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# Quantifying Differences in the Interferon Signaling Network Across Cell Types

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The interferon stimulated genes (ISGs) play a central role in the immune response, especially against viral infection.   Based on external and internal signals, cells can upregulate ISGs. In turn, ISG expression interferes with different aspects of pathogen replication.   Cell types vary in the ISGs that they upregulate both when infection is ongoing and during homeostasis, but these differences are not well understood quantitatively.  Previous work on understanding cellular ISG response has centered on gene network reconstruction or on particular ISGs in particular cell types.  In contrast, in this talk we discuss a dimensional reduction approach that allows us to characterize the ISG response in a sparse way.   The dimensional reduction is based on a sparse linear regression model, similar in spirit to the lasso.   We discuss computational challenges in fitting the model and characterize the ISG response of different cell types using the model fits.