Team Viserion: Status Update #2

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1 Alignment

To address our issue with different sequence alignments (as discussed in last week's update), we integrated our labeled data with our unlabeled data using Clustal Omega alignment software. This program takes both sets of aligned sequences and returns a single set of aligned sequences. Here, labeled data refers to sequences with experimentally confirmed RNA binding profiles. Because we have generated a single alignment for both datasets, we will now be able to generate low-dimensional representations of labeled data to fit and evaluate affinity regression.

2 Image Captioning Model

We have continued to improve and train our ResNet encoder + LSTM decoder (discussed previously, inspired by [1]). We have extracted the latent RRM representations currently being learned by the model and generated the tSNE plots in the appendix. We're unsure of the correct interpretation of the tSNE results so far, but we will consult with our mentor and try to improve this model further. We also will train a version of this model on unaligned RRM sequences instead of the current aligned sequences, so that we can compare/contrast the learned representations and the downstream affinity regression results.

3 Cho's Character Level Neural Machine Translation Model

We have continued to improve our implementation of Cho's character level model (discussed previously, adapted from [2]).

References

[1] yunjey on GitHub, "Image captioning." https://github.com/yunjey/pytorch-tutorial/tree/master/tutorials/03-advanced/image_captioning. Accessed: 2017-11-09.

[2] J. Lee, K. Cho, and T. Hofmann, "Fully character-level neural machine translation without explicit segmentation," *CoRR*, vol. abs/1610.03017, 2016.
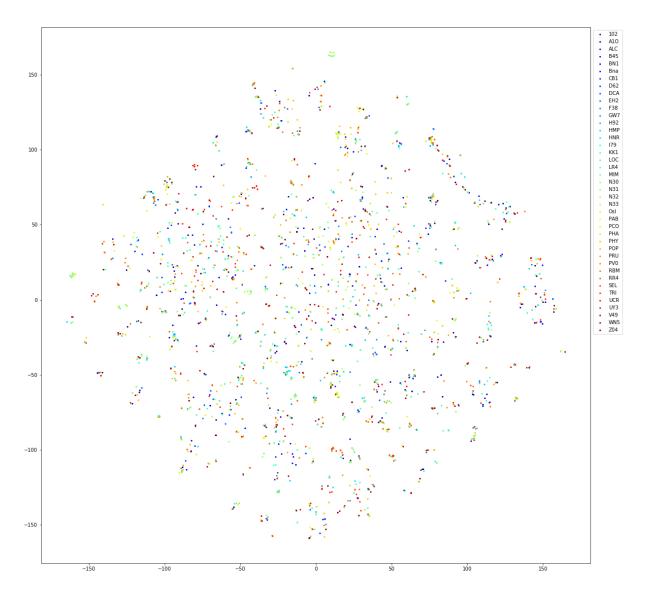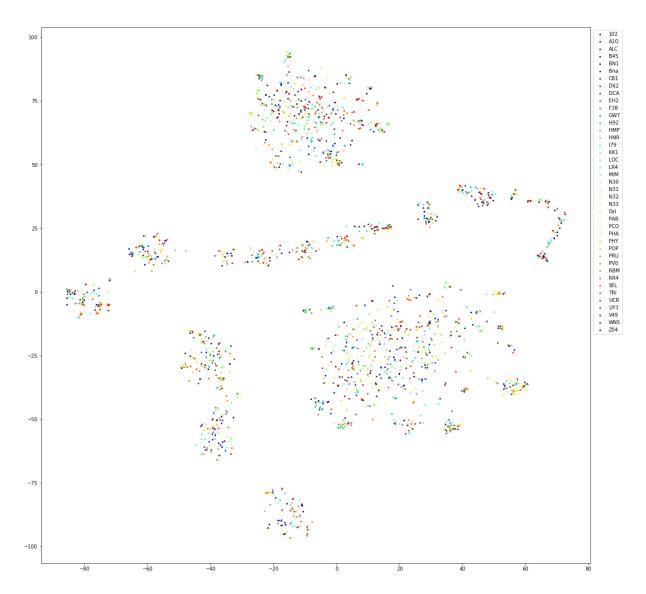
Appendix

Figures start on next page.

Figure 1: Perplexity = 10

Figure 2: Perplexity = 100