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**Simon Joyce\*** ([joyce@math.binghamton.edu](mailto:joyce@math.binghamton.edu)), 14 Washington Ave, Apt. 302, Endicott, NY 13760. *New Results in a Boolean Model of Gene Regulatory Networks*. Preliminary report.

Signed directed graphs are often used as a model for gene regulatory networks. If increasing the expression level of gene  $i$  has the effect of increasing (decreasing) the expression level of gene  $j$ , this is represented by a positive (negative) arc from  $i$  to  $j$ . In the model I'll be discussing, each gene is assigned a boolean variable  $s_i$  to represent its expression level, where  $s_i = -1$  if the gene products of gene  $i$  are absent or inactive, and  $s_i = 1$  if they are present and active. We then represent the expression level of  $n$  genes with a vector  $\mathbf{x} \in \{1, -1\}^n$ . In state  $\mathbf{x}$ , the expression levels may be changing. A function  $\mathbf{f} : \{1, -1\}^n \rightarrow \{1, -1\}^n$  is used to represent this, where  $f_j(\mathbf{x}) \neq x_j$  if the expression level of gene  $j$  is changing. We infer the influence of gene  $i$  on other genes by comparing  $\mathbf{f}(\mathbf{x})$  to  $\mathbf{f}(\mathbf{y})$ , where  $\mathbf{x}$  and  $\mathbf{y}$  differ only in the  $i$ th coordinate. Doing this, we derive a signed directed graph  $\mathcal{I}_{\mathbf{f}}$ , the gene regulatory network. I will present some facts on the relationship between  $\mathbf{f}$  and  $\mathcal{I}_{\mathbf{f}}$  and my recent results. (Received September 22, 2015)