

Identification / Classification of Chromosomes

PICT, PUNE

Project Duration: January 2022 - June 2022

Objective:

The primary objective of the Identification/Classification of Chromosomes project was to develop an advanced image processing solution that utilizes traditional segmentation approaches and machine learning techniques to accurately identify and classify chromosomes from complex biological images. The project focused on the precise segmentation of chromosomes and highlighted the largest chromosomes present in metaphase, thereby aiding in the comprehensive analysis and understanding of genetic structures.

Features:

- **Machine Learning-Based Segmentation:** Implemented machine learning algorithms for image segmentation, utilizing traditional approaches such as thresholding, edge detection, and region-based segmentation to accurately isolate and extract individual chromosomes from complex biological images.
- **Feature Extraction and Analysis:** Incorporated feature extraction techniques to capture essential characteristics of chromosomes, enabling comprehensive analysis and comparison of structural attributes, including length, width, and specific banding patterns, essential for accurate classification.
- **Metaphase Chromosome Identification:** Developed a specialized module to identify and highlight the largest chromosomes present in metaphase, facilitating the efficient recognition and analysis of critical genetic information associated with cellular development and genetic disorders.
- **Data Annotation and Model Training:** Annotated a comprehensive dataset of chromosome images, encompassing diverse genetic variations and structural complexities, to facilitate the training and validation of the segmentation and classification models, ensuring the robustness and accuracy of the system.
- **Performance Evaluation Metrics:** Employed various performance evaluation metrics, including precision, recall, and F1-score, to assess the accuracy and reliability of the segmentation and classification models, enabling continuous refinement and optimization for enhanced predictive capabilities.
- **Visualization and Reporting Tools:** Integrated advanced visualization and reporting tools to present the segmented chromosome data in a comprehensive and interpretable manner, facilitating in-depth analysis and interpretation of genetic information by researchers and geneticists.

Outcome:

The successful implementation of the Identification/Classification of Chromosomes project significantly contributed to the advancement of biological image analysis, providing researchers and geneticists with a powerful tool for accurate chromosome segmentation and classification. The project's emphasis on identifying the largest chromosomes in metaphase enhanced the understanding of genetic structures and paved the way for more precise and comprehensive genetic analysis, with potential applications in genetic research, disease diagnosis, and personalized medicine.
