Weekly Report(Up until 8th October, 2015)

Anirudh Tiwari

Work Done

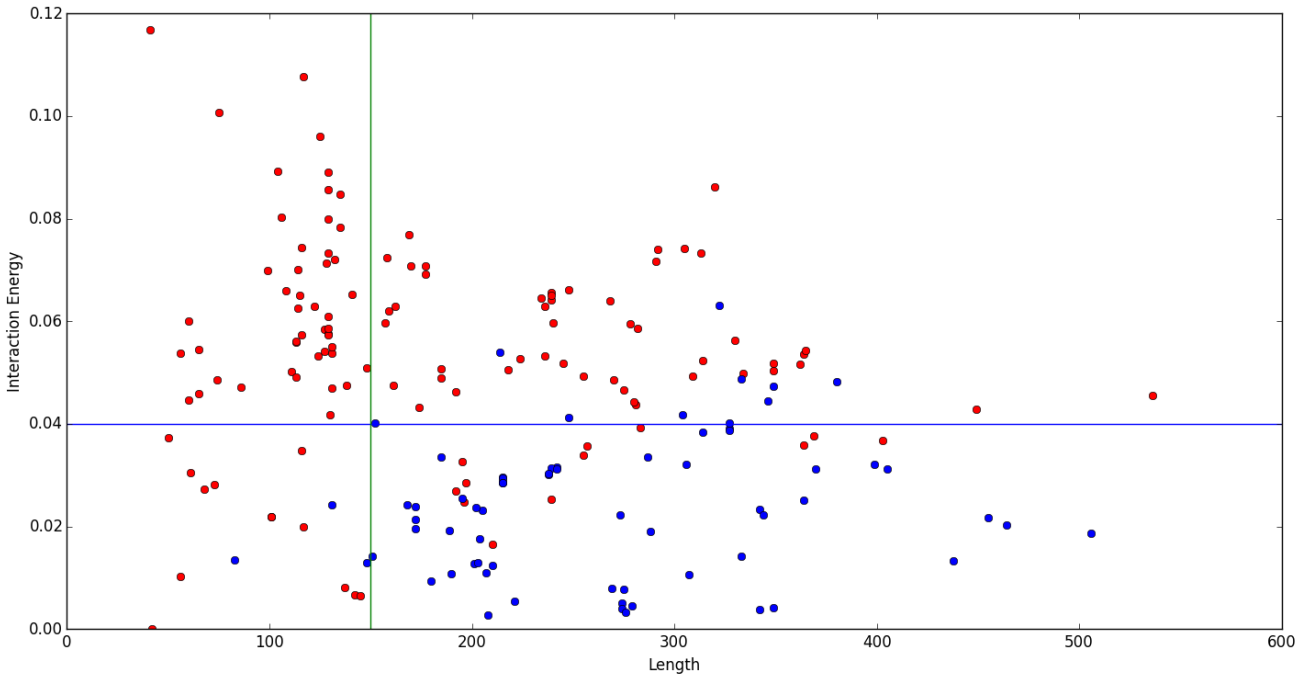
- To establish the importance of length, radius of gyration and interaction energy in classifying single domain proteins from two domain proteins. I plotted graphs(length, radius of gyration and interaction energy) for contiguous and non-contiguous two domain proteins first separately then together, comparing them with single domain proteins.

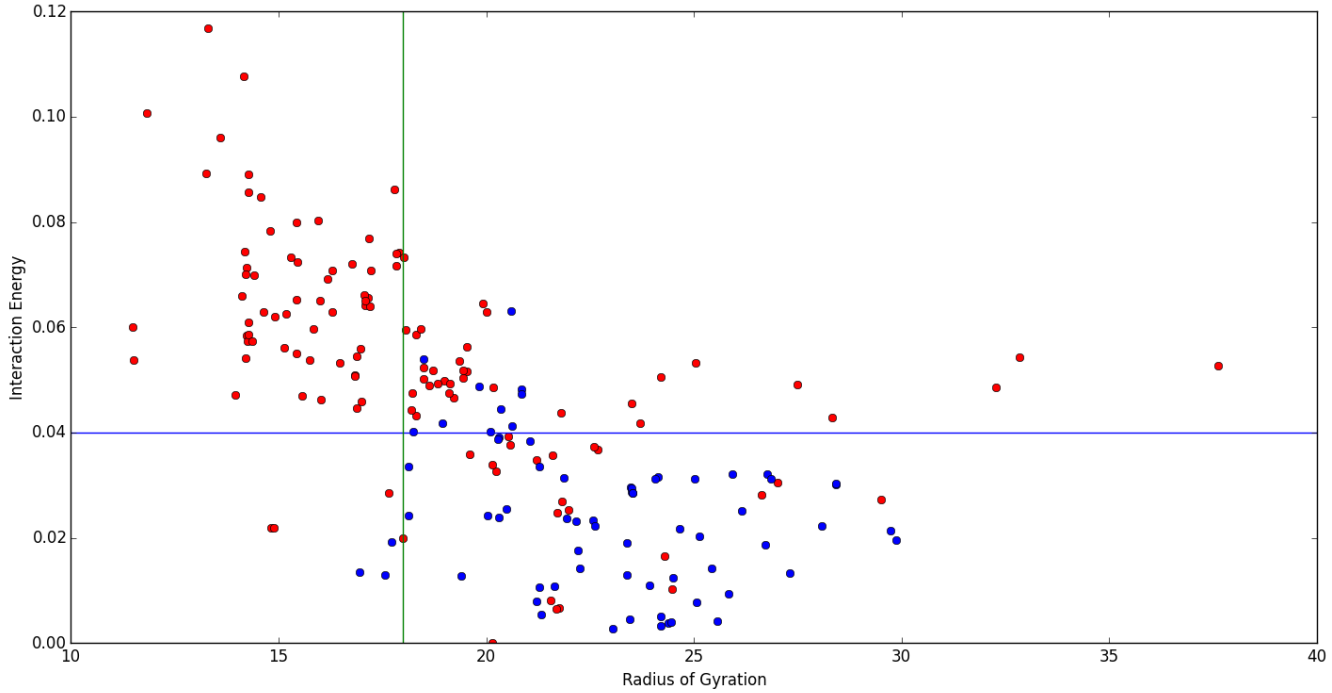
- I also extracted the class information of every domain in my data set based from SCOP.

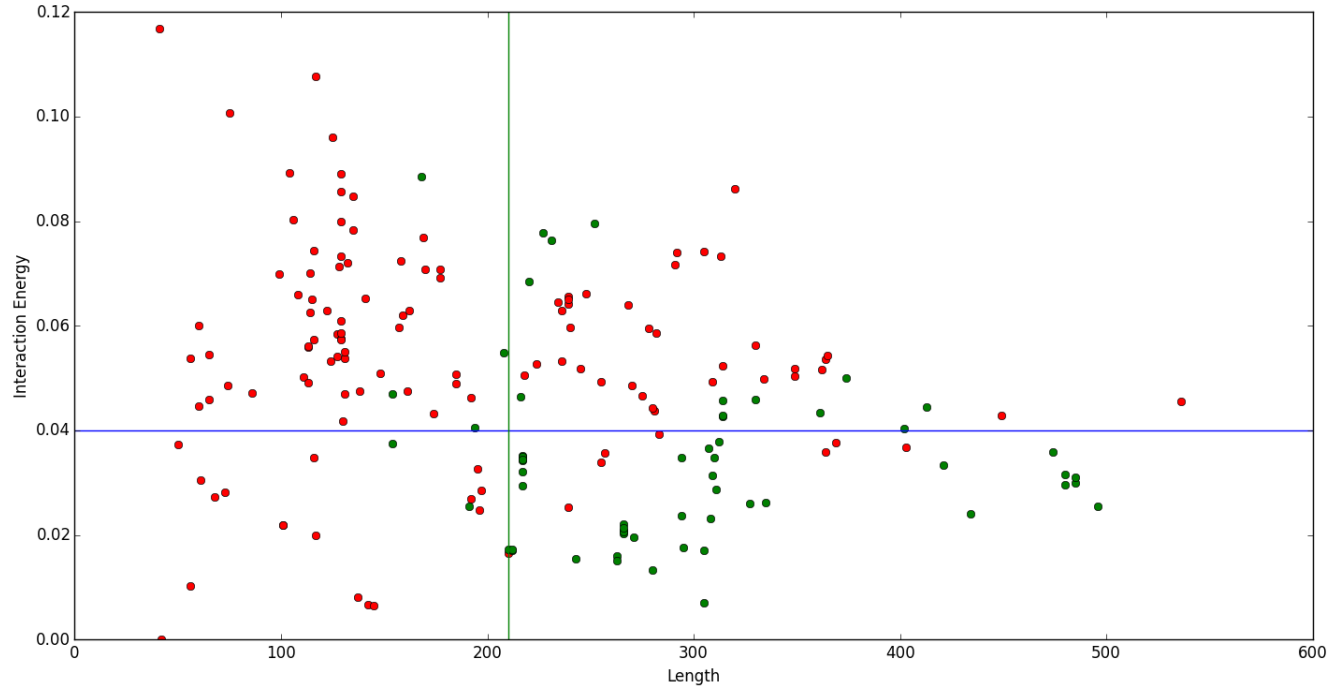
Results

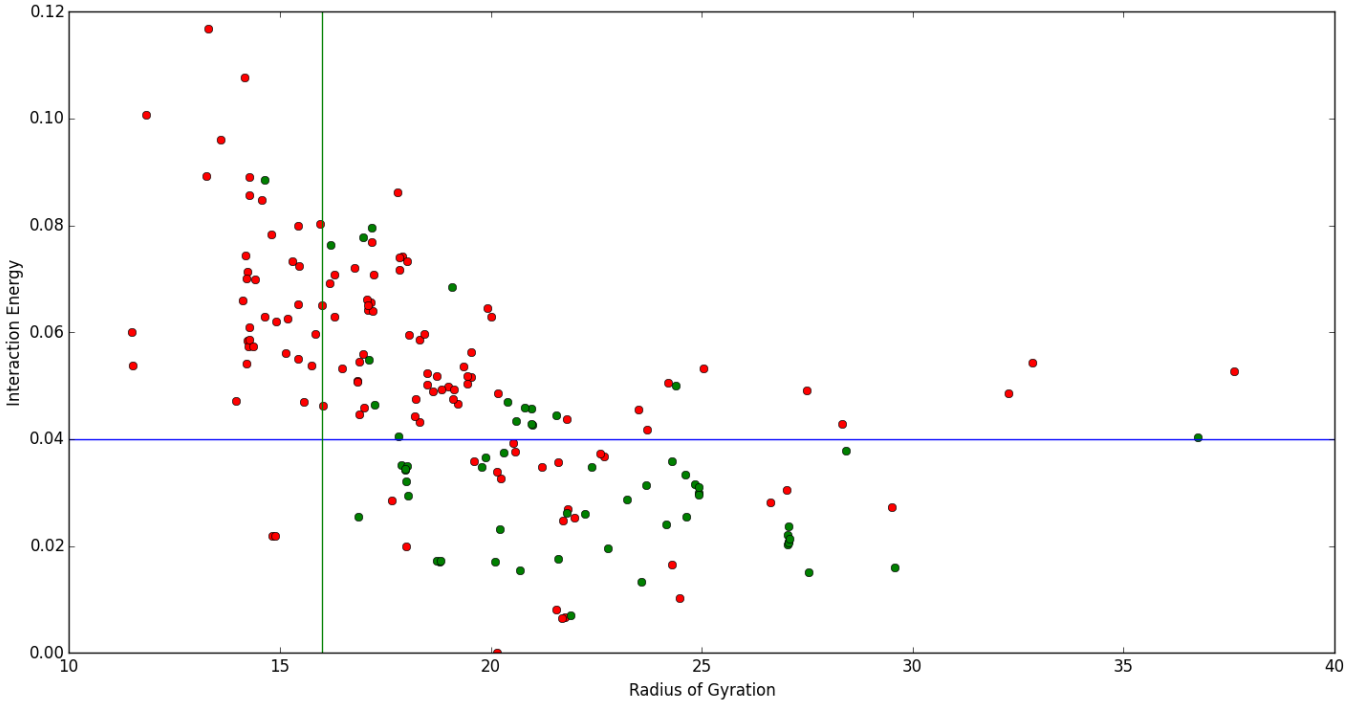
The following 6 graphs shows the results. Note:

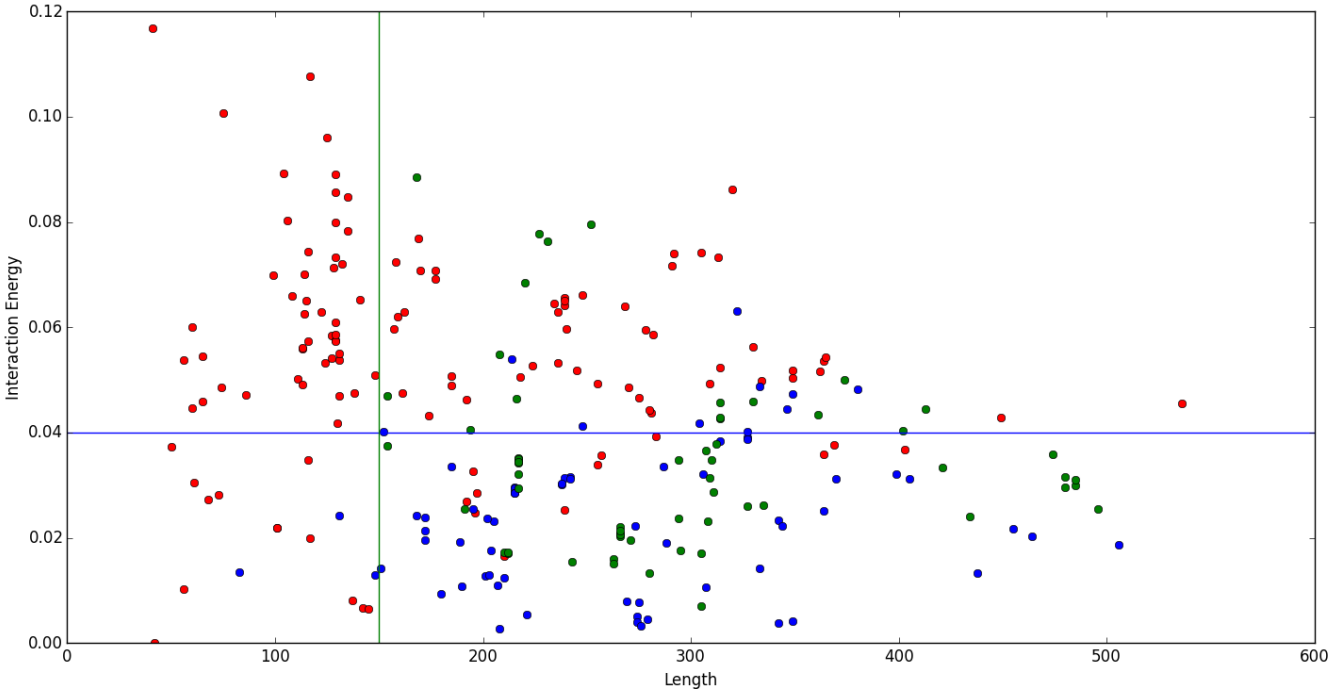
Red Dots → Single Domain Proteins
Blue Dots → Contiguous Two Domain Proteins
Green Dots → Non-Contiguous Two Domain Proteins

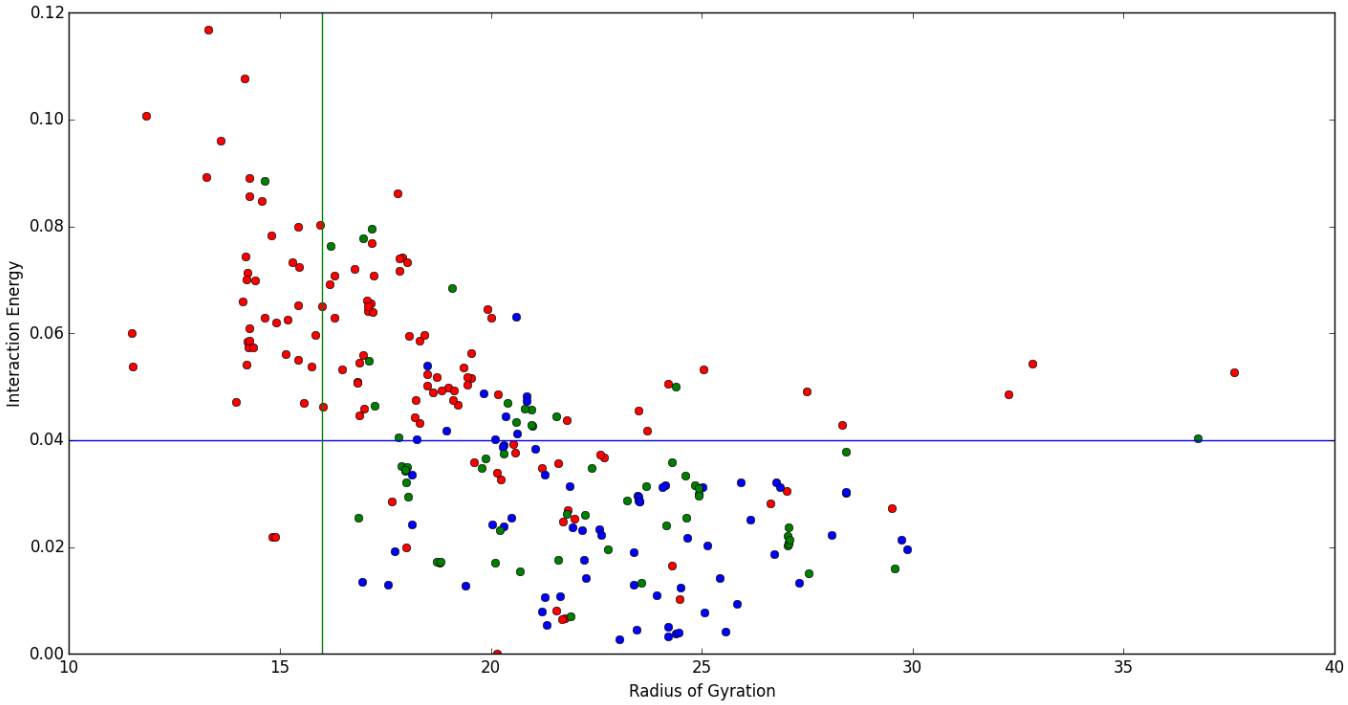



0.12
0.10
0.08
0.06
0.04
0.02
0.00
Interaction Energy
10
15
20
25
30
35
40
Radius of Gyration


0.12
0.10
0.08
0.06
0.04
0.02
0.00
Interaction Energy
0
100
200
300
400
500
600
Length


0.12
0.10
0.08
0.06
0.04
0.02
0.00
Interaction Energy
10
15
20
25
30
35
40
Radius of Gyration


0.12
0.10
0.08
0.06
0.04
0.02
0.00
Interaction Energy
0
100
200
300
400
500
600
Length



Values of Length, Interaction Energy & Radius of Gyration for distinguishing single domain proteins from two domain proteins.

	Length	**Interaction Energy**	**Radius of Gyration**	**True Positives**	**False Positives**
Contiguous	>=150	<=0.04	>=18.0	55/69	11/120
Non-Contiguous	>=210	<=0.04	>=16.0	40/59	8/120
Both	>=150	<=0.04	>=16.0	98/128	12/120

It was noted that the role of Radius of gyration was not much in distinguishing single domain from two domain proteins.

Next Steps

- Try to find out if length and interaction energy can help in distinguishing two domain from three domain and so on.

- Now with SCOP data available, repeat the same exercise and find out if the proteins are classified in a better manner.