A biochemical circuit motif for learning linear functions

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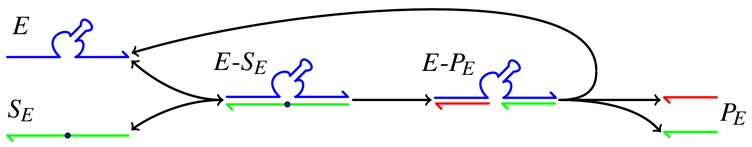
This biomolecular circuit motif learns a class of real linear functions by stochastic gradient descent, similar to classical perceptron training. The circuit architecture demonstrates a number of novel features for a synthetic biomolecular circuit, including the ability to maintain internal state and modify it according to training inputs. The circuit successfully learns and is somewhat scalable with respect to the number of inputs. Since input and weight values are represented by concentrations, all of these values must be non-negative. Also due to chemical constraints, updates must be strictly positive in all dimensions or strictly negative in all dimensions. By shifting the weight space away from the origin, we achieve good learning performance in spite of these design limitations.

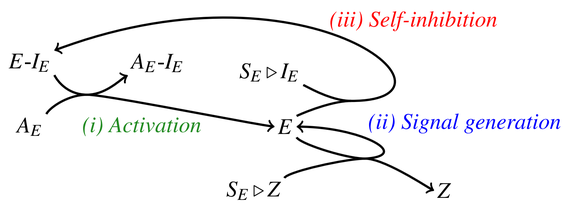
BASIC REACTIONS



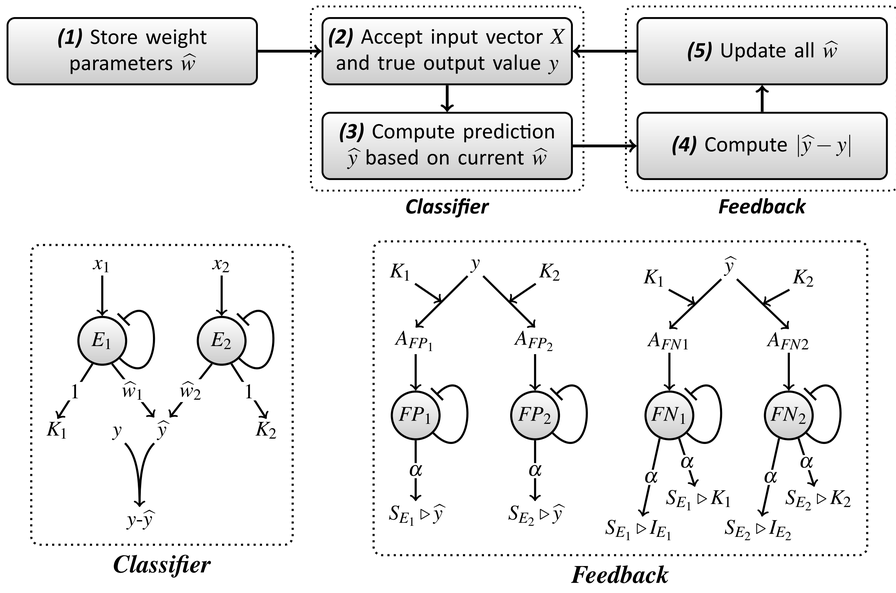
- Deoxyribozyme E catalyzes the cleavage of a substrate SE into product PE.
- E consists of a folded catalytic core flanked by 2 substrate binding arms.
- The catalytic action of E breaks the phosphodiester backbone of S at an RNA base.

The **multiplier** component's chemical reaction network consists of:

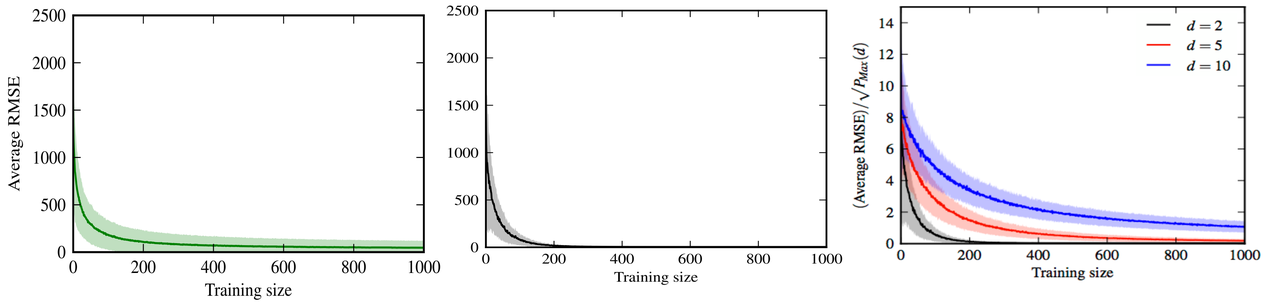
- activation
- signal generation
- self-inhibition



LEARNING ALGORITHM



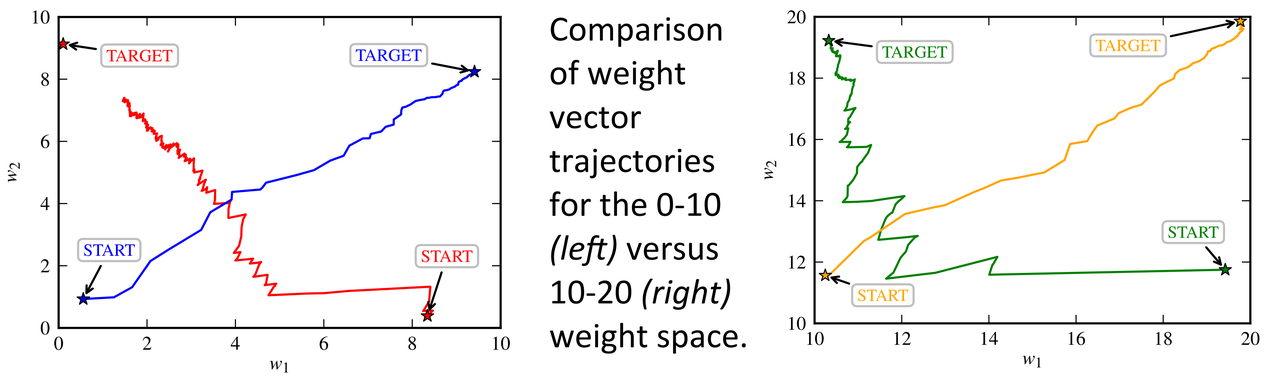
LEARNING CURVES



Comparison of learning curves for the weight range 0-10 *(left)* versus 10-20 *(right)* for 2 inputs. The RMSE values quickly bottom out to 0 in the 10-20 weight space.

Comparison of learning curves for 2, 5, and 10 inputs in the 10-20 weight space.

PATHS OF WEIGHTS

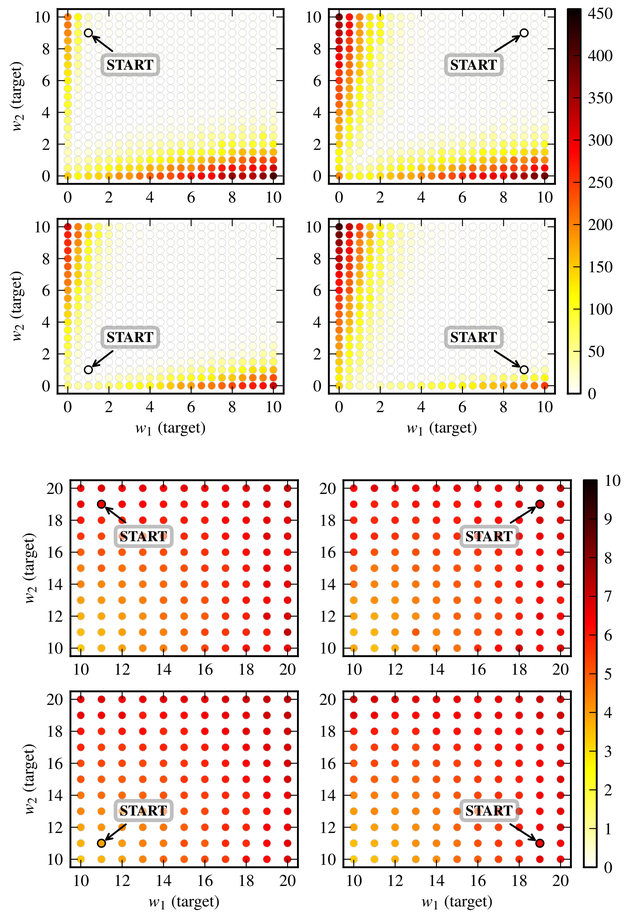


Comparison of weight vector trajectories for the 0-10 *(left)* versus 10-20 *(right)* weight space.

In the left-hand plot, the weight values take much smaller steps, increasing the number of training iterations required to reach the target weight. At each step, the updates are of the same sign for both dimensions.

SENSITIVITY TO THE TARGET FUNCTION

Scatter plots comparing RMSE (Root Mean Square Error) of prediction values in the 0-10 *(top)* versus 10-20 *(bottom)* weight spaces. RMSE values are much lower and more uniform in the weight space translated away from the origin.



This material is based upon work supported by the National Science Foundation under Grants 1027877 and 1028238, and by the National Science Foundation Graduate Research Fellowship under Grant No. DGE-0237002.