Functionally graded polar orthotropic rotating disks: investigating thermo-elastic behavior under different boundary conditions
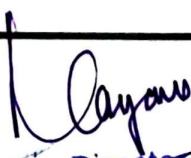
Lakshman Sondhi, Rakesh Kumar Sahu, Ritesh Kumar, Sanjay Yadav, Shubhankar Bhowmick & Royal Madan ✉

This article has been updated

Abstract

A comprehensive study has been conducted on the thermo-elastic behavior of a polar orthotropic rotating functionally graded disk, focusing on the effects of grading indices and

thermal field on various stress and displacement parameters. The normalized radial stress, tangential stress, and normalized displacement of a hollow annular disk rotating at a constant angular speed were examined under different thermal conditions and grading indices. The study posed a significant challenge in determining the stress fields in a rotating disk, which required solving a specific second-order differential equation. After validation of the proposed methodology, the problem was solved for a rotating disk under a thermal field, and the results were obtained for both free-free and fixed-free boundary conditions. The objective of this research was to investigate how the material gradation and thermal loading impact the deformation and stresses of an annular disk, which was accomplished through the use of the point collocation method—a numerical technique used to compute the normalized stress, strain, and displacement components in the radial direction. This research provides insights into the behavior of annular disks under different conditions and has practical implications for designing and analyzing various engineering applications such as rotating machinery, aerospace components, and energy systems.

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Applications and analytics of bioinformatics, healthcare informatics for modern healthcare system

Authors:

Dr-K P Singh
Dr. A.P.J. Abdul Kalam Technical University

Ashish Kumar
ITS Engineering College

Manoj Kumar GUPTA

References (18)

Abstract

Healthcare informatics emphasizes on the gathering, processing, assessment, and utilization of health records, information, and expertise. By connecting genetics, proteomics, and patient records, bioinformatics uses computational methods and tools to research and analyze huge biological datasets, completely understand illness, and grasp genetics and proteomics. Interpreting genomic and proteomic data for basic biological research, as well as for use in healthcare, drug discovery, and related fields, is the main focus. Large amounts of electronic data collection in the healthcare industry lead to the development of analytics. Data analytics is adept at enhancing healthcare, cutting costs, and preserving people. The explosion of data leads to the use of data analytics in the healthcare industry to explore understandings and make smart judgments. In order to create a better health service, this paper focuses on bioinformatics, healthcare informatics, and analytics. It examines the advantages, how each one helps to improve the health service, how bioinformatics, health informatics, and analytics connect, and lastly, what the coming times holds for healthcare informatics as well as analytics.

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Applications and analytics of bioinformatics, healthcare informatics for modern healthcare system

Kshatrapal SINGH[1*], Ashish KUMAR[2], Manoj Kumar GUPTA[3]

[1] Krishna Engineering College, Ghaziabad, India
[2] I.T.S Engineering College, Greater Noida, India
[3] School of CSE, Shri Mata Vaishno Devi University, Katra, India
mekpsingh1@gmail.com, ashishcse29@gmail.com, manoj.cst@gmail.com

*Corresponding Author: Kshatrapal SINGH
mekpsingh1@gmail.com

Abstract: Healthcare informatics emphasizes on the gathering, processing, assessment, and utilization of health records, information, and expertise. By connecting genetics, proteomics, and patient records, bioinformatics uses computational methods and tools to research and analyze huge biological datasets, completely understand illness, and grasp genetics and proteomics. Interpreting genomic and proteomic data for basic biological research, as well as for use in healthcare, drug discovery, and related fields, is the main focus. Large amounts of electronic data collection in the healthcare industry lead to the development of analytics. Data analytics is adept at enhancing healthcare, cutting costs, and preserving people. The explosion of data leads to the use of data analytics in the healthcare industry to explore understandings and make smart judgments. In order to create a better health service, this paper focuses on bioinformatics, healthcare informatics, and analytics. It examines the advantages, how each one helps to improve the health service, how bioinformatics, health informatics, and analytics connect, and lastly, what the coming times holds for healthcare informatics as well as analytics.

Keywords: Bioinformatics, Healthcare Informatics, Healthcare System, Analytics.

1. Introduction

A community must protect its citizens' mental and physical well-being in order to accomplish its dream and vision of sustainable progress. Healthcare is a crucial area of any economy. As a result, a country's ability to flourish depends on its residents' overall health, giving rise to the proverb "health is riches." So, it is highly likely that now the people will accept any innovation or method that is designed to improve the healthcare system (Flygare et al., 2016) (Ondov et al., 2016). Since the Human Genome Project's completion in 2003, there have been possibilities to obtain, analyze, and disseminate genetic data in more efficient, affordable, and trustworthy ways. Healthcare has been significantly impacted by this significant technical advancement in terms of novel prevention creation, better diagnosis, and early treatment for routine healthcare. It is predicted that these massive amounts of data from the bioinformatics as well as healthcare informatics areas, combined with analytics, will soon give preventive, predictive, and personalized healthcare solutions. It is anticipated that this will aid in the prosperity and progress of the country.

Experts now have the option to keep data, like DNA comparison, analysis, as well as interpretation, on machines in the format of databases due to bioinformatics. Even seasoned specialists cannot use biological data inside its unprocessed raw form. Therefore, the development of biological instruments to gather data from these databases to be used in the study has been made possible by bioinformatics. To understand the sequencing, structures, and activities of proteins, bioinformatics techniques are essential (Thankachan et al., 2017). A greater comprehension of an organism's biology results from having a thorough awareness of these three concepts.

Since the information in Big Data is so private, using it in healthcare comes with significant ethical and legal issues. The possibility of compromising one's privacy and autonomy, in addition to repercussions on the public's need for clarity, faith, and impartiality when using Big Data, are among the ethical and legal challenges. Critical technical and architectural concerns that could jeopardize a Big-Data-driven healthcare system include data diversity, data security, analytical processes in data analysis, and the lack of adequate infrastructures for file storage.

Standardized Phylogenetic Evolutionary Analysis based on an Alignment Free Sequence Comparison Technique

Kshatrapal Singh[1], Ashish Kumar[2], Manoj Kumar Gupta[3]

[1]Department of CSE, Krishna Engineering College, Ghaziabad, India

[2]Department of CSE, I.T.S Engineering College, Greater Noida, India

[3]Department of CSE, Shri Mata Vaishno Devi University, Katra (J&K), India

Email: mekpsingh1@gmail.com

Abstract

Phylogenetic analysis explains how species evolved throughout time. Multiple sequence alignments of proteins or genomes can be used to infer a phylogenetic tree. Understanding evolution requires phylogenetics, or reconstructing organisms' evolutionary relationships. The alignment of complete gene sequences of higher eukaryotes, as well as the construction of phylogenetic trees on the basis of these alignments, is a computationally costly and ambitious undertaking. To get around these restrictions, we compared the genomes of the Brassicales clade using alignment-free technique. A Chaos Representation (CR) can be evaluated for each nucleotide sequence, which depicts each nucleotide as a point in a square specified by the four nucleotides as nodes. As a result, every CR is a distinct fingerprint of the basic sequence. Each grid square in the CRs represents the presence of oligonucleotides of a given size in the sequence if the CRs are categorized by grid lines (Frequency Chaos Representation, FCR). To build phylogenetic trees of Brassicales species, we used distance metrics between FCRs.

Keywords: Phylogenomics, Chaos Representation, Genome-scale data, DNA sequencing, NJ trees.

1. INTRODUCTION

The term "phylogenomics" was initially used in the context of genome function prediction for genome-scale data, and then in the ambience of phylogenetic conclusion shortly after. The advancements in DNA analyzing methodology over the last two decades have given rise to the discipline of phylogenomics [1-3]. It incorporates multiple fields of research at the intersection of molecular as well as evolutionary biology, with two main objectives: (i) inferring phylogenetic relationships among taxa and gaining insights into molecular advancement mechanisms; and (ii) using multi-species phylogenetic analysis to conclude putative functions for protein or DNA sequences.

This unplanned 'noise' effects the inference of backbone nodes, possibly directing to weakly carried phylogenetic trees, due to the fewer number of phylogenetically informative characteristics accessible in one or a few genomes. Using significantly higher volumes of sequence data, this challenge can be solved satisfactorily. Traditional sequencing datasets are orders of magnitude bigger than modern phylogenomic techniques, which use hundreds to thousands of sites from across the gene [4-5]. As a result, the scale of these datasets minimizes the impact of stochastic error as well as data availability as a binding factor.

High-throughput sequence method (also known as next-generation sequence method) has produced massive amounts of genome-scale data. Next-generation sequencing methods depart from the Sanger approach for which they permit for largely parallel DNA sequencing, allowing for exceptionally high throughput from several samples at the same time at a far lower cost. Large number of DNA nucleotides could be analyzed in parallel, giving orders of enormity additional value and reducing the requirement for fragment-cloning techniques employed in Sanger sequencing [6-8]. Recent advancements in NGS technology, as well as the rapid development of bioinformatics tools, have made it possible for research groups of some amount to create massive quantity of genomic sequence for organisms of consideration.

Phylogenetic studies are important in most domains of biology, but their reproducibility is often poor, with a prediction of 60% published phylogenetic comparison being 'lost to science' as a lack of data and techniques. Because the used analytical software, software versions, software settings, as well as OS versions can be difficult or not possible to unearth or revive, produced phylogenetic research can be tough or impossible to replicate or expand [9-12]. The tracking of the input and modification of information needed to get an output, known as data provenance, is a critical aspect of reproducibility. A large number of