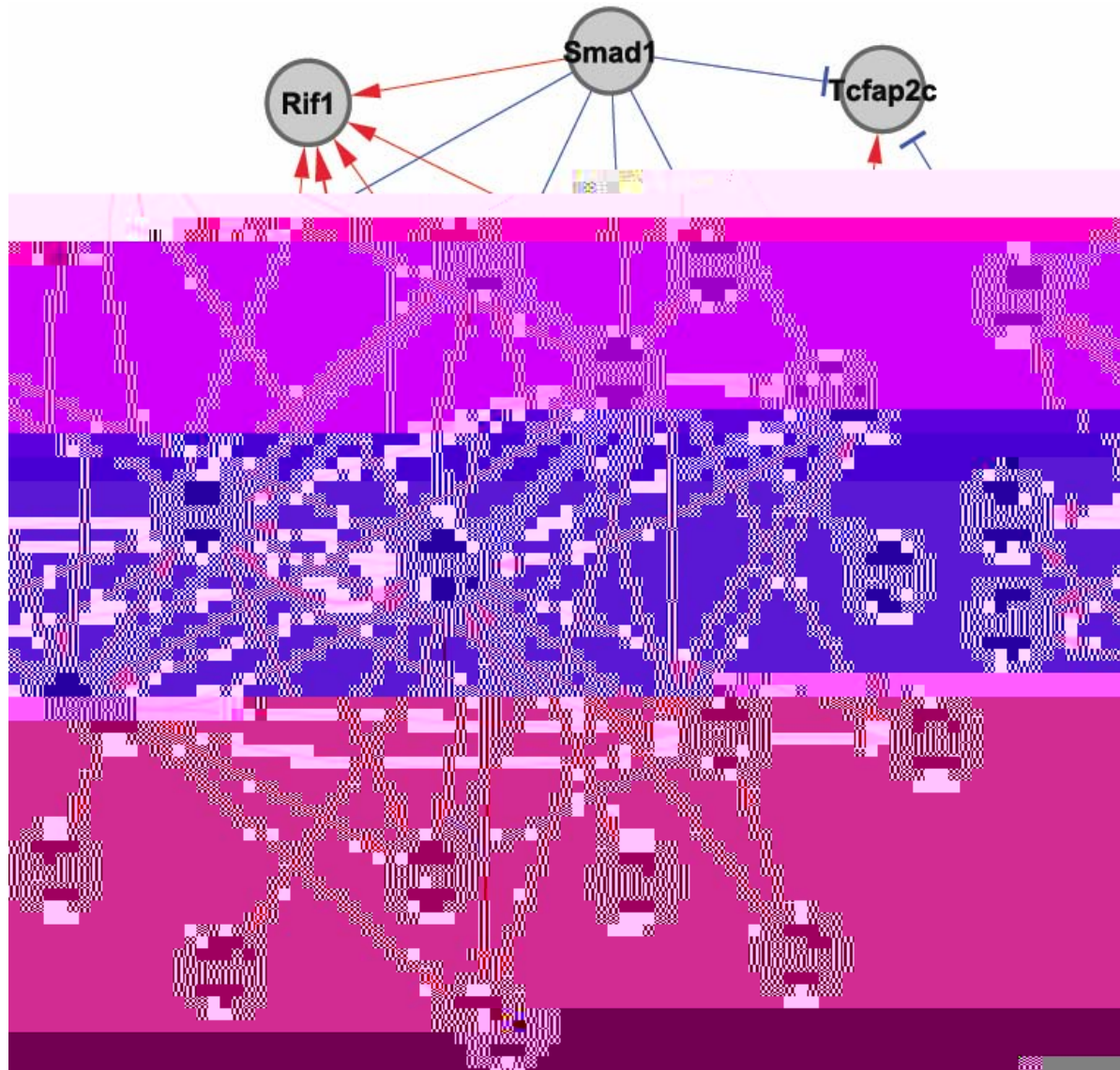
- Network reconstruction with ChIP information (ChIP-seq data from Chen et al 2008)

- Cross-validated for choice of λ
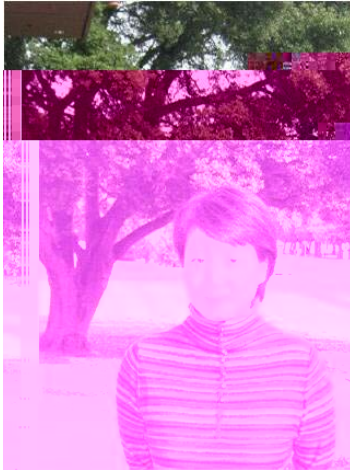
TF targets identified

- 3764 targets regulated by 10 TFs

Oct4	Nanog	Sox2	Esrrb	Stat3	Klf4	Myc	Mycn	Zfx	Smad1
2362	588	461	1169	895	277	0	0	72	163

A subnetwork for important TFs

Acknowledgement

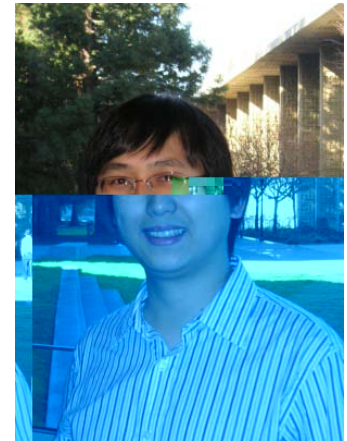**Gene perturbation:**
Xi Chen

Methods & data analysis:
Zhengqing Ouyang

Methods:
Bokyung Choi