

Bioinformatics Internship with Accommodation at Bengaluru

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Active Categories

105

Focused Areas

Bengaluru

Accommodation Location

How to View Accommodation Details and Booking Options

1. Open the Internships page or the corresponding Topics page.
2. Select the relevant focused area.
3. Select the available duration, mode and internship type.
4. Choose **Offline** mode to access accommodation booking options.
5. Continue to the fee/payment page and use the **Branches Select Option**.
6. After selecting the branch, use **Book NTHRYS Accommodation** to view accommodation fee, facility photographs, amenities and the available booking details.

Bioinformatics Internship Categories

AI Genome-Scale Data Analysis Research https://internships.nthrys.com/bioinformatics/ai-genome-scale-data-analysis-research	Machine Learning for Biotech Innovation Research https://internships.nthrys.com/bioinformatics/machine-learning-biotech-innovation-research
Machine Learning Sequence Alignment Research https://internships.nthrys.com/bioinformatics/machine-learning-sequence-alignment-research	AI Biological Database Integration Research https://internships.nthrys.com/bioinformatics/ai-biological-database-integration-research
AI Protein Structure Bioinformatics Research https://internships.nthrys.com/bioinformatics/ai-protein-structure-bioinformatics-research	AI Transcriptome Bioinformatics Research https://internships.nthrys.com/bioinformatics/ai-transcriptome-bioinformatics-research
AI Metagenomics Pipeline Development Research https://internships.nthrys.com/bioinformatics/ai-metagenomics-pipeline-development-research	AI Phylogenetics & Comparative Genomics Research https://internships.nthrys.com/bioinformatics/ai-phylogenetics-comparative-genomics
AI Network Bioinformatics Research https://internships.nthrys.com/bioinformatics/ai-network-bioinformatics-research	AI Single-Cell Bioinformatics Research https://internships.nthrys.com/bioinformatics/ai-single-cell-bioinformatics-research
AI Epigenome Bioinformatics Research https://internships.nthrys.com/bioinformatics/ai-epigenome-bioinformatics-research	Variant Calling Pipeline Optimization Research https://internships.nthrys.com/bioinformatics/variant-calling-pipeline-optimization-research
RNA-Seq Expression Quantification Research https://internships.nthrys.com/bioinformatics/rna-seq-expression-quantification-research	Protein-Protein Interaction Prediction Research https://internships.nthrys.com/bioinformatics/protein-protein-interaction-prediction-research

ChIP-Seq Data Analysis Research https://internships.nthrys.com/bioinformatics/chip-seq-data-analysis-research	Protein Folding and Structure Prediction https://internships.nthrys.com/bioinformatics/protein-folding-structure-prediction
Genome Assembly Algorithm Development Research https://internships.nthrys.com/bioinformatics/genome-assembly-algorithm-development-research	Pathway Analysis and Enrichment Research https://internships.nthrys.com/bioinformatics/pathway-analysis-and-enrichment-research
Structural Variant Detection Research https://internships.nthrys.com/bioinformatics/structural-variant-detection-research	Cancer Genomics Data Integration Research https://internships.nthrys.com/bioinformatics/cancer-genomics-data-integration-research
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Telomere and Repeat Region Analysis Research https://internships.nthrys.com/bioinformatics/telomere-and-repeat-region-analysis-research	Plant Genomics Trait Mapping Research https://internships.nthrys.com/bioinformatics/plant-genomics-trait-mapping-research
AI Ligand-Protein Docking Optimization Research https://internships.nthrys.com/bioinformatics/ai-ligand-protein-docking-optimization-research	

Bioinformatics Internship Topics and Focused Areas

AI Genome-Scale Data Analysis Research

- Machine Learning for Genomic Variant Classification
- Metagenomic Assembly and Taxonomic Profiling
- Deep Learning for Protein Structure Prediction from Genomic Data
- Comparative Genomics and Evolutionary Analysis at Scale
- Gene Expression Pattern Mining from Multi-Omics Data

Machine Learning Sequence Alignment Research

- Deep Learning Models for Protein Sequence Alignment
- Genomic Variant Calling Using Machine Learning
- Multiple Sequence Alignment Optimization with Graph Neural Networks
- Transfer Learning for Cross-Species Sequence Homology Detection
- Benchmark Development for Sequence Alignment ML Models

Machine Learning for Biotech Innovation Research

- Protein Structure Prediction and Drug Binding Analysis
- Genomic Sequence Classification and Variant Detection
- Medical Image Analysis for Disease Diagnosis
- Biomarker Discovery Through Multi-Omics Data Integration
- Natural Language Processing for Biomedical Literature Mining

AI Biological Database Integration Research

- Protein Structure Prediction Pipeline Development
- Gene Expression Pattern Mining with Machine Learning
- Genomic Variant Classification and Annotation System
- Multi-Omics Data Integration Framework
- Microbial Genome Assembly and Functional Annotation

AI Protein Structure Bioinformatics Research

- Protein Structure Prediction Model Development
- Molecular Dynamics Simulation and Analysis
- Protein-Ligand Docking and Drug Discovery
- Structure-Function Relationship Analysis
- Cryo-EM Data Processing and Structure Refinement

AI Transcriptome Bioinformatics Research

- RNA-Seq Data Processing and Quality Control
- Differential Gene Expression Analysis
- Machine Learning for Transcriptome Classification
- Pathway and Functional Enrichment Analysis
- Single-Cell RNA-Seq (scRNA-seq) Data Analysis

AI Metagenomics Pipeline Development Research

- Metagenomic Read Assembly and Binning Optimization
- Taxonomic Classification and Abundance Profiling

- Functional Annotation and Pathway Analysis
- Quality Control and Data Preprocessing Workflows
- Machine Learning for Microbiome Pattern Recognition

AI Phylogenetics & Comparative Genomics Research

- Phylogenetic Tree Construction and Validation
- Ortholog and Paralog Identification Using Comparative Genomics
- Machine Learning for Species Classification and Evolutionary Inference
- Genomic Variation Analysis and Population Phylogenetics
- Functional Annotation Integration in Comparative Genomic Studies

AI Network Bioinformatics Research

- Deep Learning for Protein Structure Prediction
- Graph Neural Networks for Drug-Target Interaction
- Genomic Data Mining and Variant Effect Prediction
- Sequence Alignment and Homology Modeling
- Network Analysis of Biological Pathways and Gene Regulation

AI Epigenome Bioinformatics Research

- DNA Methylation Pattern Analysis
- Histone Modification Mapping and Integration
- 3D Genome Structure and Chromatin Interaction
- Epigenetic Biomarker Discovery for Disease
- Non-Coding RNA Regulation in Epigenetic Pathways

RNA-Seq Expression Quantification Research

- Transcript Abundance Estimation and Quantification
- Quality Control and Data Preprocessing for RNA-Seq
- Differential Expression Analysis and Statistical Modeling
- Alternative Splicing Detection and Isoform Analysis
- Gene Expression Normalization and Batch Effect Correction

Protein-Protein Interaction Prediction Research

- Machine Learning Model Development for PPI Prediction
- Structural Docking and Molecular Simulation Analysis
- Biological Network Analysis and PPI Network Reconstruction
- Sequence-Based Feature Engineering for Interaction Prediction
- Cross-Species PPI Transfer Learning and Homology-Based Prediction

Protein Folding and Structure Prediction

- AlphaFold2 Model Optimization and Validation
- Molecular Dynamics Simulations for Protein Stability Analysis
- Structure-Function Relationship Studies via Computational Mutagenesis
- Cryo-EM Data Analysis and Structure Refinement
- Machine Learning Applications in Secondary Structure Prediction

ChIP-Seq Data Analysis Research

- Peak Calling and Quality Control
- Transcription Factor Binding Site Analysis
- Chromatin State Mapping and Epigenetic Integration
- Differential Binding Analysis Across Conditions
- Bioinformatics Pipeline Development and Automation

Structural Variant Detection Research

- Long-Read Sequencing Data Analysis for SV Detection
- Machine Learning Models for SV Classification
- Genomic Data Visualization and Annotation Tools
- Comparative Genomics and SV Population Studies
- SV Detection Algorithm Development and Benchmarking

Cancer Genomics Data Integration Research

- Tumor Mutation Signature Analysis
- Multi-omics Data Integration Pipeline Development
- Cancer Driver Gene Identification and Validation
- Clinical-Genomic Data Correlation Studies
- Cancer Subtype Classification Using Genomic Clustering

Bioinformatics Pipeline Development

- Genomic Sequence Alignment and Variant Calling
- RNA-Seq Data Processing and Gene Expression Analysis
- Metagenomic Data Analysis and Taxonomic Classification
- Protein Structure Prediction and Drug Target Identification
- Pathway Analysis and Systems Biology Integration

Clinical Genomics Interpretation Research

- Variant Annotation and Pathogenicity Prediction
- Whole Genome/Exome Sequencing Data Analysis

- Gene-Disease Association and Literature Mining
- Clinical Phenotype-Genotype Correlation Studies
- Interpretation of Copy Number Variations and Structural Variants

Drug Target Discovery Research

- Protein Structure Analysis and Target Validation
- Genomic Data Mining for Disease-Associated Variants
- Molecular Docking and Virtual Screening
- Pathway Analysis and Network Biology for Target Discovery
- Homology Modeling and Comparative Genomics for Target Characterization

Integration and Analysis of Multi-Omics Data Research

- Genomics-Proteomics Integration Pipeline Development
- Metabolomic Data Analysis and Pathway Mapping
- Transcriptomics-Epigenomics Cross-Analysis
- Multi-Omics Data Quality Control and Normalization
- Systems Biology Modeling Using Integrated Omics Data

AI Ligand-Protein Docking Optimization Research

- Machine Learning Model Development for Binding Affinity Prediction
- Molecular Descriptor Engineering and Feature Selection
- Docking Algorithm Benchmarking and Comparative Analysis
- Deep Learning Architecture Optimization for 3D Molecular Structures
- Virtual Screening Pipeline Development and Validation

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