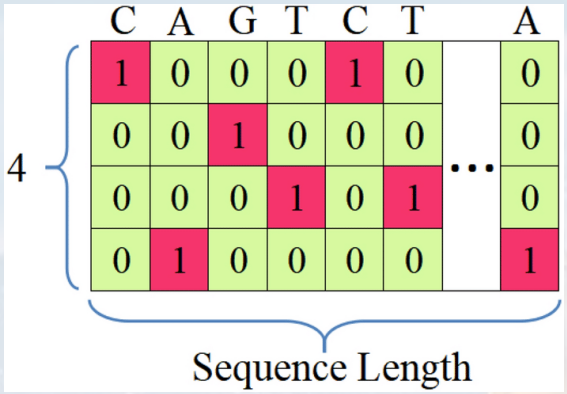
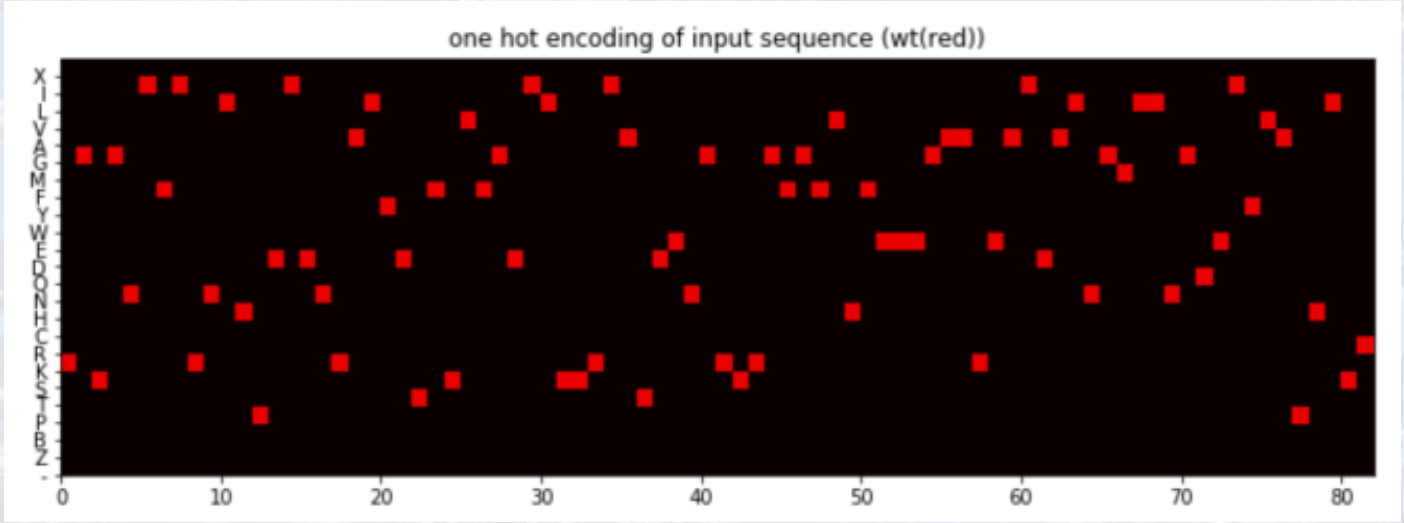
motif finding / sequence analysis



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



CNNs and Sequence Data

- 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|COI-5P
AACATTATATTTCATTTTTGGTGCTTGAGCAGGAATAATTGGAACTTCTTTAAGTCTTCTTATTCG
AGCTGAATTAAGTCAACCAGGAGTTTTTATTGGGAATGATCAAATTTATAATGTAATTGTTACAGC
TCATGCTTTTATTATAATTTTTTTTATAGTAATACCTATTATAATTGGAGGATTTGGAAATTGATT
AGTTCCTTTAATACTAGGAGCTCCTGATATAGCTTTTCCTCGAATAAATAATATAAGATTTTGAAT
ACTTCCCCCCTCATTAACACTTCTACTTTCTAGTAGTATAGTAGAAAATGGAGCTGGTACAGGTTG
AACAGTATATCCTCCTCTTTCTTCTGGAACAGCTCATGCTGGAGCTTCTGTTGATTTAGCTATTTT
TTCTTTACATTTAGCCGGAATTTCTTCAATTTTAGGAGCTGTAAATTTTATTACTACTGTAATTAA
TATGCGATCTTCTGGTATTACCCTTGATCGAATACCTTTATTTGTTTGATCAGTTGTAATTACTGC
TATTCTTTTATTATTATCTCTTCCTGTTTTAGCTGGAGCTATTACTATATTATTAACAGATCGTAA
TTTAAATACTTCTTTTTTCGATCCTATTGGAGGAGGAGATCCTATTTTATATCAACATTTATTT
>BEISA121-19|Anopheles|COI-5P
AACATTATATTTTATTTTCGGTGCTTGAGCAGGAATAGTAGGAACTTCTTTAAGTATTCTTATTCG
```

true label

sequence as image

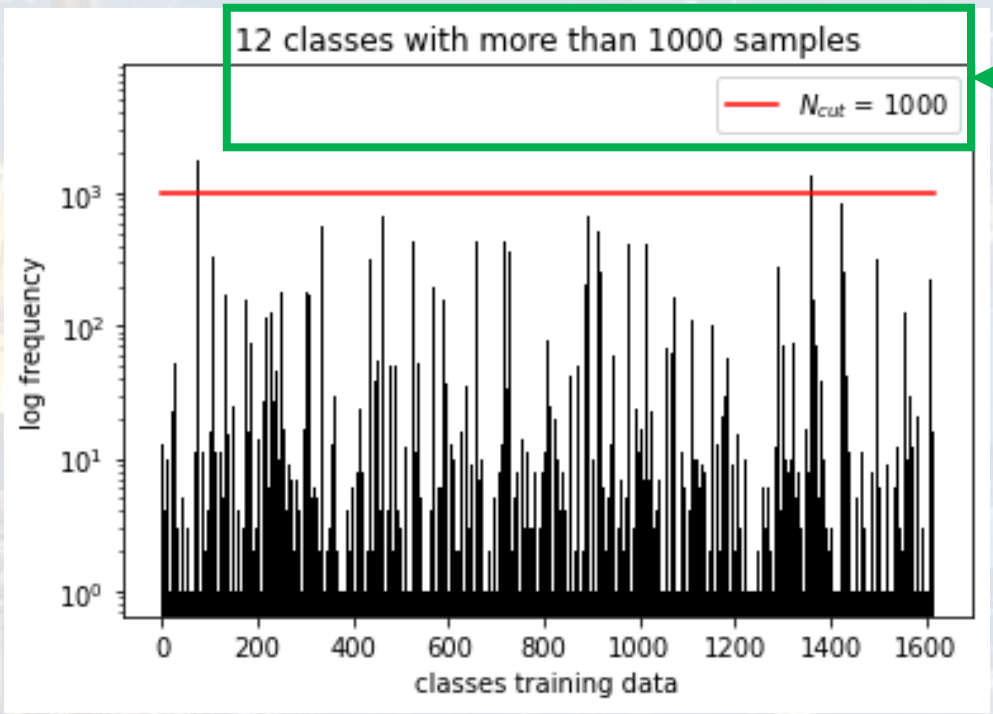
the data set:

- 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()
```



`__init__`
reads the data, one-hot encodes the nucleotides and passes only those samples where `Nsample > Ncut`

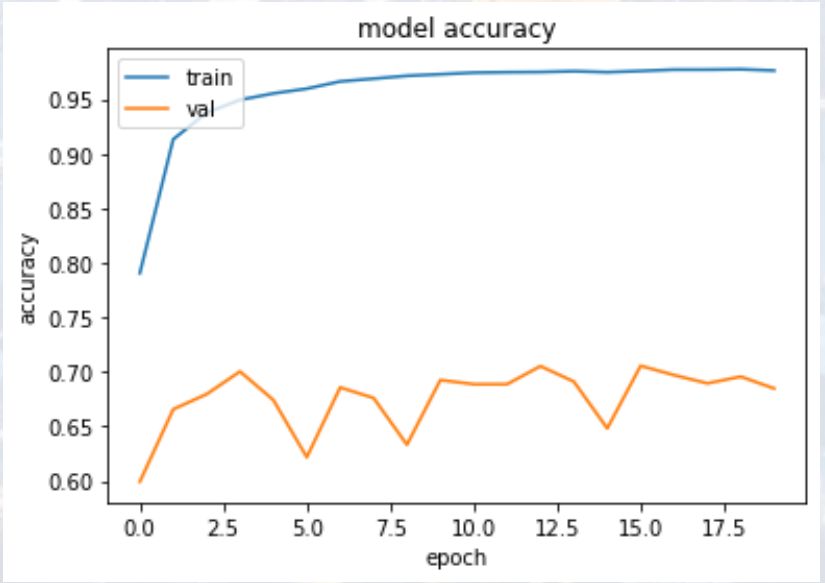
CNNs and Sequence Data

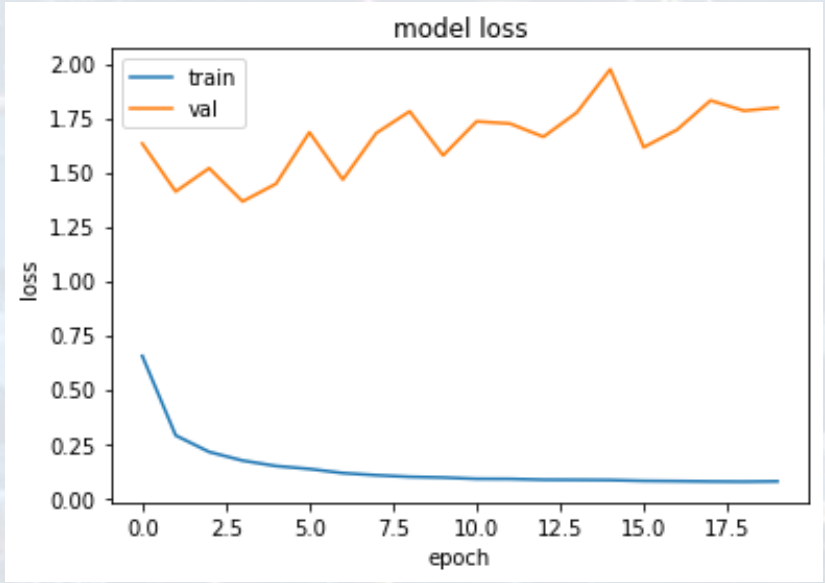
```
A.RunCNN()
```

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

`A.EvalModel()`

evaluation **(note: here with training data)**