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Sustainable innovations for harnessing marine biotechnology through advanced bioinformatics

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Abstract

Objectives

Bioinformatics has evolved into an indispensable tool across various realms of biology, pivotal in advancing scientific pursuits. Despite its ubiquitous presence in traditional life science courses, integrating hands-on training with wet lab investigations becomes imperative to foster student engagement and comprehension. This holistic approach not only bridges theoretical knowledge with practical applications but also cultivates a deeper appreciation for the interdisciplinary nature of bioinformatics. The ever-accelerating progress in omics studies has unveiled unprecedented avenues for comprehending biological structures. This surge has sparked a revolutionary transformation in the field, propelling marine studies beyond the realms of hypothetical organisms to encompass an expanding array of marine life. At the forefront of this marine exploration is the research's central focus on the practical task of unearthing novel enzymes in marine environments. The inquiry delves into the cutting-edge concept of metagenomics, a contemporary methodology that broadens the horizons of biotechnology by incorporating non-culturable microorganisms into its purview. A crucial facet of the research involves the introduction of a viral cosmid library screening probe, responding to the challenges posed by the study of marine microbiology and bioengineering. This model is used to decipher marine microorganisms' genetic patterns, further enriching the understanding of their biochemical processes. The paper meticulously delineates the objectives of marine microbiology and bioengineering projects, underscoring the need for a collaborative effort to achieve them successfully. The research outlines the goals and provides a strategic roadmap for their implementation through a synergistic collaborative approach.

Materials and Methods

This approach harnesses the collective expertise of scientists and researchers, fostering an environment conducive to breakthrough discoveries. The fusion of experimental research techniques enhances students' proficiency in fundamental bioinformatics, instilling in them a problem-solving mindset crucial for navigating the complexities of contemporary biological research.

Conclusions

The integration of hands-on training, coupled with the exploration of cutting-edge methodologies like metagenomics, marks a paradigm shift in the study of marine microbiology and bioengineering. This research contributes to the growing body of knowledge in these domains and underscores the significance of collaborative efforts in pushing the boundaries of scientific exploration.

Keywords: Biotechnology, Bioinformatics, Marine, Sustainable innovations

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Introduction

The projected value of the worldwide marine biotechnology industry is anticipated to exceed US$6.4 billion by the year 2025 (Fasim et al. 2021). When it comes to the polar areas, marine biotechnology is lagging, and the potential for many sectors has yet to be ultimately achieved. These unexplored and isolated ecosystems have great potential as sources for ecological and biological uses and might provide valuable chances for discovering new compounds and

conducting biological prospecting (Galimberti et al. 2021). Currently, it is advantageous for biologists to use web tools, information, and software to enhance the efficiency and cost-effectiveness of their designs for experiments. Hence, educating pupils using a problem-solving methodology that incorporates computational labor into a diverse experimental undertaking is advantageous. The research offers an instructional program delivered to learners enrolled in the marine and ecological biology programs (Chung et al. 2021).

The bioinformatics lesson is integrated into marine bacterial enzymes' breakdown of natural contaminants (Wang et al. 2021). The laboratory project presented to the pupils focuses on identifying an effective enzyme on a frequently encountered scaffold in contaminants and synthetic materials, known as a privileged scaffolding. The platform is indole, an N-heterocyclic heterocyclic pollution introduced into aquatic ecosystems due to industrial effluent.

The learners will search for a digestive enzyme with wide-ranging selectivity that can break down indole and other aromatic chemicals. It is well-established that only a minute proportion of naturally occurring microorganisms can thrive in traditional laboratories. Due to this rationale, several scientists have proposed that metagenomes could be a substantial source of innovative enzymes for biocatalysis, biofuels, and biological remediation (Kandasamy et al. 2021).

Evidence suggests that the processes leading to the isolation of Antarctica took place around 34 billion years ago, namely during the transition between the Eocene and Oligocene epochs. Polar marine organisms have developed specialized adaptations to survive in the severe conditions of their environment, characterized by freezing temperatures and prolonged twilight periods. These adaptations generally include the production of distinct secondary metabolic products, contributing to their distinctive survival tactics. The unique conditions and environmental challenges experienced by marine species in polar areas have a significant role in creating secondary metabolites and the development of chemicals with a wide range of biological functions. The rivalry for resources and habitat, the need to avoid predators, the danger of pathogens, and the importance of chemical exchange within the same species all contribute to promoting chemical variety in marine habitats. Maritime polar creatures need intricate metabolic and physiological modifications to endure frigid temperatures, powerful winds, limited nutrition supply, and intense UV radiation. Hence, under highly contrasting conditions, secondary metabolism products in the shape of bioactive chemicals play a crucial role in the continuing existence of marine species.

Background and Literature Summary

Marine biotechnology is integrated into many European programs, national innovative specialty plans, and international partnerships (Kawamura et al. 2021). Therefore, it requires the

cooperation of other fields and specialists. A comprehensive summary was given on the critical elements of the process in marine biotechnology, such as the species involved, areas of high biodiversity, investigation approaches, manufacturing ramping up, and application case situations. Several scientific papers have recognized Jellyfish as creatures with significant possibilities for biotechnological exploitation (Duarte et al. (2022). The levels of valuable bioactive compounds in brown seaweeds collected from the shores of Tunisia were evaluated. Conopeptides of the novel kind were extracted from the cone snail species Conus quercinus. A comprehensive analysis was conducted on 37 marine invertebrates from extreme polar areas. These organisms were examined for their diverse spectrum of biological activities, and the molecular makeup of the primary bioactive substances was thoroughly investigated. The authors studied the underutilized possibility of cephalosporins, protein-based poisons generated by the salivating glands of coleoids, namely Octopuses, squids, and jellyfish (Gonçalves and Costa 2021). Utilizing fish skin is a significant waste valorization method to reduce the trash generated from fishing and agribusiness. The study also examined other waste methods, focusing on marine creatures and their biological polymers (Wang et al. 2021). These methods included the production of biofuels, fertilizers, supply, packaged food, and bioremediation, among other applications in many sectors.

The potential of marine microbes, specifically those found in association with microbes, has often been underestimated as a valuable biotechnology asset (Mu et al. 2021). The researchers examined the capabilities of the fungal strain Aspergillus sp., which was obtained from a red seagrass Grateloupia filicina. The authors discussed the possibility of bacteria connected with the Brazilian indigenous ascidian Euherdmania sp (Streit et al. 2021). The research comprehensively analyzed the prospective uses of physiologically active peptides produced by marine creatures and their microscopic microorganisms. They also discussed the methodologies used for searching and the possible industrial applications of these proteins.

The biotechnological capabilities of aquatic phytoplankton were addressed (Das and Kumar 2022). The scientists conducted a biotechnological assessment of diatoms, focusing on their diverse silica shells and their ability to thrive in severe settings. An evaluation was born on the dinoflagellate Prorocentrum spp. as a prospective origin of phycotoxins, with a thorough examination of methods to augment their generation. These methods included chemical and genetic engineering approaches and various culture procedures. A study was conducted on the possibility of marine microbes, namely Stenotrophomonas maltophilia, found in rock specimens and connected with deep-sea crustaceans in the undersea volcano in the Canary Islands in France (García et al. 2022). Crucially, many approaches are employed for enhancing the synthesis of the

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desired metabolites for biotechnology purposes. An optimization study was conducted to improve the co-culturing of the astaxanthin-producing marine and the lactic acid-producing bacterial species Escherichia fermentum (Pirmanesh et al. 2022). The study focused on optimizing the medium parameters for this co-culturing process. These activities are evident in marine biology via the publication of white articles, research studies, innovative projects, governance campaigns, efforts to promote ocean knowledge, and exposure in the press. These need the participation of interdisciplinary communities.

Proposed Marine Biotechnology and Bioinformatics

Creating large amounts of high-quality proteins, marine fats, and other desired secondary metabolic products necessitates using biochemistry and genetic engineering techniques. Figure 1 depicts an exploded view of the variables that must be considered throughout the bioprospecting procedure. This process begins with the choice of marine life, followed by their farming to synthesize valuable bio-components and investigate their application in different sectors.

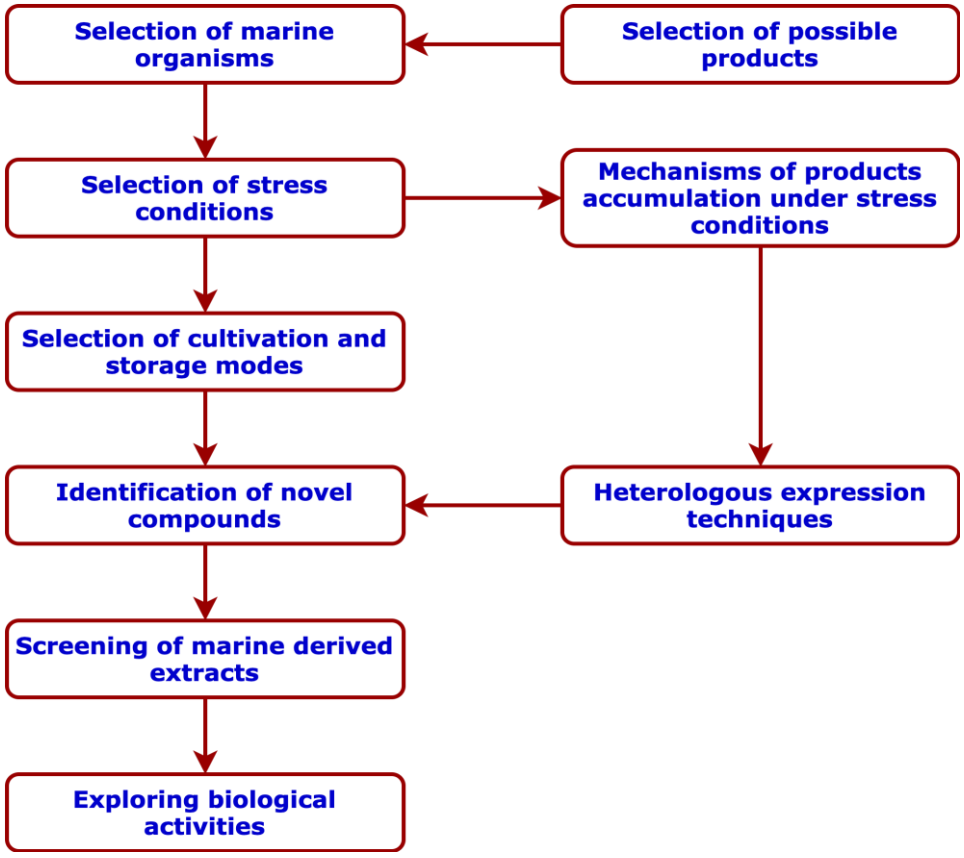

Figure 1. Bioprospection Pipeline of Marine Biotechnology with Bioinformatics

It is assumed that learners are involved in research to discover a new bacterial protein from a specimen of saltwater metagenomics. For this reason, the study presumes that an archive has been created using cosmids and has to be examined. This tutorial introduces a biological technique for designing a probe to identify the intriguing clone (Figure 2).

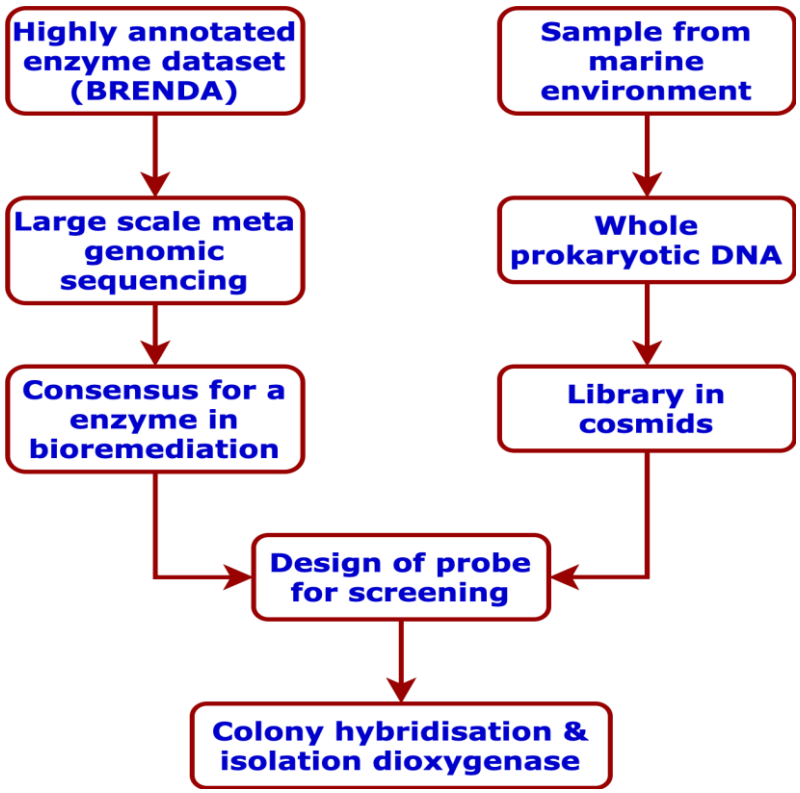

Figure 2. Flowchart of Training in Marine Biotechnology with Bioinformatics

Initially, learners will search the enzyme records in BRENDA to identify a prokaryotic enzyme capable of using a specific category of contaminants as precursors (https://www.brenda-enzymes.org). BRENDA examines enzyme agonists using chemical similarities and components. The tutorial selects indole as a case study as to its status as a privileged scaffolding. Several natural and artificial chemicals that can attach to various targets share a biologically active structure. Regrettably, conducting a sophisticated search that involves drawing a framework is currently not feasible.

It is imperative to follow a two-phase protocol that appears redundant to identify an enzyme in the classroom active on a specific substrate defined by its chemical makeup and produced by microbes. During the first step, the composition is the starting point to get the precise name of the studied substrates. During the second stage, the accurate nomenclature and taxonomy of species are used, along with improved functionalities. Various kinds of enzymes exhibit activity towards compounds that have a resemblance to indole. Naphthalene 1,2-dioxygenase (N-DO) has wide-

ranging selectivity and plays a role in the breakdown of several aromatic chemicals (Liu Y et al. 2021). By selecting the quantity, learners can access a wealth of material organized into several parts. The most pertinent ones for the scenario being examined are those about enzyme-ligand conversations, which provide insights into the full range of materials that can interact with enzymes of this kind.

Pertinent details regarding organism-related data and protein buildings can be found with links to UniProt. The learners will not discover any N-DO originating from a bacterial sea creature. The only bacterial enzyme thoroughly described is created from *Aeruginosa putida*. The subsequent stage involves retrieving the sequence of N-DO derived from *Pseudomonas putida* in UniProt. *Pseudomonas putida* is phylogenetically distinct from the marine prokaryotes found in the marine water samples used for library construction. The learners will search for sequences with homology derived from marine bacteria. They will use many uncharacterized gene sequences acquired via extensive genomic and metagenomic sequencing initiatives. BLAST will be used for this study, with N-DO of *Pseudomonas putida* as the query. The search will be restricted to metagenomic proteins stored in the dataset.

The Omega Clustal will align several sequences in the third stage. The students will analyze the structure of N-DO from the homologous bacteria *Pseudomonas putida* to find preserved sections. They will then use Cons to generate a consensus transcript.

The fourth phase involves performing retrotranslation of the protein agreement pattern using bioinformatics techniques. The learners will discover that retrotranslation fails to offer a distinct DNA sequencing until a codon most often utilized for every amino acid in microorganisms is selected. The result of this lesson is a series of probes used for the assessment via colony recombination.

Training Process

Step 1. Querying the enzyme repository to identify a microbiological enzyme that can break down indole.

The system retrieves information from the BRENDA database. It illustrates the molecule of fascination, a bicyclic structure composed of six-membered benzene rings bonded to a five-membered pyrrole compound ring. To receive the precise name of the chemical, the user can visit the BRENDA webpage and choose Ligand Structural Searching. Before conducting the investigation, a sub-structure search with a maximum search duration of 120 seconds is necessary, limited to Substrates.

It gets the precise nomenclature of several compounds with the form it depicted and chooses indole. Return to the BRENDA site and do a sophisticated search by entering microbes in the category field and substrate in the type field. Use the precise name of the chemical, indole.

BRENDA displays a comprehensive list of all the enzymes in the registry that employ indigo as the substrate. Based on the findings, the enzyme N-DO from Aeruginosa was selected for this training. This trait is seen in several bacteria and exhibits a wide range of specific substrates. Kindly click on the number to get comprehensive biochemical information on the peptide.

Refer to the enzyme architectures section to locate the patterns that include the linkages to Uni-Prot. The organism selected is Pseudomonas putida. Click on the UniProt code to access the proteome sequencing repository.

Select the Sequence option on the UniProt page and download the amino acid sequencing in FASTA formats.

Step 2. Protein BLAST (BLASTp) performs a neighborhood matching to contrast an amino acid sequencing with the proteome from metagenomic data stored in a repository (https://blast.ncbi.nlm.nih.gov).

Launch a fresh web page using the BLAST application and choose Protein BLAST to align the amino acid patterns.

Copy and insert the sequence obtained from UniProt into the designated Enter Query String section, selecting Metagenomic enzymes as the repository. Under the Method variables section, choose 500 as the value for Max targeted sequencing and execute the BLAST operation.

Choose and get every marine metagenome sequence in the FASTA type.

Step 3. Clustal omega is a tool for doing multiple pattern positions, which helps predict relationships and similarities among nucleotides.

Access the Clustal Omega navigation tool by visiting the website and opening an additional Web page. Use this tool to carry out multiple alignments.

Insert the sequencing into the provided space using Pearson/FASTA as the final style. Keep the other options at their default settings and complete the task.

Step 4. EMBOSS exploration tool for generating a consensus nucleotide from an array of alignments

Access the EMBOSS Browser and go to the cons option on the left edge of the webpage. Transfer the acquired multiple alignments in FASTA style and insert them into the space (https://www.ebi.ac.uk/).

Extract a segment (choosing around 30 amino acid repeats) to generate a DNA probe of about 100 base pairs while avoiding areas with excessive X occurrences.

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Step 5: Convert an amino acid pattern into the sequence of nucleotides with the highest probability.

Utilize the online program Reverse Translation to convert a protein acid pattern into the most likely nucleotide series, employing the standard codon structure from E. coli.

Insert the duplicated sequence into the space and complete the task.

Bioinformatic Pipeline

To identify the genetic factors that contribute to the ability of marine Streptomyces to break down keratin, a comparable evaluation of the genomes of three distinctive streptomycetes was done. These strains exhibit moderate, high, and no keratolytic action. Searching for proteases began with genomic tagging utilizing three computers. Based on the dataset, the proteins were individually curated using Blastp and categorized into peptidase groups. A thorough examination of the three strains' chromosomes revealed proteolytic orthogroups common to all triple streptomycete genes and proteins specific to every theme (Figure 3). Based on this study, the genes of particular relevance were explicitly associated with keratinolytic variants. Among these strains, 17 enzymes were discovered solely in instance G11C and three peptidases in forming ortho groups had been identified across isolates CHD11 and G11C.

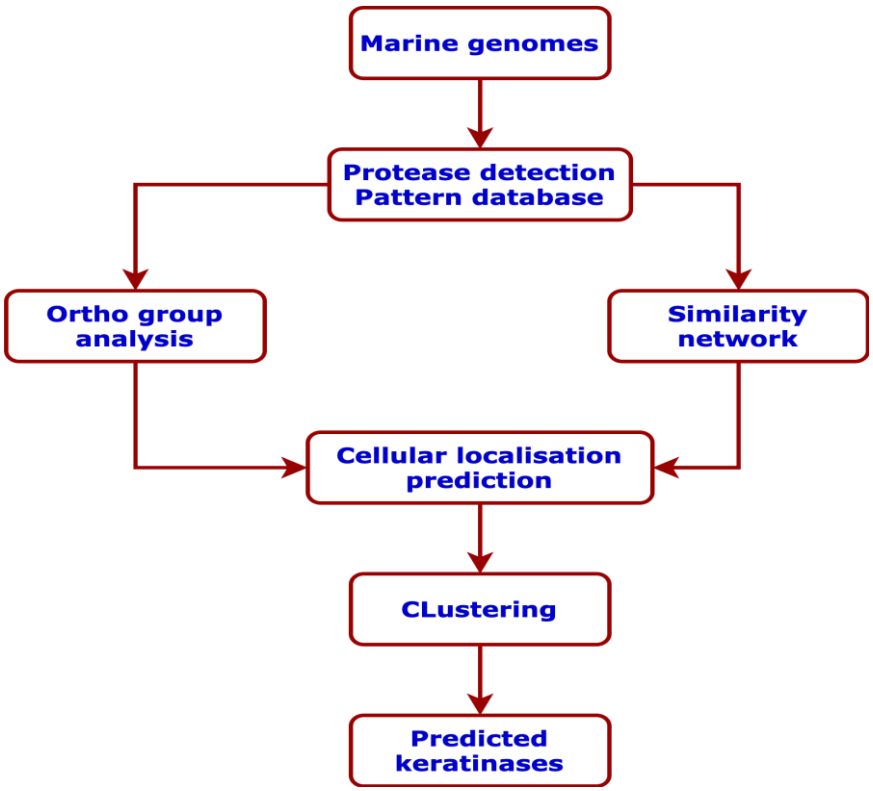

Figure 3. Bioinformatics Pathway to Predict the Keratinases

A similarity network study was conducted on the proteins from the three varieties, along with two records containing useful keratinases and hypothetical non-keratinases. This investigation revealed the presence of three separate groups associated with functional keratinases, which are classified under peptidase households S1, S8, and M4—eleven proteases originating from Streptomyces sp. This investigation identifies G11C. The data from similarities networking and p-ortho group investigation were combined with a cell localization study using t-SNE-based grouping to ascertain additional keratinase proteases. The study facilitated the discovery of three clusters, including external proteases designated as groups t-SNE 0, 1, and 2. Based on the investigation, the strain G11C had many distinct amino acids and amino acids expected for both the keratinolytic isolates CHD11 and G11C. It was hypothesized that these peptidases are located inside the cell. Their unique association with the keratinolytic varieties remains intriguing since their existence might account for the variations in keratinolytic ability seen among the three isolates. The amino acids anticipated to be located outside of cells in the t-SNE groups were analyzed using a phylogenetic analysis that included the tool Ancestors state rebuilding. This tool allocates a range of probabilities to every ancestral node in the tree, indicating the likelihood that it falls into the following categories: Practical keratinase, keratinase-linked proteins, three-strain grouping, and non-keratinase. Following the application of choosing for selection to analyze the groups of the tree of phylogeny, seven code patterns for interest extracellular keratinases emerged in Streptomyces sp. These choosing standards included the existence of a helpful keratinase, a G11C order, and a 50% likelihood in the ancestral node containing this enzyme or a keratinase-linked pattern.

The study focuses on two types of proteins: (1) proteases specific to keratinolytic varieties and (2) external proteins associated with functional keratinases. These proteins have been suggested as potential explanations for the variations in keratolytic action observed among the three varieties.

Advancement of Marine Biotechnology with Bioinformatics

Marine nanotechnology with bioinformatics has five overarching goals:

Description of Marine Biodiversity: The understanding of marine biodiversity remains constrained. There is a significant variation across regions regarding the distribution of species and the extent of taxonomic information about them. The scarcity of specialists in the classification of marine life, the presence of duplicate or inconsistent data in the primary nucleotide records, the absence of designated type organisms, and the existence of multiple lineages within generally created taxa contribute to the misidentification or failure to identify

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numerous species or varieties. Many of these unknown organisms possess significant potential for use in biotechnology. These problems are equally substantial for marine natural product initiatives. Therefore, it is necessary to use personnel, investigations, and cost-effective ways to address the existing information gap about the biological and chemical variety in marine environments. These issues are resolved using high-throughput techniques that expedite organisms' identification, categorization, and distribution.

High-throughput techniques for tracking biodiversity have yet to be widely implemented, and the standardization of the biodiscovery course is often lacking. Indeed, the use of bioinformatics processes and the analysis of large data are significantly transforming the field of marine biological sciences since around 18,000 newly discovered species are documented each year. Marine nanotechnology with bioinformatics will provide operational protocols for discovering biodiversity utilizing efficient methodologies, including barcoding with DNA. In situ hybridization methods use these approaches to quantitatively analyze and locate particular microbial groups within the surrounding matrices. Biological analysis is essential to tracking and exploiting marine creatures. The environmental effects of physical searching are deemed negligible during the first sampling phases when the gathered samples are modest. It is essential to standardize the biodiscovery method due to the significant variation in geodiversity within the same species, which occurs across spatial and ecological gradients and periodically and during the entire lifespan of animals.

Natural Product Discovery: This procedure involves simultaneous separation and biological screening methods to identify and isolate bioactive substances, which are then subjected to structural elucidation. Should the target molecule from one species demonstrate biotechnological promise, the amplification of manufacturing and distribution would inevitably result in a heightened environmental effect. Creating the molecule using chemical synthesis, albeit time-consuming and costly, or utilizing synthetic biology to produce the desired component often resolves the need for recurrent gathering and excessive use of the natural environment. Marine nanotechnology with bioinformatics aims to create a comprehensive collection of processes and techniques, known as pipelines, based on specific case studies. These pipelines will cover various stages, including the establishment of marine biorepositories, the detection of gathered organisms through integrative systems biology, the assessment of bioactivities relevant for certain businesses, the recognition and environmentally friendly manufacturing of bioactive molecules, creating a company plan, and the formulation of a marketing strategy. Throughout this process, marine nanotechnology with bioinformatics will prioritize legal and ethical considerations and adhere to stringent regulations for safeguarding the planet and ecological sustainability. These pathways will function as frameworks and instructional materials for future creations while

facilitating knowledge exchange across different fields. These pathways will emphasize the synergistic transdisciplinary nature of marine biotechnology and its connection to other biotechnology domains. To the concepts of sustainability, supply chain decision-making necessitates the incorporation of economic and social variables in addition to environmental factors. The action will implement a comprehensive methodology for assessing a product's or process's sustainability over its entire life cycle, known as Life Cycle Sustainability Analysis (LCSA). The approach would include a physical Life Cycle Assessment (LCA) that accounts for several environmental effect subcategories, such as warming temperatures, a process known as acidity, during various lifespan stages (partial LCA).

It will incorporate social LCA (SLCA) and Life Cycling charging (LCC) following the United Nations Environment Program (UNEP)/ Society of Environmental Toxicology and Chemistry (SETAC) recommendations. This action will use the methodology employed in previous studies. It shall adhere to the methodology structure for performing LCA as specified by the International Standards Organization (ISO) 14040 range.

Sharing Infrastructure: There is a growing need to connect academic and creative capacities and the corporate sector. This encompasses the presence of educational infrastructures, giving access to various novel instruments and resources to foster the flourishing of marine biology. The methods employed in marine biology are extensively utilized in several research and technology domains. Participating in cooperative research initiatives is a means of granting accessibility to these resources and promoting interdisciplinary research. Marine nanotechnology with bioinformatics will facilitate the exchange of knowledge and resources among various participants, primarily via short scientific expeditions and novel collaboration initiatives. Priority will be provided to consumers from countries with lower study intensity or to beginning scientists who need accessibility to advanced analytical machinery, microbiological communities, or screening procedures.

Responsible Research and Innovation: Observing and sustainably managing the ocean to optimize its scientific and societal advantages while minimizing detrimental impacts on the marine ecosystem is crucial. The issue will be resolved by implementing the Responsibility Research and Innovation (RRI) model, founded on six fundamental principles.

- **Ethics:** Each individual is responsible for maintaining the balance and stability of the ecosystems on Earth. This study will identify and solve ethical concerns and difficulties, which will then be utilized in advocating for the safeguarding of marine environments and promoting sustainable utilization of resources and laws about the environment, along with raising public awareness.

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- **Open Access:** To effectively collaborate in knowledge generation and benefit from previous studies, it is crucial to prioritize openness, effectiveness, accountability, data accessibility, reciprocal relationships, biological safety, protection of nature, and information transfer to other nations.
- **Gender Equality:** The action will enhance gender parity by encouraging young professionals and female employees to aspire for management jobs and eventually create and oversee coalitions for the valuation of marine biotechnology goods.
- **Governance:** Geographical boundaries do not limit marine biodiversity, but the Agreement on Biological Diversity establishes guidelines for accessing ecological assets. This convention aims to protect biodiversity, promote sustainable utilization of biological organizations, and ensure an equitable distribution of those assets. The Protocol from Nagoya also addresses this issue by establishing a legal structure to ensure the just and equitable distribution of advantages that result from using genetic assets, which might sometimes impede or hinder specific study endeavors (Knauf et al. 2019).
- **Public Engagement:** The attendees of the initiative will use various communications platforms and activities to provide more information to legislative leaders, investigators, and businesses. The objective is to ease the regulatory constraints often hindering international cooperation.
- **Science Education:** The research will prioritize educating the next cohort of investigators, especially early career analysts. The main emphasis will be on nations with lower research intensity, sometimes called inclusivity nations. These nations have formulated their national tactical objectives within the EU Smart Specialization Strategies (S3) framework to promote equitable development across areas. Given the extensive presence of marine biotechnology and its many goods and uses across all national S3 goals, now is an opportune moment to establish educational programs that go beyond the conventional school curriculum and focus on enhancing capacity-building. The research will address learning disparities via three distinct approaches.

(i) Short-term missions in science refer to movement initiatives that include direct, hands-on engagement and experience overseas.

(ii) By providing financial incentives for individuals to actively engage in meetings focused on any areas connected to marine biotechnology.

(iii) The workshops and meetings, which will be publicly advertised, will focus on issues that include academia, technical centers, and business.

This plan will mitigate the hazards of educating a marine-related profession that the marketplace could not absorb by providing diverse skills.

Knowledge Co-creation and Integration: The Action aims to be regionally comprehensive by creating an open-access registry of commercially viable organisms for marine biology in the member nations of marine nanotechnology with bioinformatics. This Activity will primarily concentrate on species that are believed to have promise for biotechnological applications, as well as on the World Registry of Ocean Resources.

(i) The Action will encompass all species, irrespective of their kingdom, ranging from algae and microbes to plankton and other exploitable organisms, in a comprehensive biological perspective.

(ii) The attendees will systematically include all stages of the biotechnological pipelines, including bioprospecting, culture, biological assessment, compound loneliness, improvement of the isolation procedure, and structural deconstruction.

This action is genuinely multidisciplinary, encompassing a wide range of knowledge and involving specialists from diverse fields such as marine (micro)biology, chemical engineering, food sciences, farming, medicine, safeguarding the environment, technology, power, information technology, omics methods, research, law, policy producing, finances, business strategy, and more. The system will facilitate the transfer of information from conventional universities to sectors focused on exploitation. This will result in the development of ecological services aligned with the interests of policy producers, citizens, businesses, and small and medium-sized enterprises.

Conclusions: To promote a long-lasting blue bioeconomy in the Atlantic region, it is necessary to (i) consistently establish a robust and all-encompassing study network, (ii) facilitate synchronized international research that covers the entire Atlantic Ocean, and (iii) encourage enhanced ocean literacy and recognition of marine microbes. In line with the marine nanotechnology with bioinformatics principles of global collaborations, the formation of a Marine Bioengineering and Marine Microbes action grouping would:

- Establish cooperative alliances across government, educational, and corporate sectors to advance marine biotechnology and marine microbial solutions for environmental and societal concerns.
- Foster partnerships to establish research initiatives throughout the Atlantic region, explicitly targeting marine microbes, the aquaculture sector, drug research and growth, and other pertinent marine methods to bolster the maritime economy, particularly endeavors centered on carbon sequestration.

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- Facilitate knowledge transfer across different industries and nations and encourage the establishment of fresh marine biological enterprises in the Atlantic Ocean region.
- Facilitate the establishment of connections and active participation among partners to enhance their skills and knowledge in ocean studies and technological advances, as well as in ocean leadership, to foster an environment for practice that is open and varied.
- Foster curiosity and enhance understanding of blue biological sciences, fish farming, microbes, and their capacity to tackle existing difficulties.

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چکیده

هدف: بیوانفورماتیک به یک ابزار ضروری در حوزه‌های مختلف زیست‌شناسی تبدیل شده است که در پیشبرد فعالیت‌های علمی بسیار مهم است. علیرغم حضور همه جانبه آن در دوره های سنتی علوم زیستی، ادغام آموزش عملی با تحقیقات آزمایشگاهی برای تقویت تعامل و درک دانشجویان و مخاطبین ضروری است. این رویکرد جامع نه تنها دانش نظری را با کاربردهای عملی مرتبط می‌کند، بلکه درک عمیق‌تری را برای ماهیت بین‌رشته‌ای بیوانفورماتیک ایجاد می‌کند. پیشرفت روزافزون در مطالعات اومیکس راه‌های بی‌سابقه‌ای را برای درک ساختارهای بیولوژیکی آشکار کرده است. این افزایش جرقه یک دگرگونی انقلابی را در این زمینه ایجاد کرده است و مطالعات آبزیان را فراتر از قلمرو موجودات فرضی سوق داده تا مجموعه‌ای از حیات دریایی در حال گسترش را در بر بگیرد. در خط مقدم این اکتشاف دریایی، تمرکز اصلی پژوهش بر روی وظیفه عملی کشف آنزیم‌های جدید در محیط‌های دریایی است. این تحقیق به مفهوم پیشرفته متاژنومیکس می پردازد، روشی معاصر که افق های بیوتکنولوژی را با ترکیب میکروارگانیسم‌های غیرقابل کشت در حوزه کاری خود گسترش می‌دهد. جنبه حیاتی این تحقیق شامل معرفی یک کاوشگر غربالگری کتابخانه کیهانی ویروسی است که به چالش های ناشی از مطالعه میکروبیولوژی دریایی و مهندسی زیستی پاسخ می‌دهد. این مدل برای رمزگشایی الگوهای ژنتیکی میکروارگانیسم‌های دریایی استفاده می‌شود و درک فرآیندهای بیوشیمیایی آنها را غنی‌تر می‌کند. این مقاله به دقت اهداف میکروبیولوژی دریایی و پروژه های مهندسی زیستی را مشخص می‌کند و بر نیاز به تلاش مشترک برای

دستیابی موفقیت‌آمیز به آنها تأکید می‌کند. این تحقیق اهداف را ترسیم می‌کند و یک نقشه راه استراتژیک برای اجرای آنها از طریق یک رویکرد مشارکتی هم افزایی ارائه می‌دهد.

مواد و روش‌ها: این رویکرد، تجربیات و دستاوردهای دانشمندان و محققان را تجمیع می‌کند و محیطی را برای اکتشافات مهم ایجاد می‌کند. تلفیقی از تکنیک‌های تحقیق تجربی، مهارت مخاطبین و دانشجویان را در بیوانفورماتیک بنیادی افزایش می‌دهد و ذهنیت حل مسئله را در آنها القا می‌کند که برای پیمایش پیچیدگی‌های تحقیقات زیست‌شناسی معاصر ضروری است.

نتیجه‌گیری: ادغام آموزش عملی، همراه با اکتشاف روش‌های پیشرفته مانند متاژنومیکس، تغییر پارادایم در مطالعه میکروبیولوژی دریایی و مهندسی زیستی را نشان می‌دهد. این تحقیق به افزایش دانش در این حوزه‌ها کمک می‌کند و بر اهمیت تلاش‌های مشترک در پیشبرد مرزهای اکتشاف علمی تأکید می‌کند.

کلیدواژه‌ها: بیوتکنولوژی، بیوانفورماتیک، دریایی، نوآوری‌های پایدار

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