

A DISSERTATION / THESIS TEMPLATE IN L^AT_EX

by

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A Dissertation (Thesis) Submitted in Partial Fulfillment of the Requirements for the
Degree of

The Degree

in

My Chosen Field

Middle Tennessee State University

December, 2020

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Dr. Greathearted, *Chair*

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Dr. Dooalot

Dr. Heliopolis

This page is optional. Students wishing to dedicate the thesis or dissertation to someone may do so using this page. This page does not include a heading, and the text should be brief and centered on the page. Pagination is centered, in lowercase Roman numerals.

ACKNOWLEDGMENTS

This page is optional and can be used to include brief statements of appreciation or recognition. This page has the heading “ACKNOWLEDGEMENTS,” and the heading must be centered and written in all capital letters. Pagination is centered, in lowercase Roman numerals.

ABSTRACT

Every thesis or dissertation is required to include an abstract. This should be approximately 350 words for dissertations and 150 words for theses. The student and the committee will determine the content of the abstract. The page must be titled “ABSTRACT,” and the heading must be centered and written in all capital letters. Pagination is centered, in lowercase Roman numerals.

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CHAPTER I : PROLOGUE

This is the introduction chapter, use it to introduce the audience to what this Thesis/Dissertation represents. Maybe your work is biology related and deals with proteins. Good graphics help assist with the introduction, see Figures 1.1 and 1.2. You might also want to mention your related publications.

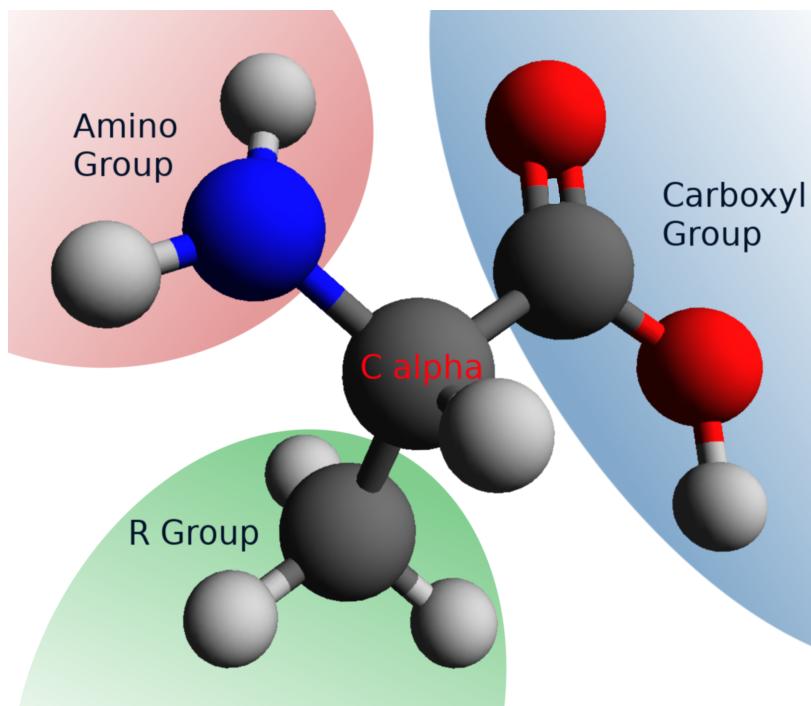


Figure 1.1: The amino acid Alanine showing the amino group (red shading) bound to the alpha carbon CH (center) that is bound to the carboxyl group (blue shading). The R group (green shading) for Alanine is CH_3 . Carbon is depicted as dark gray, hydrogen is light gray, oxygen is red and nitrogen is blue. Amino acid produced by Avogadro (Hanwell et al., 2012).

The following are related publications:

“Still Working on this Awesome Paper” (In preparation)

Me, and You. “A Paper I Submitted and Currently Have a Preprint on BioRxiv.”
BioRxiv, Cold Spring Harbor Laboratory, June 2020, the doc id and url. (Submitted
for publication)

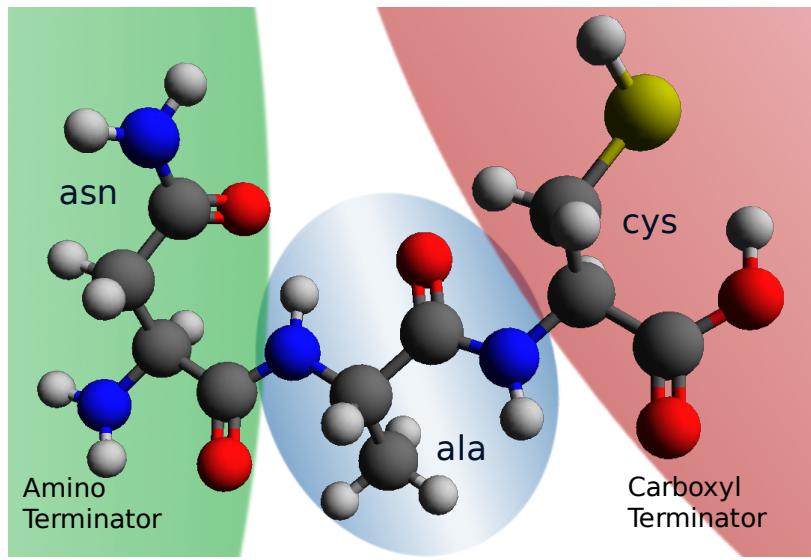


Figure 1.2: A simple protein chain with shading to distinguish each amino acid: Asparagine (green), Alanine (blue), and Cysteine (red). The amino terminal is to the left and the carboxyl terminal is to the right. Carbon is depicted as dark gray, hydrogen is light gray, oxygen is red, sulfur is yellow and nitrogen is blue. Protein chain produced by Avagadro (Hanwell et al., 2012).

Me, You, and Another ...

CHAPTER II : BACKGROUND INFORMATION

The First Subsection

This is the background chapter, make the case for your dissertation. more graphics help and break it down by subject with subsections and subsubsections.

Another Section

More information on another aspect of the subject

CHAPTER III : MAYBE A CHAPTER ON HOW WE GOT THE DATA

This research extends upon previously developed methods to determine something about some thing. A figure here helps get the message across.

My New Approach

The pipeline of Stieh et al. (2013) is enhanced through the use of full structure assemblies, energy minimization, advanced compression techniques and a fully automatic execution environment. Notice the citation format, this is an inline citation used to call out a specific article, see the source code of this chapter. I may want to cite it as a matter of fact, in which case I want it to appear like this (Stieh et al., 2013).

More graphics help get the message across

Some Specific Details of Part A

Structure modeling is facilitated through comparative modeling by Modeller (Sali and Blundell, 1993).

More Figures as needed

Some Specific Details of Part B

Once theoretical models are generated by Modeller, the structures are energy minimized by Gromacs (Berendsen et al., 1995; Lindahl et al., 2001).

CHAPTER IV : METHODS

Background

Some background information about your specific methods will help readers understand where all this started.

Dynamic Electrophoretic Fingerprinting

Electrophoretic mobility (EM) is an experimental measure of surface charge used to characterize and separate micro-organisms (Mehrishi and Bauer, 2002; Richmond and Fisher, 1973). Researchers hypothesized the method could be applied across saline and pH ranges relevant to mucosal environments where transmission is common and results in systemic infection. The method was employed to study trimeric gp120/gp41 from clade B HIV-1 strain BX08 (Stieh et al., 2013) in the bound and unbound conformations by evaluating the difference between the two states. The results described surface charge variations across titrations indicating decreased gp120 surface charge in mucosal environments, complementing the positive charge of the CD4 receptor surface. This potentially could be the result of variations in gp120 protein structure and the interactions of surrounding solvent where blood plasma and mucous vary in pH and saline levels. This technique is used to validate the pipeline process in the methods that follow.

My First New Method

With a colorized table. I would suggest <https://www.tablesgenerator.com/> as a place to generate tables of this nature.

Results

These results are a product of ...

Check the source here to see how to manually insert hyphenation points in long character strings such as: Z242MPL25JAN03PCR23ENV1.1-DT and Z242MPL25JAN03PCR-

Table 4.1: Visually compelling tables make a greater impact.

Unbound Data for Each Sequence						
Model/pH	3.0	3.1	3.2	3.3	...	9.0
Model_1	0.008658	-1.246752	0.441558	1.229436	...	-1.290042
Model_2	0.017316	1.25541	-0.017316	0.580086	...	-1.16883
...
Model_N	0.019243	1.142856	-1.55844	1.549782	...	1.090908

Seq_1	PCA	BESI	BESI compares the first 2 principal components of each sequence against the first 2 principal components of the control.
Seq_2	PCA		
...	...		
Seq_N	PCA		

33ENV1.1-DNT gp120. It's a little painful at first and especially if you manuscript contains a lot of them. Some minor programming skills in Python (Van Rossum and Drake Jr, 1995) can make easy work of it.

Discussion

The results here have shown ...

My Next Method

My next method and how data is extracted; visually represented in Figure 4.1.

Results

The first set of results comes from ...

For the purposes of expressing these data, all theoretical data will be normalized for clarity using:

$$x' = \frac{x - set_{min}}{set_{max} - set_{min}}$$

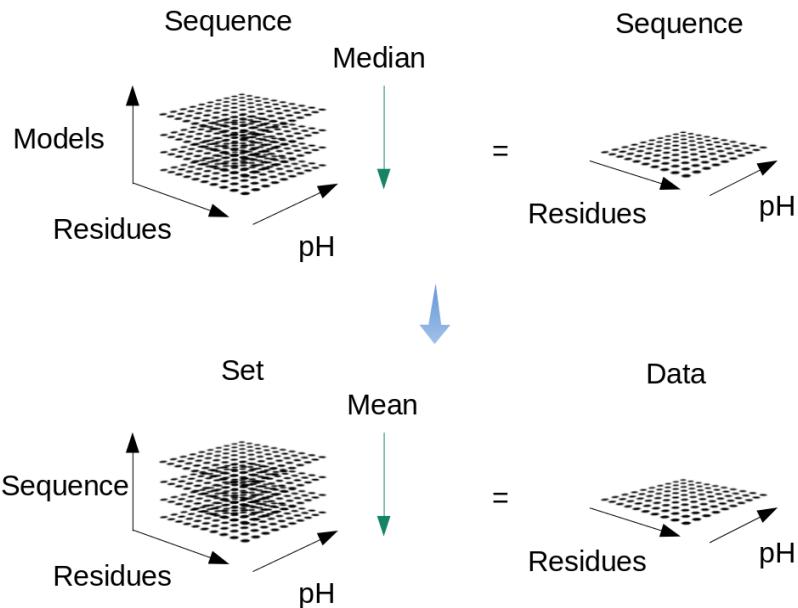


Figure 4.1: Visualization of the process to extract variance data from residue electrostatics. Models of residue data are reduced to 2 dimensions by taking the median of the set across models/residue to eliminate the effects of outliers on the data. Once each sequence/model set is processed, the mean across the sequence set is taken to produce the residue data for which the variance is extracted for each residue across the pH range.

Where x is the theoretical value, set_{min} is the minimum value of all theoretical data produced, set_{max} is the maximum value of all theoretical data produced, and x' is the normalized value returned.

Discussion

Motifs provide no evidence that the range of ...

Comparing Soandso to Supervised Machine Learning

This section is presented as validation of the unsupervised methods ...

Binary Classifier

Figure 4.2 shows the model construct for the binary classifier using sixty-one inputs with a one hundred and twenty eight node hidden layer to a single node output. Figure 4.3 provides a visual representation of the binary classifier. Dropout layers are only used

during training to prevent over-fitting the data and are not depicted in the figure. The neural network is dense (fully meshed) and utilizes Rectified Linear Unit (ReLU) activation for the input and hidden layers. Output is sigmoid activated to complete the binary classifier.

```

model = keras.Sequential(
    [
        layers.Dense(128, input_dim=61, activation='relu'),
        layers.Dropout(0.5),
        layers.Dense(128, activation='relu'),
        layers.Dropout(0.5),
        layers.Dense(1, activation='sigmoid')
    ]
)

model.compile(loss='binary_crossentropy',
               optimizer='rmsprop',
               metrics=['accuracy'])

history = model.fit(x_train, y_train,
                     epochs=100, batch_size=50,
                     validation_data=(x_val, y_val),
                     verbose=1)

test_data = np.genfromtxt('inputdata.txt', delimiter=' ')
test_data_labels = np.genfromtxt('sequence.list', delimiter=' ')
results = model.predict(test_data)

```

Figure 4.2: Model construct of a binary classifier using 61 inputs tied to a 128 node hidden layer that feeds a single output node.

Results

Scoring by the binary classifier can be see in Table 4.2 for all 252 ...

This is an example of a multi-page table:

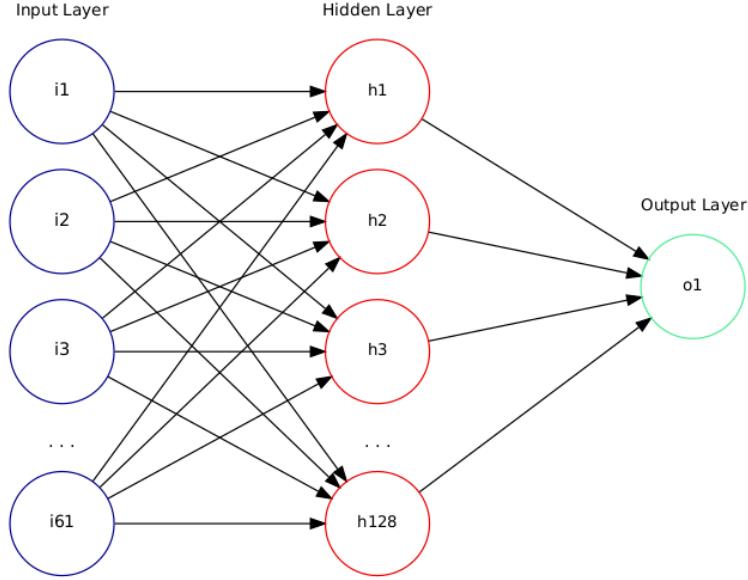


Figure 4.3: Graphic representation of binary classifier showing individual layers. Dropout layers are not expressed and are only used during training to control over and under fitting.

Table 4.2: Scoring from binary classifier showing under-fitting by the neural network.

Sequence	Score	Sequence	Score
Z238FSW15A6_plasmid_6v	0.9819	Z201FPL07feb03102-1	1
Z238FSW15G4_plasmid_4i	0.9999	Z201FPL07feb03103-1	1
Z238FSW15H8_plasmid_3ii	1	Z201FPL07feb03105-1	1
Z238FSW29oct0215A11	1	Z201FPL07feb0350-2	1
Z238FSW29oct0215A6v	0.9767	Z201FPL07feb0351-1	0.8955
Z238FSW29oct0215G4	0.9999	Z201FPL07feb0368-2	1
Z238FSW29oct0215H8	1	Z201FPL07feb0372-1	1
Z238MPL17_plasmid_a	0.8942	Z201FPL07feb0390-1	1
Z238MPL9_plasmid_c	0.3827	Z201FPL100_plasmid_8-1	1
Z242FPL25JAN03PCR23ENV1.1	0.9998	Z201FPL102_plasmid_7-1	1
Z242FPL25JAN03PCR8ENV1.1	1	Z201FPL103_plasmid_4-1	1
Z242FPL25jan038_plasmid	1	Z201FPL105_plasmid_3-1	1

Table 4.2 – *Continued on next page*

Table 4.2 – *Continued from previous page*

Sequence	Score	Sequence	Score
Z242MPL25JAN0326	0.8888	Z201FPL50_plasmid_5-2	1
Z242MPL25JAN0327-1	1	Z201FPL51_plasmid_1-1	0.913
Z242MPL25JAN0327-2	0.9999	Z201FPL68_plasmid_6-2	1
Z242MPL25JAN0327-3	1	Z201FPL72_plasmid_9-1	1
Z242MPL25JAN03PCR23ENV1.1-DT	1	Z201FPL7FEB03ENV1.8	1
Z242MPL25JAN03PCR33ENV1.1-DNT	0.0016	Z201FPL7FEB03ENV2.1	1
Z242MPL25jan0323_plasmid	1	Z201FPL7FEB03ENV3.3	1
Z242MPL25jan0326_plasmid	0.9648	Z201FPL7FEB03ENV4.1	1
Z242MPL25jan0328_plasmid_8-1	1	Z201FPL7FEB03ENV5.2	1
Z242MPL25jan0328_plasmid_8-2	1	Z201FPL7FEB03ENV6.1	1
Z242MPL25jan0328_plasmid_8-3	0.9998	Z201FPL7FEB03ENV7.1	0.8914
Z242MPL25jan0333_plasmid	0.0018	Z201FPL90_plasmid_2-1	1
Z242MPL26_plasmid	0.9942	Z201FSW07feb03DNA13D1	1
Z242MPL28_plasmid_8-1	1	Z201FSWDNA13D1_plasmid_4i	1
Z242MPL28_plasmid_8-2	1	Z201MPB7FEB03ENV2.1	1
Z242MPL28_plasmid_8-3	1	Z201MPB7FEB03ENV4.1	1
Z292FCA12A52_plasmid_9v	1	Z201MPB7FEB03ENV5.1	0.9999
Z292FCA24may0512A52	1	Z201MPL07feb0352a	1
Z292FCA24may0512A52_plasmid_9v	1	Z201MPL07feb0352aa	0.9995
Z292FCA24may0512A58_plasmid_6v	0.9656	Z201MPL07feb0352e	0.9998
Z292FCA24may0512D10_plasmid_5iii	1	Z201MPL07feb0384c	0.9999
Z292FCF12E26_plasmid_10iv	1	Z201MPL52_plasmid_a	0.9999
Z292FCF24may0512D18_plasmid_4i	1	Z201MPL52_plasmid_aa	0.9999
Z292FCF24may0512E26	1	Z201MPL52_plasmid_e	0.9998
Z292FCF24may0512E26_plasmid_10iv	1	Z201MPL7FEB03ENV2.1	0.9998
Z292FPL24may05105_plasmid_5-1	1	Z201MPL7FEB03ENV3.1	1
Z292FPL24may05136_plasmid_7-1	1	Z201MPL7FEB03ENV4.1	1
Z292FPL24may05152_plasmid_1-3	0.9999	Z201MPL84_plasmid_c	0.9957

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Sequence	Score	Sequence	Score
Z292FPL24may05160_plasmid_4-1	1	Z205FPB27MAR03ENV1.1	0.8165
Z292FPL24may05164_plasmid_9-2	1	Z205FPB27MAR03ENV4.2	0.7305
Z292FPL24may05172_plasmid_6-1	1	Z205FPL27MAR03ENV4.1	0.019
Z292FPL24may0535_plasmid_3-3	1	Z205FPL27MAR03ENV5.2	1
Z292FSW24may0512E12_plasmid_3v	0.9996	Z205FPL27MAR03ENV6.3	0.6004
Z292FSW24may0512E20_plasmid_2i	1	Z205MPB27MAR03ENV4.1	1
Z292MPL113_plasmid_e	1	Z205MPB27MAR03ENV6.1	1
Z292MPL150_plasmid_b	1	Z205MPB27MAR03ENV9.1	0.0816
Z292MPL24may05113_plasmid_e	1	Z205MPL27MAR03ENV1.1NF	1
Z292MPL24may05113e	1	Z205MPL27MAR03ENV2.3	0.341
Z292MPL24may05150_plasmid_b	1	Z205MPL27MAR03ENV3.1NF	0.9999
Z292MPL24may05150b	1	Z205MPL27MAR03ENV6.3	1
R56FPL21apr05B6_plasmid_a	0.9777	Z216FC17jan04RNAB37	0.9996
R56FPL21apr05B6_plasmid_b	0.9807	Z216FCF17jan04RNAB44	0.0097
R56FPL21apr05E7_plasmid_a	0.5807	Z216FCFRNA11B44_plasmid_2iv	0.0064
R56FPL21apr05E7_plasmid_b	0.9906	Z216FCRNA11B37_plasmid_7i	0.9998
R56MCA21aug0516_plasmid_9iii	0.9999	Z216FPB112_plasmid_e	1
R56MCA21aug053_plasmid_5i	1	Z216FPB85_plasmid_f	0.9289
R56MCA21aug056_plasmid_6iii	1	Z216FPB98_plasmid_e	0.9447
R56MCF21aug0511_plasmid_1v	1	Z216FPL129_plasmid_6-1	1
R56MCF21aug0514_plasmid_2iv	1	Z216FPL138_plasmid_8-3	0.9963
R56MCF21aug0519_plasmid_3ii	1	Z216FPL17jan04112e	1
R56MPL21apr05C2_plasmid_7-1	1	Z216FPL17jan04129	1
R56MPL21apr05C5_plasmid_6-4	1	Z216FPL17jan04138	0.9872
R56MPL21apr05G5_plasmid_5-3	1	Z216FPL17jan04190	0.9994
R56MPL21apr05H3_plasmid_1-3	1	Z216FPL17jan046	0.0008
R56MPL21apr05K4_plasmid_4-1	1	Z216FPL17jan0483	0.0069
R56MPL21apr05K6_plasmid_2-4	1	Z216FPL17jan0485f	0.9793

Table 4.2 – *Continued on next page*

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Sequence	Score	Sequence	Score
R56MPL21apr05P5_plasmid_8-1	1	Z216FPL17jan0492	1
Z153FPB13MAR02ENV1.1	0.828	Z216FPL17jan0498e	0.8215
Z153FPB13MAR02ENV2.1	0.9979	Z216FPL190_plasmid_5-1	0.9999
Z153FPB13MAR02ENV3.1	0.3384	Z216FPL6_plasmid_4-4	0.0028
Z153FPB13MAR02ENV4.1	0.9996	Z216FPL83_plasmid_7-2	0.1336
Z153FPB13MAR02ENV5.1	0.9989	Z216FPL92_plasmid_1-1	0.9999
Z153FPL13MAR02ENV1.1	0.9033	Z216FSW17jan04DNA15	0.975
Z153FPL13MAR02ENV2.1	0.2734	Z216FSWDNA11I5_plasmid_5v	0.9916
Z153FPL13MAR02ENV3.1	0.0002	Z216MPL133_plasmid	0.9964
Z153FPL13MAR02ENV4.1	0.9996	Z221FPB7MAR03ENV10.3	1
Z153FPL13MAR02ENV5.1	0.0015	Z221FPB7MAR03ENV11.3	1
Z153FPL13MAR02ENV6.1	0.0014	Z221FPB7MAR03ENV6.4	1
Z153MPB13MAR02ENV1.1	0.9998	Z221FPB7MAR03ENV9.1	0.935
Z153MPB13MAR02ENV2.1	0.8576	Z221FPL08mar0335	0.9796
Z153MPB13MAR02ENV3.1	0.9998	Z221FPL08mar0344	0.0004
Z153MPB13MAR02ENV4.1	1	Z221FPL08mar0348	0.4223
Z153MPB13MAR02ENV5.1	0.9999	Z221FPL08mar0351	0.9989
Z153MPL13MAR02ENV1.1	0.9996	Z221FPL08mar0355	0.0619
Z153MPL13MAR02ENV2.1	0.9995	Z221FPL08mar0371	0.9597
Z153MPL13MAR02ENV3.1	0.9631	Z221FPL08mar0380	1
Z153MPL13MAR02ENV4.1	0.9997	Z221FPL35_plasmid_7-1	0.8827
Z153MPL13MAR02ENV5.1	0.9996	Z221FPL44_plasmid_4-1	0.0008
Z185FPB24AUG02ENV1.1	0	Z221FPL48_plasmid_5-1	0.3918
Z185FPB24AUG02ENV2.1	0	Z221FPL51_plasmid_2-2	0.9996
Z185FPB24AUG02ENV3.1	0	Z221FPL55_plasmid_6-2	0.0259
Z185FPB24AUG02ENV4.1	0	Z221FPL71_plasmid_9-1	0.9746
Z185FPB24AUG02ENV5.1	0	Z221FPL7MAR03ENV1.2	0.9677
Z185FPL17AUG02ENV1.1	0.0003	Z221FPL7MAR03ENV10.4	0.9999

Table 4.2 – *Continued on next page*

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Sequence	Score	Sequence	Score
Z185FPL17AUG02ENV2.1	0	Z221FPL7MAR03ENV2.3	1
Z185FPL17AUG02ENV3.1	0.0018	Z221FPL7MAR03ENV3.3	0.9987
Z185FPL17AUG02ENV4.1	0	Z221FPL80_plasmid_8-3	1
Z185FPL17AUG02ENV5.1	0	Z221FSW08mar0314H16iii	0.7743
Z185MPB17AUG02ENV1.2	0.0038	Z221FSW08mar0314H16iv	0.9668
Z185MPB17AUG02ENV1.5	0.0021	Z221FSW14H16_plasmid_6iii	0.9665
Z185MPB17AUG02ENV7.4	0	Z221FSW14H16iv_plasmid_6iv	0.9941
Z185MPB17AUG02ENV7.5	0	Z221MPB7MAR03ENV4.1	0.9832
Z185MPB17AUG02ENV7.6	0	Z221MPB7MAR03ENV5.4	0.8951
Z185MPB17AUG02ENVB17	0	Z221MPB7MAR03ENV6.4	0.2915
Z185MPB17AUG02ENVB6	0	Z221MPL08mar0375a	0.8709
Z185MPB17AUG02ENVC17	0	Z221MPL08mar0375f	0.9939
Z185MPB17AUG02ENVC18	0	Z221MPL75_plasmid_a	0.9284
Z185MPB17AUG02ENVC8	0.0034	Z221MPL75_plasmid_f	0.9941
Z201FCA07feb0313C8	0.9999	Z221MPL7MAR03ENV2.1	0.9861
Z201FCA07feb03DNA13G10	1	Z221MPL7MAR03ENV4.2	0.9195
Z201FCA13C8_plasmid_2iii	0.9999	Z221MPL7MAR03ENV6.4	0.8982
Z201FCADNA13G10_plasmid_6i	1	Z238FCA15C6_plasmid_1v	0.8263
Z201FCF07feb03DNA13C18	1	Z238FCA29oct0215C6	0.8369
Z201FCF07feb03DNA13G13	1	Z238FCF15A39_plasmid_9ii	1
Z201FCF07feb03DNA13H13	0.9999	Z238FCF15C13_plasmid_2ii	1
Z201FCF07feb03DNA13H9	0.4086	Z238FCF29oct0215A39	1
Z201FCFDNA13C18_plasmid_3ii	1	Z238FCF29oct0215C13	1
Z201FCFDNA13G13_plasmid_7i	1	Z238FPL12_plasmid_1-2	1
Z201FCFDNA13H13_plasmid_10i	0.9991	Z238FPL16_plasmid_2-3	1
Z201FCFDNA13H9_plasmid_8v	0.3429	Z238FPL29nov0212	1
Z201FPB7FEB03ENV1.1	1	Z238FPL29nov0216	1
Z201FPB7FEB03ENV5.1	1	Z238FPL29nov024	1

Table 4.2 – *Continued on next page*

Table 4.2 – *Continued from previous page*

Sequence	Score	Sequence	Score
Z201FPB7FEB03ENV6.1	0.9996	Z238FPL4_plasmid_6-1	1
Z201FPL07feb03100-1	1	Z238FSW15A11_plasmid_7ii	1

Discussion

Comparing Soandso to artificial neural networks designed to ...

CHAPTER V : DISCUSSIONS

Discuss my methods and the value they present.

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APPENDICES

APPENDIX A : MY THING

Its the Appendix, Appendix A specifically.

APPENDIX B : MY OTHER THING

Appendix B