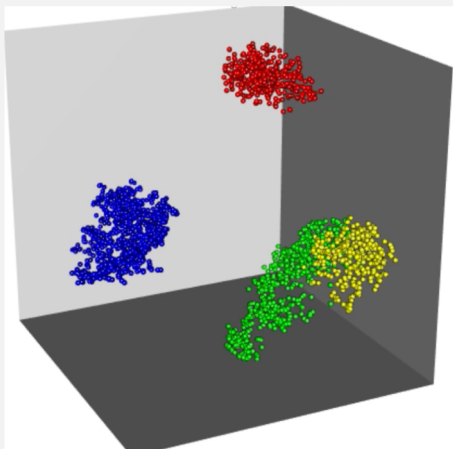
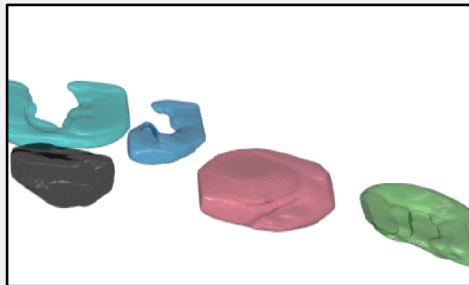
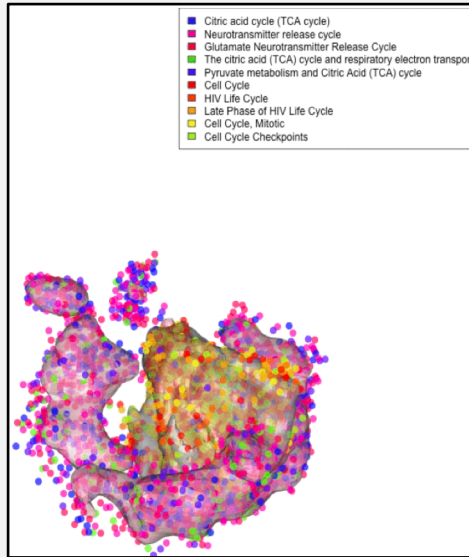




# POSTDOC FELLOW IN COMPUTATIONAL BIOLOGY



In contrast to a cell's DNA, its RNA – the transcriptome – is a highly dynamic machinery which operates within ranges, orders of magnitudes wider than those of the genome. Its role in shaping clonal evolution and implementing a cell's response to its environment is undoubted, yet nowhere close to understood. We seek applications from a computer scientist with a PhD and strong background in machine learning to develop general metrics of cell fitness using supervised machine learning approaches. This project is part of our NIH-awarded K99/R00. Successful candidate will work with a powerful combination of single-cell RNA sequencing data and live-cell imaging to learn various aspects about a clone's fitness from its transcriptome.

Experience with machine learning approaches, especially supervised methods such as Bayesian MKL, deep neural networks (Bayesian neural nets, LSTM, convolutional) is required. Experience with PyTorch or TensorFlow is also needed. Prior work with very large datasets, such as CIFAR-10 and imaging data pre-processing is preferred but not required. Experience with Java and OO programming concepts is also a plus. Successful candidate will work closely together with mathematicians towards steering the fitness landscape of coexisting cancer clones in a systematic, directed fashion.

Moffitt Cancer Center is the top-ranked NCI-designated comprehensive cancer center in the Southeastern US. The Integrated Mathematical Oncology department at Moffitt integrates mathematicians, computer scientists, and physicists together with evolutionary biologists, geneticist and imaging specialists as well as clinical and experimental oncologists to better understand, predict and treat cancer.

More information under [cloneredesign.com](http://cloneredesign.com).

Please send your CV and cover letter to [noemi.andor@moffitt.org](mailto:noemi.andor@moffitt.org).