

# Structural Bioinformatics Training Workshop & Hackathon 2018

## Spark Machine Learning

Mars Huang

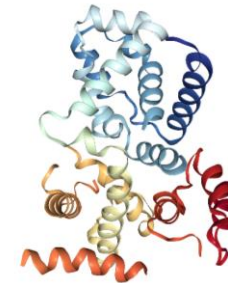
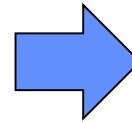
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UC San Diego*

# Example Problem

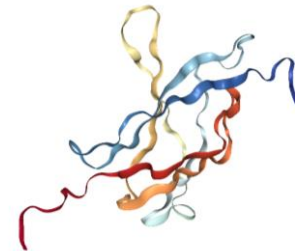
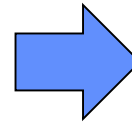
*Classify protein fold as either all alpha or all beta given the protein sequence.*

MHHHHHHSSGRENLYFQGMTVREKTRLEKFRQLLSSQNTDLDELKCS  
WPGVPREVRPITWRLLSGYLPANTERRKLT LQRKREEYFGFIEQYYDSR  
NEEHHQD TYRQIHIDIPRTNPLIPLFQQPLVQE IFERILFIWAIRHPASGYV  
QGINDLVTPFFVFLSEYVEEDVENFDVTNLSQDMLRSIEADSFWCMSK  
LLDGIQDNYTFAQPGIQKKVKALEELVSRIDEQVHNHFRRYEVEYLQFAF  
RWMNNLLMRELPLRCTIRLWD TYQSEPEGFSHFHLYVCAAFLIKWRKEI  
LDEEDFQGLLMLLQNLPTIHWGNEEIGLLLA EAYRLKYM FADAPNH YRR



*PDB ID: 3DZX – all alpha*

GSSGSSGLPQVEAYSPSACSVRGGEELVLTGSNFLPDSKVVFIERGPD  
GKLQWEEEATVNRLQSNEVTLTLTVPEYSNKRVS RPVQVYFYVSNRR  
KRSPTQSFRFLPVICKEE

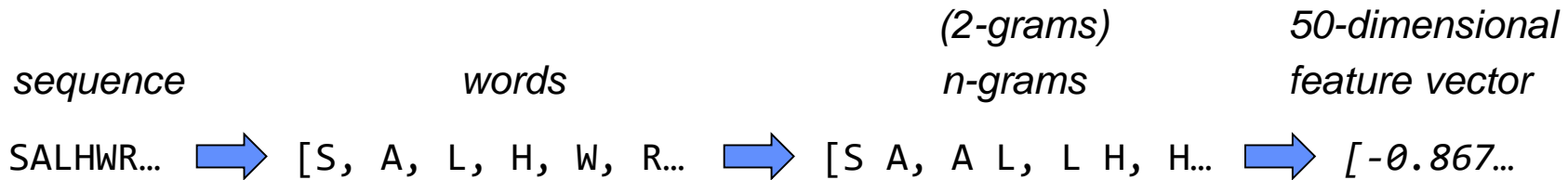


*PDB ID: 2YRP – all beta*

# PySpark Machine Learning

- **pyspark.ml**
  - Uses Dataset
- **pyspark.mllib (maintenance mode)**
  - Uses RDD

# Feature Vector Creation



Feature Engineering Pipeline:

**NGram**

**Word2Vec**

alpha	beta	coil	foldType	words	ngram	features
0.7194245	0.0	0.28057554	alpha	[S, A, L, H, W, R...]	[S A, A L, L H, H...]	[-0.8678886349164...
0.4090909	0.0	0.59090906	alpha	[S, H, L, K, S, K...]	[S H, H L, L K, K...]	[-0.2172588950821...
0.015151516	0.5808081	0.4040404	beta	[M, A, H, H, H, H...]	[M A, A H, H H, H...]	[-0.6485012823101...
0.7916667	0.0	0.20833333	alpha	[M, G, S, S, H, H...]	[M G, G S, S S, S...]	[-0.7672874573129...
0.028846154	0.52884614	0.44230768	beta	[M, E, K, A, T, K...]	[M E, E K, K A, A...]	[-0.7308713050851...
0.6904762	0.011904762	0.29761904	alpha	[P, T, I, H, D, H...]	[P T, T I, I H, H...]	[-0.7869252321949...
0.8108108	0.0	0.1891892	alpha	[G, A, M, E, P, E...]	[G A, A M, M E, E...]	[-0.8350848566740...
0.022900764	0.39694658	0.5801527	beta	[I, V, N, G, E, E...]	[I V, V N, N G, G...]	[-0.6840203473201...
0.8021978	0.0	0.1978022	alpha	[M, T, P, D, V, L...]	[M T, T P, P D, D...]	[-0.7698143909806...

<https://github.com/sbl-sdsc/mmtf-pyspark/blob/master/mmtfPyspark/ml/proteinSequenceEncoder.py>

# N-gram, Word2Vec

- N-gram: Slice and group a string with a window size of N
- Word2Vec: Projecting a string to an n-dimensional vector

## Word-level unigrams

Text

One Two Three Four  
One Two Three Four  
One Two Three Four  
One Two Three Four

## Word-level bigrams

Text

One Two Three Four  
One Two Three Four  
One Two Three Four

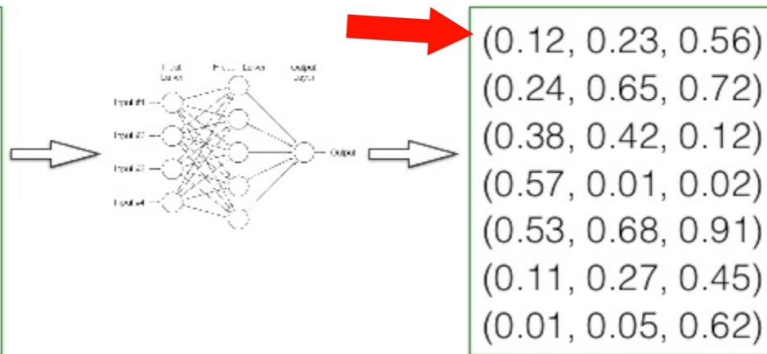
## Word-level trigrams

Text

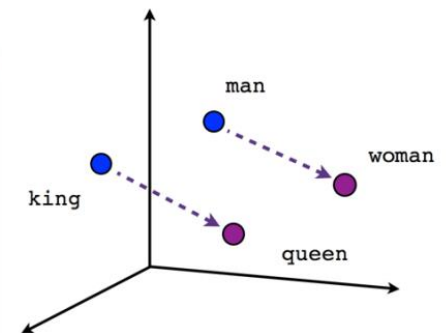
One Two Three Four  
One Two Three Four

word

The  
Cardinals  
will  
win  
the  
world  
series



vector



Male-Female

<https://spark.apache.org/docs/latest/mllib-feature-extraction.html#word2vec>



# Create Class Labels

	alpha	beta	coil	foldType
0.7194245	0.0	0.28057554	alpha	
0.4090909	0.0	0.59090906	alpha	
0.015151516	0.5808081	0.4040404	beta	
0.7916667	0.0	0.20833333	alpha	
0.028846154	0.52884614	0.44230768	beta	
0.6904762	0.011904762	0.29761904	alpha	
0.8108108	0.0	0.1891892	alpha	
0.022900764	0.39694658	0.5801527	beta	
0.8021978	0.0	0.1978022	alpha	

# The Dataset for Classification

*We save this dataset as .parquet file:*

```
data.write.mode("overwrite").format("parquet").save(filename);
```

class label				features		
alpha	beta	coil	foldType	words	ngram	features
0.7194245	0.0	0.28057554	alpha	[S, A, L, H, W, R...]	[S A, A L, L H, H...]	[-0.8678886349164...
0.4090909	0.0	0.59090906	alpha	[S, H, L, K, S, K...]	[S H, H L, L K, K...]	[-0.2172588950821...
0.015151516	0.5808081	0.4040404	beta	[M, A, H, H, H, H...]	[M A, A H, H H, H...]	[-0.6485012823101...
0.7916667	0.0	0.20833333	alpha	[M, G, S, S, H, H...]	[M G, G S, S S, S...]	[-0.7672874573129...
0.028846154	0.52884614	0.44230768	beta	[M, E, K, A, T, K...]	[M E, E K, K A, A...]	[-0.7308713050851...
0.6904762	0.011904762	0.29761904	alpha	[P, T, I, H, D, H...]	[P T, T I, I H, H...]	[-0.7869252321949...
0.8108108	0.0	0.1891892	alpha	[G, A, M, E, P, E...]	[G A, A M, M E, E...]	[-0.8350848566740...
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0.8021978	0.0	0.1978022	alpha	[M, T, P, D, V, L...]	[M T, T P, P D, D...]	[-0.7698143909806...

# Demos

- **Create a dataset**
- **Fit several classification models with pyspark.ml**
- **Fit several classification models with scikit-learn**



# Problem 1

- **Change the code to a 3-state classification problem:**
  - alpha, beta, alpha+beta
- **Rerun the classification with Decision Tree Classifier**

# Resources

- **Pyspark.ml API**
  - <http://spark.apache.org/docs/2.2.0/api/python/pyspark.ml.html>
- **Extracting, transforming and selecting features**
  - <http://spark.apache.org/docs/2.2.0/api/python/pyspark.ml.html#module-pyspark.ml.feature>
  - N-gram
    - <http://spark.apache.org/docs/2.2.0/api/python/pyspark.ml.html#pyspark.ml.feature.NGram>
  - Word2Vec
    - <http://spark.apache.org/docs/2.2.0/api/python/pyspark.ml.html#pyspark.ml.feature.Word2Vec>
- **Classification and regression**
  - <https://spark.apache.org/docs/2.2.0/ml-classification-regression.html>
- **Parquet files (columnar format)**
  - <https://spark.apache.org/docs/latest/sql-programming-guide.html#parquet-files>

# Funding

This workshop was supported by the National Cancer Institute of the National Institutes of Health under Award Number U01CA198942. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

