

### **Bioinformatics Summer Training**

NTHRYS provides Bioinformatics Summer Training for interested candidates at its Hyderabad facility, Telangana. Please refer below for more details including Fee strctures, Eligibility, Protocols and Modules etc.,. Please do call / message / whatsapp for more details on 9014935156 [India - +91]

**Eligibility**: BSc / BTech / MSc / MTech / MPhil / PhD in any Life Sciences studying or completed students

### **Protocols / Techniques Covered**

In the present scenario as the demand for accurate, faster and qualitative research increased, this led to the advent of bioinformatics. Bioinformatics as a tool where errors made can be corrected to open newer approaches in R&D fields. With the advent of Bioinformatics we can develope and carry out research in various areas like nanotechnology, biochemistry, crop research, environmental biotechnology. The basic information of biology one can gains through training in bioinformatics is now a prerequisite for any life sciences graduate. The recent rise in organism specific genome projects coming up from scientist desks, bioinformatics becomes the foundation to start these projects. It helps to develope research, start new research, maintain and organize the data and decode the results. On a global perspective in order to receive faster results bioinformatics is a necessary tool to embark on a career in life sciences division is bioinformatics.

Bioinformatics Training Program at NTHRYS is provided under three different modules:

## 1. Basic Bioinforrmatics Training Module

| Module I                |                      |  |
|-------------------------|----------------------|--|
| Theory                  | Practical            | Tools                                  |
| History                 | Biological Databases | NCBI,MMDB,EMBL,DDBJ,SwissProt          |
| Origin                  | Structure DB         | PDB,CATH,SCOP,InterproScan,Signal      |
|                         |                      | Scan                                   |
| Scope of Bioinformatics | Importance of Tools  | N/A                                    |
| Origin of Tools         | Sequence DB's        | Scan, Prosite, Prodom, MotifScan, PFam |
| Sequence File Formats   | Types                | Genebank file format,FASTA             |
|                         |                      | format,EMBL                            |
|                         |                      | format,UniprotKB/Swiss-Prot format,    |
|                         |                      | PIR/NBRF format                        |

| Module II                                    |                               |                           |  |  |
|--|-------------------------------|---------------------------|--|--|
| Application of Bioinformatic                 | s Gene Prediction & Functiona | ol ORF finder,            |  |  |
|  | Analysis                      | GeneScan,GeneMark,Webgene |  |  |
| Sequence Comparison                          | EXPASy, EMBOSS                | BLAST,Clustalw,DIALIGN    |  |  |
| Structure File Formats                       | Repeat detection              | Repeat Masker, dnadot     |  |  |
| General Introduction to                      | Hydrophobicity                | Protparam                 |  |  |
| Molecular Biology                            |                               |                           |  |  |
| Restriction Site Mapping                     | Restriction site Detection    | Webcutter, NEBCutter      |  |  |
| Visualiztion Software                        | System Biology Vs /w          | RasMol,SPDBV,JMol,Cn3D    |  |  |
| Phylogenetic Analysis                        | Evolutionary Relationship     | Phylogeny,HHperd, Biology |  |  |
|  |                               | workbench                 |  |  |
| Bioinformatics Dogma                         | Thermodynamics                | ProTherm                  |  |  |
| Minor Project Concerning the concepts learnt |                               |                           |  |  |

# ${\it 2.}~ \textbf{Advanced Bioinformatics Training Module}\\$

| Theory  | Practical  | Tools  |  |
|---|--|--|--|
| Module III  |  |  |  |
| Statistical significance of Alignments  | RNA sequence Analysis  | Expasy   |  |
| Sequence Databases for similar sequences  | RNA fold Recognition   | MFOLD,PFOLD  |  |
| RNA sequence analysis   | Secondary Structure Prediction                                   | GOR4, ChouFasman, Predator,<br>Phobious, HMMTOP  |  |
| RNA structure Prediction  | Abinitio Structure Prediction                                    | QUARK,Bhageerath   |  |
| Submitting Sequence   | To NCBI  | N/A  |  |
| Scoring Types   | PAM,BLOSUM   | N/A  |  |
| Types of Alignment  | Global & Local   | Grapics Sequences Pairwise BLAST<br>& EMBOSS Aligns  |  |
| Module IV   |  |  |  |
| Molecular Phylogeny Prediction  | Molecular evolutionary genetic<br>Analysis                       | MEGA5,PHYLIP   |  |
| EST and Gene Discovery  |  | dbEST  |  |
| Genome Analysis   |  | Genid,FGNEGH,GLIMMER,GRAIL   |  |
| Comparative modeling  | Homology Modeling  | MODELER, Swiss Model   |  |
| Fold recognition  | Threading  | RAPTOR,3DPSSM,HHPRED   |  |
| Model Evaluation  | Structure Refinement   | WHATCHECK,SAVES Server   |  |
| Structure Validation  | RMSD plot  | CASP Server  |  |
| Module V  |  |  |  |
| Molecular Dynamics  | Molecular Simulation   | GROMACS,HOOMD blue,PYMOL   |  |
| Molecular Modeling  |  | CHARM-GUI,Amber  |  |
| Primer Desinging  | Three Primer designing tools along with concepts of behind tools | FastPCR,PRIMER3,Gene Fisher  |  |
| Concepts of<br>Biostatistics,biophysicsand<br>biochemistry to help in dealing with<br>databases/tools | Various tools used to useges, of subject with bioinformatics     | Risk assessment tools,KinCohort<br>software MultAssoc,Genetic Pathway<br>analysis software |  |
| N.  | linor project work in desired to                                 | pic  |  |

#### Major project in desired topic

Note: Major project as well as Minor project can also done by the student after selected time and respective certification can be issued on the respective date. For example if a MSc first year student joins in this training module he/she can complete the training module and take Training and take training certificate at the time and later come back after few months continue doing the minor project and then collect the certificate and come later at the time of final year academic project time and do the major project and collect the certificate for the same in respective dates and make use of the three certifications for a single fee structure.

This module was designed after considering the advices given by the Bioinformatics Head of the departments of many reputed universities.

### 3. Pofessional Bioinformatics Training Module

| Theory  | Practicals                        | Tools Used   |  |  |  |
|---|-----------------------------------|--|--|--|--|
| Module VI   |                                   |  |  |  |  |
| Reconstruction Of Metabolic Pathway                                   |                                   | Various pathway construction tools including KEGG  |  |  |  |
| Pathway Databases   |                                   | KEGG [all<br>databases ]                           |  |  |  |
| Monte Carlo Simulation  |                                   | Molecular dynamics tools                           |  |  |  |
| Docking of Small Molecules  | Docking<br>Software               | GOLD,<br>HYPERCHEM,<br>AutoDOCK,<br>Hex, Argus Lab |  |  |  |
| Module VII  | •                                 |  |  |  |  |
| Energy minimization   | QSAR Studies                      | Build QSAR   |  |  |  |
| Geometry Optimization   | Descriptor<br>Database            | E-Dragon   |  |  |  |
| Force Fields  | Primer<br>Designing               | Primer3,<br>FastPCR                                |  |  |  |
| Descriptors   |                                   |  |  |  |  |
| BioPERL   | BioPERL /<br>PERL<br>programming  |  |  |  |  |
| Antibody engineering  | Designing and modeling antibodies |  |  |  |  |
| HTML concepts   | HTML                              |  |  |  |  |
| Concepts on designing a bioinformatics database                       |                                   |  |  |  |  |
| Concepts on various biotechnology aspects                             |                                   |  |  |  |  |
| Major project work in any one of the fields present Projects section. | nt in NTHRYS I                    | Bioinformatics                                     |  |  |  |

# **Expertise Training Module on QSAR**

|                                | Module VIII  |   |  |
|--------------------------------|--|---|--|
| Topic                          | Practical Approaches   | Software / Tools  |  |
| Free Energy<br>Relationships   | Hansch method: Linear Free Energy Relationships (physicochemical properties) Martin & Kubinyi: Non Linear Free Energy Relationships (physicochemical properties) Free Wilson mathematical model (structural elements)  | QSAR-PC: PAR  |  |
|                                | Curation   | KNIME   |  |
|                                | Molecular Descriptors (0D, 1D, 2D, 3D, 4D, 5D, 6D)   | Chemistry Development<br>Kit, PADel, RDKit, MOE,<br>PubChem, Chemotypes                         |  |
| Molecular<br>Modeling          | Modeling Methods 1. K-Nearest Neighbors (kNN) 2. Random Forest 3. Support Vector Machines (SVM)  | ACD/ChemSketch,<br>ACD/3D Viewer, Biome<br>MOLEKEL, The<br>Molecular Modelling<br>Toolkit etc., |  |
| Quantum<br>Mechanical<br>Model | 1. Linear Scaling Methods 2. QM/MM (Quantum Mechanics /Molecular Mechanics) 3. QM Simulation 4. Protonation States 5. Cation-π and π-π interactions 6. Using QM to calculate molecular properties 1. QM derived FFs (Force Fields) 2. QM Derived Partial Charges 3. QM Descriptors in QSAR/QSPR (Quantitative Structure Property Relationship) 4. Molecular Quantum similarity measures 5. Variation particle number approach for molecular design | AlgoGen, ProToss, Epik etc.,  |  |

| Topological<br>Method    | 1. The Wiener Index 2. The Platt and Gordon-Scantlebury Indices 3. The Hosoya Index 4. The Zagreb Indices 5. The Balaban J Index 6. Information Content Indices 7. Autocorrelation Descriptors 8. WHIM Descriptors 9. Topochemical Atom Indices 10. The Centric Index 11. Triplet Indices 12. The Randi? Index 13. Molecular Connectivity Indices 14. Kappa Indices 15. Flexibility Indices 16. The Variable Connectivity Index 17. Topological Descriptors in Inverse QSAR 18. Electrotopological State Indices 19. Biodescriptors 20. Chirality | ADAPT, CODESSA,<br>MathChem, MDL QSAR,<br>TOPIX, etc., |
|--------------------------|---|--|
| Pattern<br>Recognization | -   |  |

### Fee for Module VIII

Module VIII (Online Mode Only) - \$1500 for 1 Month Duration (Training + 1 Minor Project), \$3000 for 3 Months Duration (Training + 1 Major Project + Publication Assistance as Co author Only), \$2000 additional for First Authorship Publication Project Assistance along with training.

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| Fee details in Rs per student           |       |       |       |       |         |
|---|-------|-------|-------|-------|---------|
| Fee 5 Days 10 Days 20 days 1 Month 45 D |       |       |       |       | 45 Days |
| Individual                              | 11900 | 12500 | 15800 | 19600 | 23200   |
| Group 2 - 4                             | 11400 | 11400 | 15100 | 18700 | 22100   |

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| Group 5 - 7  | 11200 | 11200 | 14900 | 18500 | 21900 |
|--------------|-------|-------|-------|-------|-------|
| Group 8 - 10 | 11100 | 11100 | 14800 | 18300 | 21700 |