

Bioinformatics a Tool for Studies of Climate Change

S Rehan Ahmad*

Assistant Professor, Hiralal Mazumdar Memorial College for Women, Kolkata, W.B, India

*Corresponding Author E-mail: zoologist.rehan@gmail.com

Received: 20.1.2023 | Revised: 31.03.2023 | Accepted: 13.04.2023

ABSTRACT

The problem of climate change is one of widespread concern, and research on it includes analysis from both socio-economic and scientific perspectives. All relevant fields of research and technology, including bioinformatics, have a significant impact on limiting climate change. A more thorough investigation of this matter can significantly aid in finding a solution to this global issue. The sequencing of the microbial genomes of those bacteria that can lower carbon dioxide and other greenhouse gas levels and ultimately may play a significant part in stabilising global climate change is the subject of a bioinformatics study.

Keywords: Greenhouse Gases; CO₂ Climate Change; Bioinformatics.

INTRODUCTION

According to the 2014 Synthesis Report of the UN Intergovernmental Panel on Climate Change (IPCC), India is in danger since climate change will negatively affect food production there and impede sustainable development. The Indian economy is heavily reliant on climatically vulnerable industries like agriculture, fishery, forestry, and even the production of energy.

But those who are most impacted by climate change are the poorest individuals. For instance, 58 per cent of our population relies completely on agriculture, so any new variations in rainfall or temperature can impact the entire nation's economy and food security

(Barros et al., 2014). The IPCC Synthesis Report 2014 also details future threats for Asia, including an increase in flood-related harm to communities, livelihoods, and infrastructure; heat-related human mortality; and an increase in drought-related water and food shortages. A substantial layer of gases envelops the Earth, keeping it warm and enabling the existence of plants, animals, and bacteria. This gas acts as a blanket. Without this cover, the Earth would be 20 to 30 degrees Celsius colder and considerably less conducive to life. However, the Earth's gaseous shroud is becoming noticeably thicker (Gupta et al., 2014).

Cite this article: Ahmad, S. Rehan (2023). Bioinformatics, a tool for studies of Climate Change , *Emrg. Trnd. Clim. Chng.* 2(1), 40-43. doi: <http://dx.doi.org/10.18782/2583-4770.120>

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The planet is warming as a result of these gases trapping more heat in the atmosphere. Global warming is happening as a result of this, and climate change is taking place due to the rise in global temperatures. They are referred to as greenhouse gases.

Greenhouse Gases and Microbes

The three most significant greenhouse gases are carbon dioxide, methane, and nitrous oxide (Pidwirny et al., 2006), and human activity has significantly boosted these gases in recent years. The Earth is a "closed system," which implies that it generates all the resources required for the survival and development of its inhabitants. Nature uses chemical cycles like the carbon cycle to regulate and maintain the equilibrium of the gases that surround the Earth. All carbon atoms in the universe revolve through a complicated set of operations called the carbon cycle. This indicates that the carbon atoms in your body today have been employed in a variety of other compounds from the beginning of time, such as the carbon in the atmospheric molecule carbon dioxide. Since microbes can recycle and change vital components like carbon and nitrogen that make up cells, they play a significant role as either producers or consumers of these gases in the environment. The 'cycles' of all the fundamental elements involve bacteria and archaea (Pachauri, IPCC 2004; USGCRP – 2009; & Oreskes et al., 2004). Methanogenesis is the process through which methanogens turn carbon dioxide into methane as part of the carbon cycle (Thauer et al., 1998). As part of the nitrogen cycle, nitrogen-fixing microorganisms like *Rhizobium* fix nitrogen, which means they transform atmospheric nitrogen into biological nitrogen that plants can use to produce plant proteins (Postgate et al., 1998). Other microbes are also involved in these cycles, such as photosynthetic algae and cyanobacteria, which perform photosynthesis and serve as the foundation of the food webs in the oceans (Sayre et al., 2010). As they decompose organic waste and release carbon dioxide back into the atmosphere, fungi and soil bacteria are important players in the carbon cycle.

Role of Microbes to Reduce Global Climate Change:

Microbes are thought to make up roughly 60% of the biomass on the planet and are crucial to natural biogeochemical cycles. Scientists are now beginning to understand their potential and function in processes that affect the global climate. The use of genetically modified bacteria as living sensors (biosensors) to detect harmful chemicals in soil, air, or water, energy generation and the development of renewable energy sources, management of environmental carbon dioxide related to climate change, detection of disease-causing organisms and monitoring the safety of food and water supplies, and understanding how microbes work are just a few applications of microbes.

One-celled cyanobacteria *Prochlorococcus* and *Synechococcus* are the tiniest but most prevalent photosynthetic marine organisms (Biller). Per litre of seawater, there are around 100 million *Prochlorococcus* cells (Genomes of Tiny Microbes Yield Clues to Global Climate Change, News, 2003). *Prochlorococcus* and *Synechococcus* are thought to extract roughly 10 billion tonnes of carbon from the atmosphere annually, which is more effective than other phytoplankton and accounts for about two-thirds of the total carbon fixation that takes place in the oceans (Hartmann et al., 2014). Scientists have fully analysed the genomes of these two bacteria.

With this understanding, scientists can perhaps comprehend why these two microorganisms are particularly successful at photosynthesis. If such microbial power could be harnessed, global warming could be slowed, and other greenhouse gases, like carbon dioxide, could be reduced.

Bioinformatics Studies on Microbes Genome:

Studies on climate change benefit from the use of bioinformatics. Numerous genome sequencing and metagenomic projects have produced large volumes of genetic information about cyanobacteria over the past ten years. This plethora of information offers researchers a new foundation for the study of cyanobacterial molecular adaptability,

ecology, and evolution, as well as for the creation of biotechnological applications. Additionally, it makes it easier to combine multiple methods, such as expression profiling, with high-throughput tools like microarrays, RNA-seq, and proteomics. However, exploration and analysis of these data are difficult tasks that frequently call for sophisticated computational techniques.

In order to use them to make trustworthy biological judgments, they must also be incorporated into the body of information already in existence. Systems biology offers useful tools in this situation. Particularly, the creation and analysis of molecular networks have become an effective systems-level framework for integrating such data and improving our understanding of the biologically significant processes occurring in these animals. To draw the reliable biological inference that may be employed in environmental remediation, multiplex data from genomic, transcriptomic, proteomic, and metabolomics investigations on cyanobacteria must be evaluated with an informatics method. Additionally, research is being done to use comparative genomics to examine and classify the changes in the gene content of cyanobacteria.

In order to evaluate the gene content of 100 different species of cyanobacteria and identify core genes, species-specific genes that are phylogenetically related, and genome-specific genes, this study developed a computer pipeline.

The DOE established the Microbial Genome Initiative in 1994 to sequence the genomes of microorganisms valuable for energy production, environmental remediation, toxic waste reduction, and industrial processing thanks to advancements made by the Human Genome Project.

As a result of that effort, six bacteria that can survive in situations of high pressure and temperature have been sequenced. Researchers may employ the bacteria and their enzymes for useful applications such as waste control and environmental remediation by

studying the specific protein structure of these microbes.

Prochlorococcus, the smallest unicellular cyanobacterium with a genomic size of about 2 Mb and a widely distributed photosynthetic microorganism (Partensky et al., 1999) in the ocean that predominates temperate and tropical oceans is one of these bacteria. It performs a considerable portion of photosynthesis in the world's oceans despite lacking the phycobilisomes that distinguish cyanobacteria from other types of bacteria. For instance, it typically accounts for 50% of the total chlorophyll in the subtropical Pacific.

Because of this, it can effectively absorb blue light at low light intensities and blue wavelengths typical in the deep euphotic zone. It produces between 30 and 80 per cent of all photosynthesis in oligotrophic oceans and, as a result, has a considerable impact on the Earth's climate and the global carbon cycle.

Our understanding of the regulation of these critically important activities on a global scale will be considerably improved by the description of *Prochlorococcus marinus* entire genome. *Prochlorococcus* is a prime candidate for complete genome sequencing because it is the smallest known phototroph, has a small genome (1.8 Mb), is widespread and abundant, is simple to identify and count in situ using flow cytometry, and can be easily accessed thanks to its distinctive photosynthetic pigment (divinyl chlorophyll). Additionally, at least two *Prochlorococcus* ecotypes coexist in the oceans.

Another microbe, *Deinococcus radiodurans*, is employed to clean up harmful chemical waste sites because of its radiation resistance. Numerous creatures rely only on carbon dioxide as a supply of carbon, and rising carbon dioxide emissions are one of the main factors contributing to the world's changing climate. Bioinformatics makes it feasible to investigate the genomes of these microorganisms, which aids in the formulation of suggestions for lowering carbon dioxide levels. The MGP launched by DoE has revolutionised the field of microbiology, and more work must be done in this area with the

aid of bioinformatics in order to regulate waste and clean up the environment.

CONCLUSION

In conclusion, it can be concluded that bioinformatics can be an intrinsic part of and play a significant role in the research of climate change. The bioinformatics field hasn't done much work in this area, and more regionally specific research is needed to consider the CO₂ abatement potential of local bacteria.

Declarations:

Ethics approval and consent: This study has nothing to do with human and animal testing.

Consent for Publication: All the authors give their consent to publish the current manuscript.

Competing Interest: The authors declare that they have no conflict of interest.

Funding Declaration: It hereby declares that any agency did not fund the current project.

ORCID id: <https://orcid.org/0000-0003-0796-5238>

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