

SYED ABBAS BUKHARI

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RESEARCH INTERESTS

My research covers following major areas of Bio-Informatics.

- Prediction/Analysis of Transcriptional Regulatory Elements/Modules in genome of an organism.
- Statistical and computational genomics.

QUALIFICATION

MS-Bioinformatics 2010–Present

Graduate Student, at U of I, IL, USA.

BS-Bioinformatics (CGPA 3.53)

CIIT, Islamabad, PAKISTAN.

PROFESSIONAL EXPERIENCE

Research Associate in Bioinformatics

2009 – 2010 CIIT, PAKISTAN.

PUBLICATIONS

Malik Nadeem Akhtar, **Syed Abbas Bukhari**, Zeeshan Fazal, Raheel Qamar, Ilham Shahmuradov “POLYAR, a new computer program for the prediction of Poly (A) signals in Human Genome.” BMC Genomics, 2010.

AWARDS / ACTIVITIES

- Received certificate of recognition for academic performance by Gamma Delta Society.
- MS-Scholarship Funded by CIIT, Pakistan.
- Two Months Internship at UIUC in Professor Dr. Gustavo’s Lab; Funded by CIIT, Pakistan.
- I have been awarded two silver Medals.
- Four Merit scholarships during BS-Bioinformatics.
- First Prize in CIIT poster competition
- Second prize in CIIT biological Model competition

PROJECTS

- ☐ Phylogenomic analysis of Protein Architectural Patterns following the route of reductive evolution and suggesting a complex Eukarya like Ancestor.

- ▣ Unravelling Promoter Architecture of Co-Expressed Orthologous genes in Human, Fly, Worm and Yeast.
- ▣ PAS-based approach for Prediction of Transcription Termination Regions in Human Genome.
- ▣ POLYAR, a new computer program for the prediction of Poly (A) signals in Human Genome.

▣ COURSE PROJECTS

1. Data mining and Genetic Algorithm based Gene/ SNP selection
2. Identification of genes and their functions from the DNA sequence of unknown patient (In collaboration with SUSSEX University, UK).
3. Implementation of Sankoff Algorithm C++
4. Implementation of Boyer Moore Algorithm C++
5. Implementation of Needleman Wunch and Smith-Waterman Algorithm C++
6. Homocystein, a Risk Factor for Cardiovascular Diseases

BIOINFORMATICS SKILLS

- **Programming Languages:** Java, SAS, C#.NET.
- **Biological databases Analysed:** Genbank, Ensembl, Ghosh's set of Transcription Factors, AMIGO, SCOP, CATH, Superfamily, GENE3D.
- **Softwares used:** Molquest, PAUP, Pajack (Network construction), NSITE.

COURSE-WORK

Courses [Semester 1 and 2, GPA = 4.0]	Grade
• Biological Modelling	(A)
• Applied Statistical Methods 1	(A+)
• Evolutionary Genomics	(A+)
• Applied Statistical Methods 2	(A)
• System Biology and Bioinformatics	(A)
• Applied Bioinformatics	(A)

REFERENCES

Will be provided on request.