

# Self Organizing Maps on the GPU

Mark Kim  
University of Utah  
Scientific Computing and Imaging Institute  
Los Alamos National Laboratory  
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# Organization

- What's a SOM?
- How's it used?
- Creating a SOM
- CUDA
- Future Works

# Self-Organizing Map

- Purpose
  - Make high dimensional data manageable
    - Neucleotide frequency count
    - $4^4 = 256$  vector size
      - AAAA, AAAT, AAAC, AAAG, AATA, AATT, AATC, AATG...
  - visualize the characteristics in data
    - $M \times N \times \text{Vector size} \xrightarrow{\text{reduce}} M \times N$ 
      - $150 \times 350 \times 256$  reduces to a  $150 \times 350$  image

# SOM (cont.)

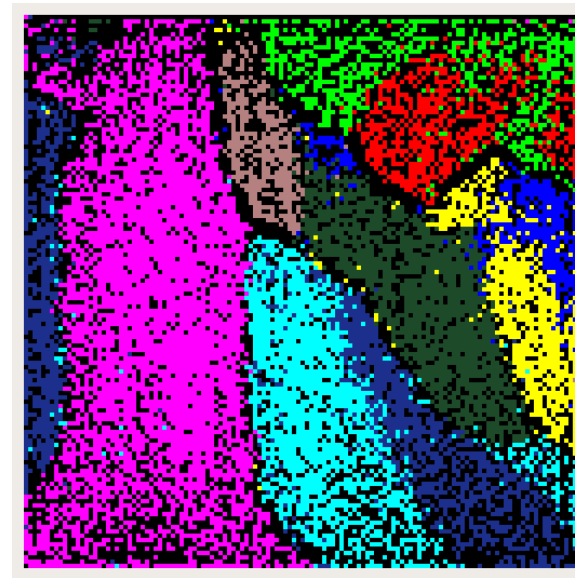
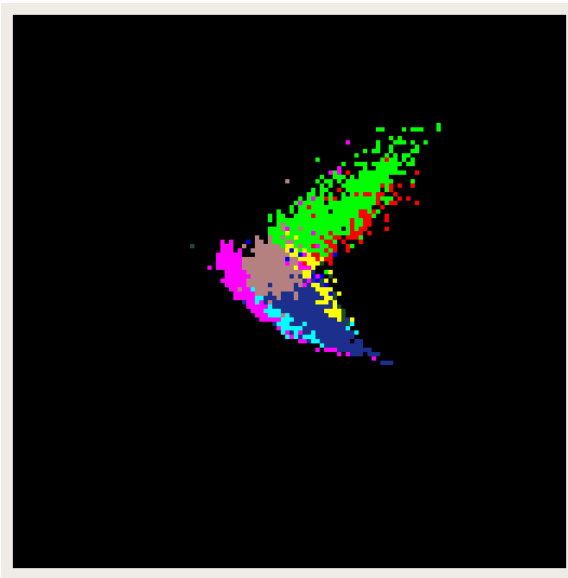
- Unsupervised learning
- Depending on the literature, neural network
- Produces 2D images from multi-dimensional data
  - While keeping the characteristics of the data intact

# How a SOM is Used

- Characterize unknown data with known data
  - Similar to using a neural network
  - Color different data groups, run through SOM
  - Run unknown data, see where it lands in the SOM.

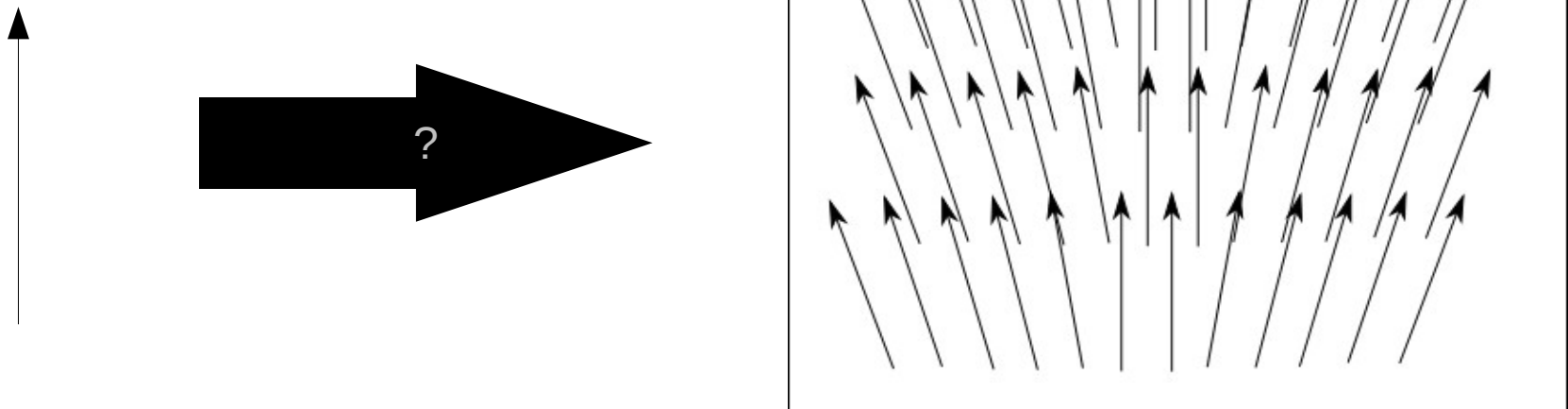
# SOM (cont)

- 9 eukaryotic genomes
  - Vector size 256 ( $4^4$ ) (only used 16 for images)
  - 40 iterations



# Building a SOM, briefly

- Initialize the weight map with PCA
- For T iterations
  - For every vector in our data set
    - Find the “closest” weight vector
    - Adjust the weight vector plus its neighbors



# Initial Weight Map

- Random or Principle Component Analysis?
  - Random may require more iterations
    - But should get you there anyways
  - PCA could create poor starting point
    - Vectors skewed via abnormally large portions of the data
    - Normalize count should take care of that
- I used PCA to create the initial weight vectors



# Principal Component Analysis

- Is there another basis that reveals hidden structure in the data?
  - If we constrain this other basis to a linear combination of the original basis of the data, then yes
- We can use the covariance of the dataset
  - Then run PCA on the covariance

# PCA (cont)

- Figure out the covariance and solve using SVD
  - Get new eigenvectors (we need the first two)
- Initialize Weight Map
  - $\vec{w}_{ij} = \vec{x}_{av} + \frac{5 * \sigma_1}{I} * [\vec{b}_1 * (i - I/2) + \vec{b}_2 * (j - J/2)]$
  - Where  $b_1$  and  $b_2$  are eigenvectors of the first and second principal components, and  $\sigma_1$  is the standard deviation.
  - $X_{av}$  is the mean of the dataset
  - $I, J$  are the weight map sizes

# Distance Measure

- Given an  $M \times N$  weight vector map and a data vector
  - How do you determine “close”
- As always, it depends on your data
  - I used  $\|(\vec{X}_k - \vec{W}_{ij})^2\|$

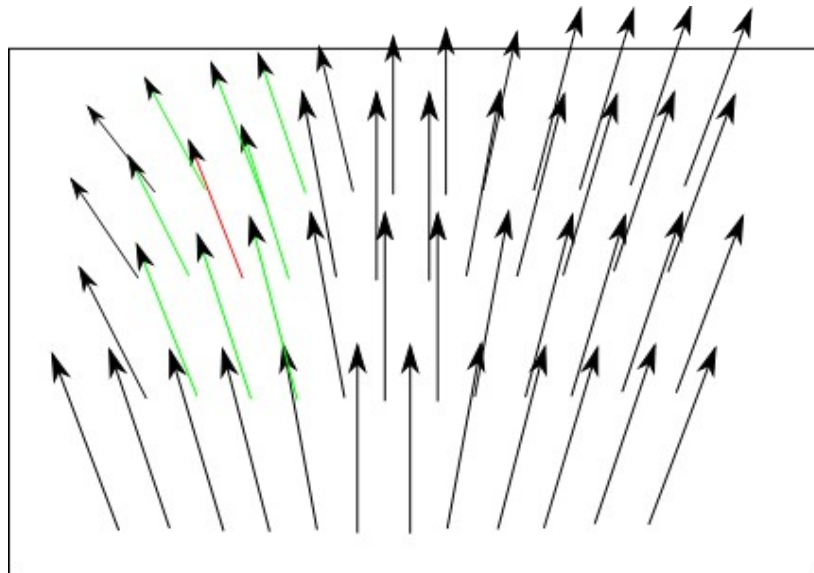
# Update Weight Map

$$\vec{w}_{ij}^{(new)} = \vec{w}_{ij} + \alpha(r) * \left( \frac{\sum \vec{x}_k}{N_{ij}} - \vec{w}_{ij} \right)$$

- Where alpha is a learning coefficient
  - After every iteration, alpha is updated
  - $\alpha(r) = \max(0.01, \alpha(1) * (1 - r/T))$ 
    - Where  $\alpha(1)$  is the initial value of alpha, and T is the total number of iterations
- r is the iteration number

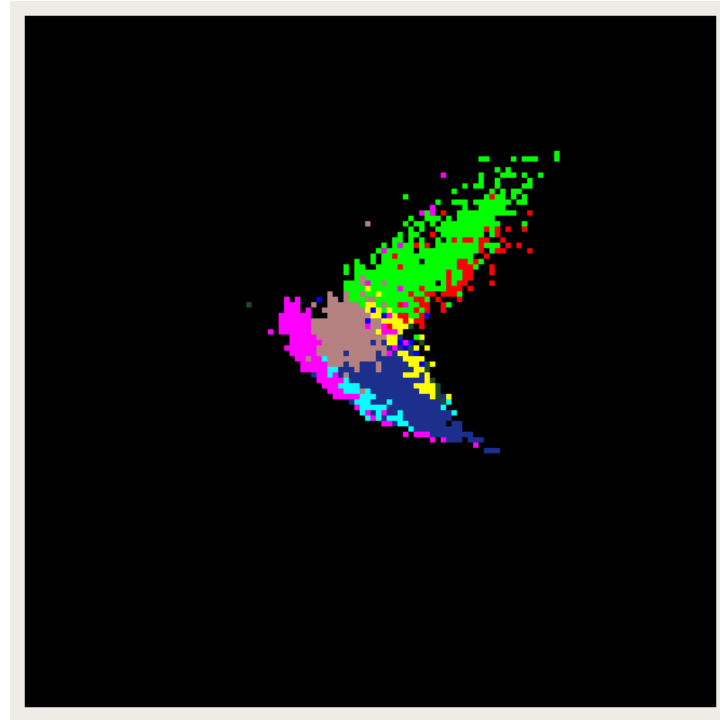
# Update Weight Map (cont)

- Use a window
  - Use beta to control the size
  - After each iteration beta is updated
    - $\text{Beta}(r) = \max(0, \text{Beta}(1) - r)$
    - Where  $\text{Beta}(1)$  is the initial value of beta



# Other Useful Information

- Density



# CUDA?

- PCA is host side (C++), SOM is CUDA
- Difficulties
  - Memory constraints in general
  - Memory constraints using SGEMM
    - Weight map width \* weight map height \* size of data
    - $64 \times 64 \times \sim 10,000 = \sim 3.6\text{GB}$  of RAM
  - Reduction required using SGEMV
  - Rolling my own matrix multiplier

# Future works

- stuff that needs to be finished soon.
  - Finish writing a CUDA PCA
  - Do some speed measurements
- Big picture
  - Adapt it for detecting “fracture”
    - Canny Edge Detection



# Questions?