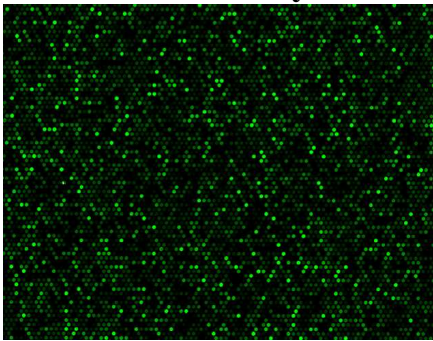*Jose Martinez Lomeli*

University of California, Riverside

Prediction of Transcription factors (proteins) binding sites

Protein Binding Microarray

Identify SNPs that alter Transcription Factor DNA binding

- Most of the transcription factors have a preference for a particular DNA sequence to bind

- Disruptions like mutations in a DNA sequence will affect the ability of transcription factor to bind

- The *in vivo* method made use of protein binding microarrays (PBMs)

- A PBM experiment allows to test hundreds of different DNA sequences for several proteins

- We trained a machine learning model base on the PBM data to predict new DNA binding sites

Jose Martinez Lomeli

University of California, Riverside

In the field of bioinformatics, we always look to improve the way we visualize the data

We look for more efficient ways to employ machine learning to analyze PBM, ChIP-seq, RNA-seq and other data

We would like to improve some of the current pipelines to reduce the large amount of resources that are required at different steps

We would like to use a state of the art deep learning models to improve transcription factor binding prediction

The current published models that predicts transcription factors binding sites made use of CUDA and we would like to port or create a more friendly tool using TensorFlow