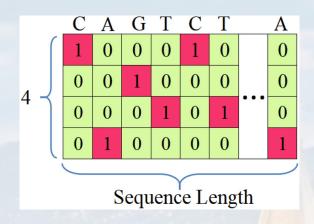
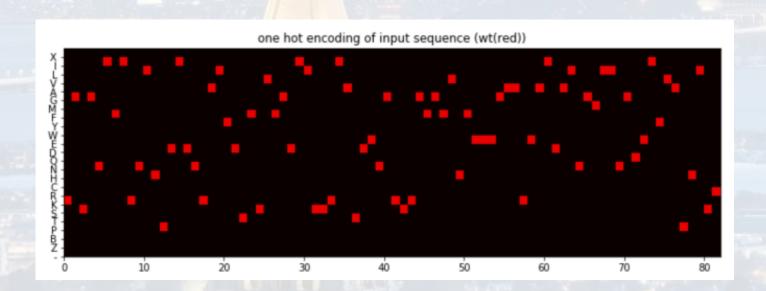
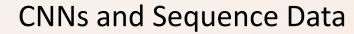


motif finding / sequence analysis



one – hot encoded NT or AA sequences can be interpreted as b/w images!





true label

sequence

as image

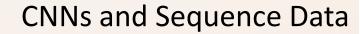


- barcodes are short DNA sequence for identifying species
- we want to see, if we can us a CNN for classification
- loading a so called fasta file

>BEISA025-19 Culex | GOI 5P

>BEISA121-19|Anopheles|COI-5P

AACATTATATTTTATTTTCGGTGCTTGAGCAGGAATAGTAGGAACTTCTTTAAGTATTCTTATTCG





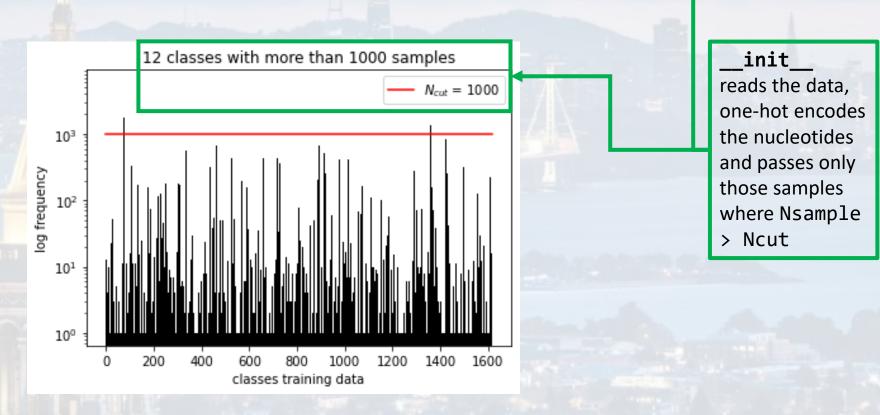
the data set:

- 86k samples
- 1.6k classes
- classes are not evenly distributed

→ picking only those with > 1k samples (12 classes)

run the package AnalyzBarcode2.py

A = Analyzer()

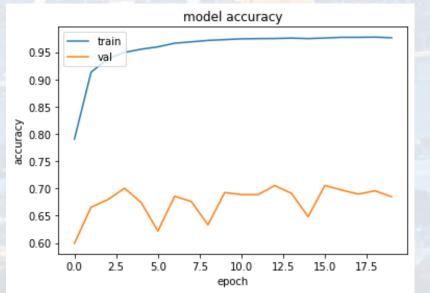


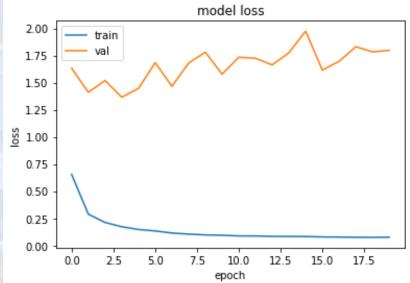


A.RunCNN()

Layer (type)	Output Shape	Param #
conv2d_6 (Conv2D)	(None, 1256, 1, 24)	408
flatten_6 (Flatten)	(None, 30144)	0
dense_12 (Dense)	(None, 84)	2532180
dense_13 (Dense)	(None, 12)	1020

Total params: 2533608 (9.66 MB) Trainable params: 2533608 (9.66 MB) Non-trainable params: 0 (0.00 Byte) runs very simple CNN





results are not great, but it shows the principle



CNNs and Sequence Data

A.EvalModel()

evaluation (note: here with training data)

