During training (600 steps), the fibration symmetries were computed using different thresholds (0.1, ..., 1). In the plots, each color is associated with a threshold. The bottom plot shows how many fibers appear in the first hidden layer during training.

Once the fibers are known, one can obtain a collapsed model. The middle plot displays the number of parameters in the collapsed model (at a given time) relative to the original model. The top plot shows the performance of that collapsed model.

For example, if we set threshold = 0.8 (purple curves) and at time t = 600, we observe a little over 150 fibers in layer 1. If we collapse the model at that moment, the total number of parameters in the collapsed network is approx. (0.13 × the number of parameters in the original network). That collapsed model achieves approx. 95% performance.
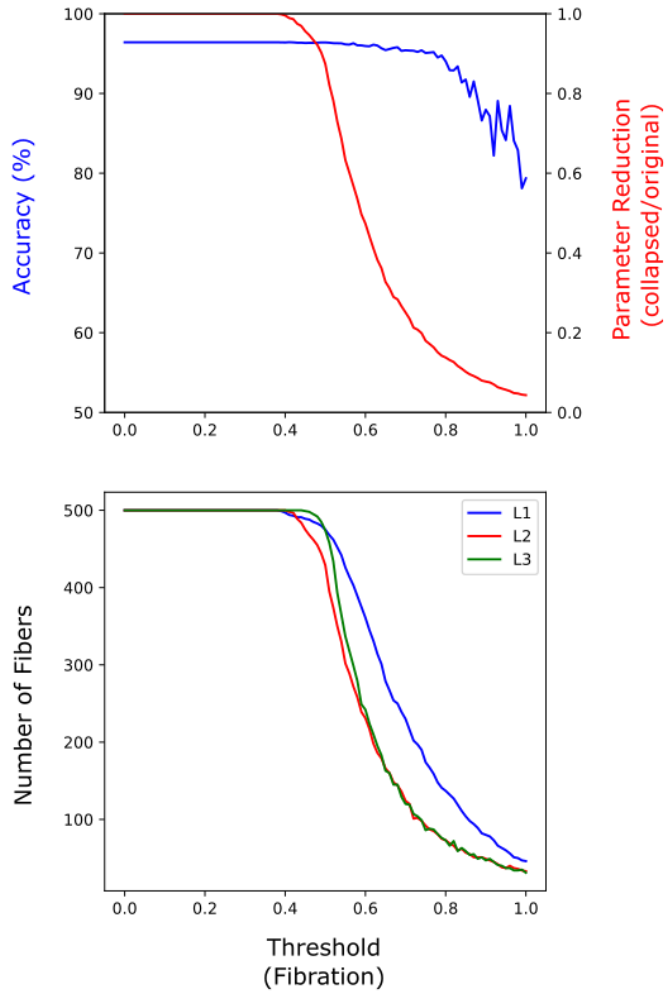
After training (t=600), we analyzed how the performance of the collapsed model depends on the threshold. The top plot shows that up to a threshold = 0.8, there is no significant loss in performance (blue curve).

However, the reduction in the number of parameters is substantial (red curve).

As mentioned earlier, the number of fibers in the hidden layers (L1, L2, L3) depends on the threshold. See the bottom plot.
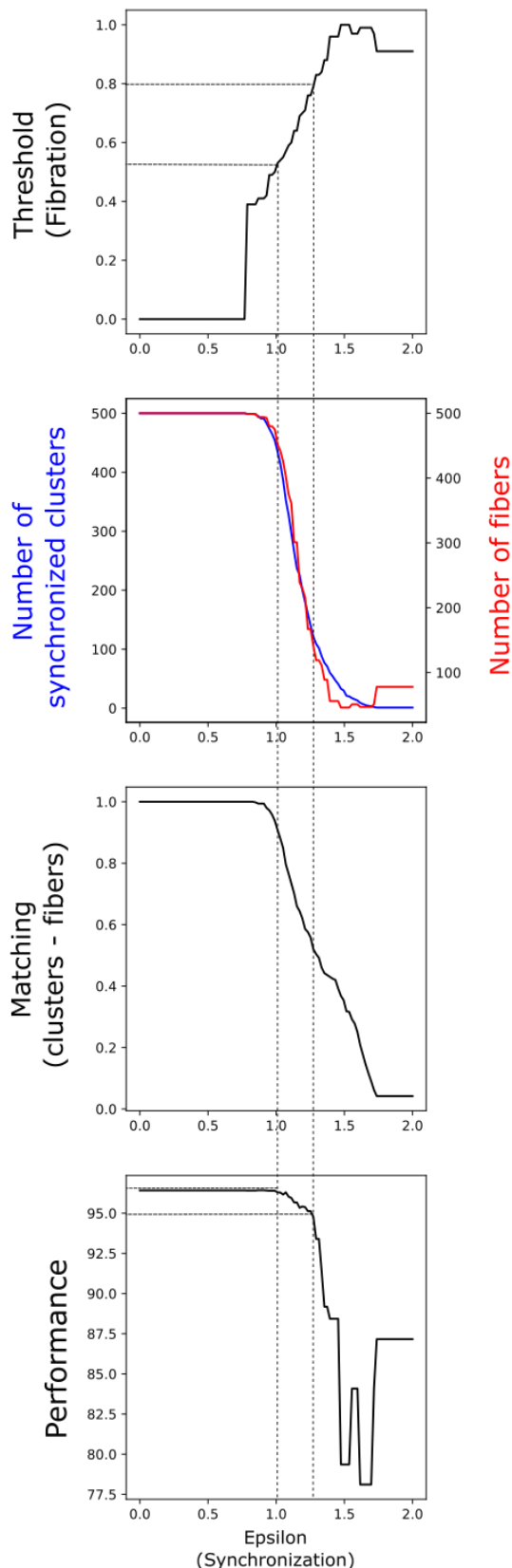
To compute synchronization clusters, a parameter 'epsilon' must be fixed.
For each 'epsilon', there exists a 'threshold' that maximizes the overlap between synchronization clusters and fibers. This relationship is shown in the top plot.

The second plot shows that for each 'epsilon' and its corresponding 'threshold', the number of clusters and fibers coincide.

The degree of overlap/matching between the partitions varies as a function of these 'epsilons' and 'thresholds' (see the third plot). A matching score of 1 indicates perfect agreement, while 0 means the partitions are entirely different.

Since there is a relationship between 'epsilon' and 'threshold', one can plot how the performance of a collapsed model changes as a function of 'epsilon' (bottom plot).

For epsilons between 1 and 1.25, the thresholds lie in the range of 0.5 to 0.8. The matching scores for the corresponding partitions exceed 0.5, and the performance of the collapsed models remains above 95%.