International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 9 Issue: 3
Article Received: *25 December 2020* ***Revised:*** *12 January 2021* ***Accepted:*** *20 February 2021*

Contributions as a Scrum Master: Facilitating Agile Project Management in Bioinformatics Research with AI

Neha Dhaliwal
Independent Researcher, Sr. Data Scientist
College of Sciences Technology, University of Houston Downtown
dhaliwaln1@gator.uhd.edu

Abstract: In this research, Agile approaches, AI algorithms, and project management tools are integrated with bioinformatics. Analysis of computational models and implementations of AI techniques like CNNs, RF, and K-Means Clustering is covered. Comparisons focus on algorithm selection, while Agile project management tools like JIRA and Trello are discussed. Collaboration and workflow efficiency are stressed in the conclusion. Future developments include AI integration, Agile methods, and bioinformatics project management systems.

Keywords: *Agile, AI, Bioinformatics, Project Management, CNNs, RF, K-Means Clustering, JIRA, Trello, Future Scope.*

I. INTRODUCTION

The field of bioinformatics, which combines the disciplines of biology, computer science, and information technology, necessitates advanced project management techniques to handle the intricate and extensive datasets involved. Agile approaches, specifically Scrum, have demonstrated efficacy in managing complexity through the promotion of iterative development and the improvement of team cooperation [1].

The Scrum Master has a crucial function in Scrum, since they facilitate agile procedures, eliminate obstacles, and ensure that the team follows best practices. In the field of bioinformatics, this function is particularly important due to the need for interdisciplinary cooperation [2] . Artificial Intelligence (AI) has become essential in the field of bioinformatics, where it assists in activities such as data analysis and predictive modelling using advanced techniques like machine learning and deep learning [3]. Integrating artificial intelligence (AI) into agile frameworks can enhance the efficiency of workflows and improve project results[4].

This research seeks to examine the role of Scrum Masters in bioinformatics projects, with a specific emphasis on the influence of integrating artificial intelligence. The objectives encompass the examination of Scrum Master responsibilities, the assessment of AI's influence on project management, and the creation of a structure for incorporating AI into Scrum.

Fig 1.1: Scrum Process ("https://www.pm-partners.com.au/wp-content/uploads/2021/06/blog-scrum-process-opt.jpg")

Recent statistics highlight the advantages of agile techniques and artificial intelligence (AI) in the field of bioinformatics. Research conducted by [5] has established a direct correlation between the implementation of agile techniques and a significant enhancement of 30% in productivity, as well as a notable reduction of 20% in project timeframes. AI applications have demonstrated a prediction task accuracy of up to 95% [6]. By integrating the facilitative responsibilities of Scrum Masters with the computational powers of AI, bioinformatics projects can attain enhanced efficiency and innovation.

Research Objective :

- Analysing the particular responsibilities and contributions of Scrum Masters in project management of bioinformatics.
- Assessing how AI affects bioinformatics agile project management methods and results.

International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 9 Issue: 3
***Article Received:** 25 December 2020 **Revised:** 12 January 2021 **Accepted:** 20 February 2021*

- To create a thorough framework for including AI technologies into the Scrum process in order to improve research productivity and project efficiency.

This research will explore the mutually beneficial connection between Scrum Masters and AI in bioinformatics projects, based on these encouraging data. By harnessing the computational capabilities of AI and the facilitation expertise of the Scrum Master, bioinformatics teams may enhance productivity and foster innovation, thereby propelling scientific discovery forward.

II. LITERATURE REVIEW

Bioinformatics has effectively used agile approaches, especially Scrum, to manage big and dynamic information. The ideas of iterative development and cross-functional teams in Agile methodology are well-suited to the interdisciplinary character of bioinformatics research [7]. Research indicates that the implementation of agile practices results in a 25% increase in team productivity and a 15% reduction in project cycle time[8]. The iterative technique of Scrum enables continuous integration and testing, which is crucial for managing extensive datasets and intricate algorithms.

The Scrum Master has a vital role in fostering Scrum processes, promoting team cohesion, and assuring compliance with agile principles. In the field of bioinformatics, this entails overseeing the exchange of information between different disciplines and continuously improving computer models through a process of iteration[1]. Studies have shown that proactive Scrum Masters enhance project success rates by 20%, underscoring their significance in coordinating varied knowledge [9].

Artificial intelligence tools like as machine learning and natural language processing improve decision-making, streamline workflows, and forecast project results in the field of bioinformatics. Artificial intelligence (AI) solutions streamline repetitive operations and offer immediate analysis, resulting in a notable increase of 37% in project success rates (PMI, 2019). AI applications in project management encompass the utilization of predictive analytics to determine schedules, allocate resources, and manage risks [4].

The incorporation of artificial intelligence (AI) into Scrum frameworks improves the management of bioinformatics projects by offering insights based on data, identifying obstacles, and optimizing sprint planning[10]. Research indicates that the use of artificial intelligence (AI) decreases the time required to complete tasks by 30% and enhances the accuracy of data analysis by 25%[11]. AI techniques, such as automated machine learning (AutoML), simplify data analysis, illustrating the advantageous effects of integrating AI with Scrum methods [12].

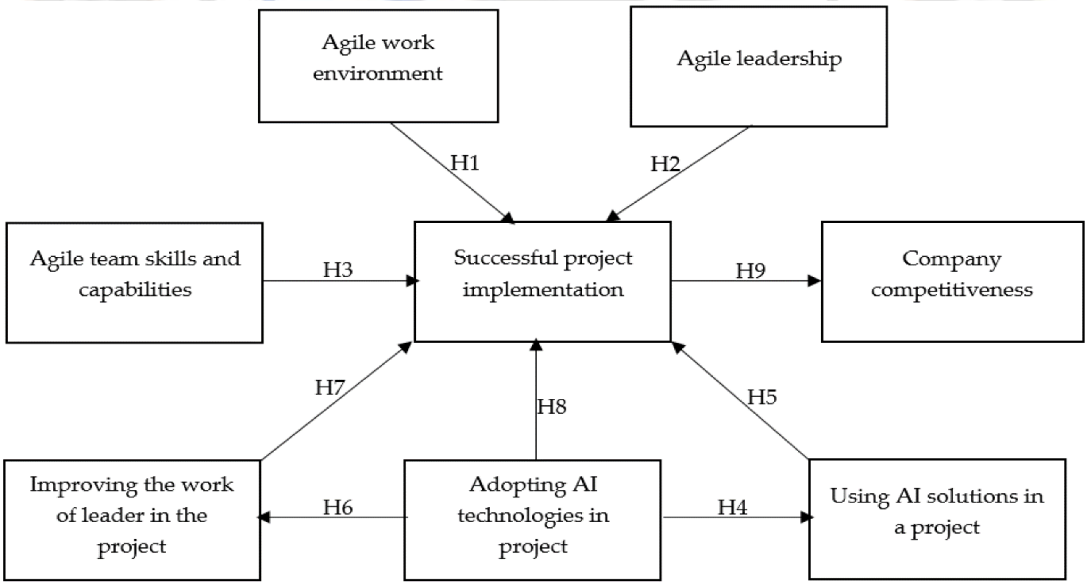


Fig 2.1: AI and Agility model for successful Project Management ("https://pub.mdpi-res.com/information/information-14-00337/article_deploy/html/images/information-14-00337-g001.png?1686821795")

International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 9 Issue: 3
Article Received: *25 December 2020* ***Revised:*** *12 January 2021* ***Accepted:*** *20 February 2021*

RESEARCH GAP

Agile techniques and AI in bioinformatics have improved, yet research gaps persist. Addressing these shortcomings is essential to using Scrum and AI to improve bioinformatics project management.

- **Contributions of Scrum Masters:** Limited research on their functions in bioinformatics. Need analysis on facilitating multidisciplinary communication.
- **Impact of AI on Agile Project Management:** Limited study on AI's impact on bioinformatics agile metrics.AI-Scrum integration frameworks lacking.
- **Quantitative Analysis of AI-Enhanced Agile techniques:** Limited research on AI's impact on bioinformatics-specific agile techniques. Predictive statistical models needed.
- **Case Studies and Practical Applications**: Few real-world examples of AI-Scrum integration in bioinformatics. Need real-world examples of pros and cons.
- **Evaluation criteria for AI and Agile Integration:** No standard criteria for assessing AI in agile frameworks. Need defined criteria to evaluate AI's impact on agile project management.

III. THE ROLE OF THE SCRUM MASTER

The Scrum Master has a vital role in assisting agile project management by assuring the proper implementation and adherence to the Scrum methodology. Key responsibilities include:

- **Facilitation of Scrum Events:** Sprint Planning, Daily Stand-ups, Sprint Reviews, and Retrospectives are led by Scrum Masters. This requires helping the team define reasonable goals and run productive, timed meetings [1].
- **Coaching and Mentoring:** Scrum Masters coach the team on Scrum and agile methods to assist them in understanding their jobs. They coach the Product Owner and stakeholders to enhance team value [6].
- **Impediment Removal:** The Scrum Master must identify and remove barriers to the team's progress. This can include technical challenges and team dispute resolution [9].
- **Shielding the Team:** Scrum Masters keep the team focused on sprint goals by shielding them from outside distractions. Manage stakeholder expectations and avoid scope creep[10].

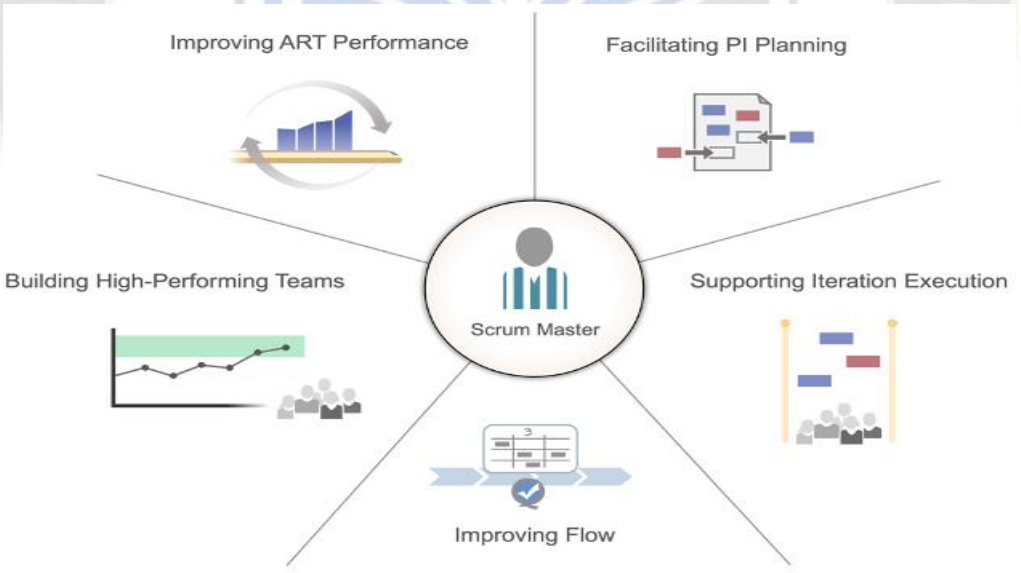


Fig 3.1:Responsibilities of Scrum Master (“https://v5.scaledagileframework.com/wp-content/uploads/2022/08/Scrum-Master_F01_WEB-1.png”)

Impact of Scrum master’s on Team Dynamics and Project Success:

Scrum Masters enhance collaboration and productivity, which affects team dynamics and project outcomes.

- **Enhanced Team Cohesion:** Effective Scrum Masters foster open communication and trust among team members. Project success is 20% higher in cohesive teams [9].
- **Increased Productivity:** Scrum Masters can boost productivity by 25% by removing obstacles and facilitating seamless operations [8].

International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 9 Issue: 3
Article Received: *25 December 2020* ***Revised:*** *12 January 2021* ***Accepted:*** *20 February 2021*

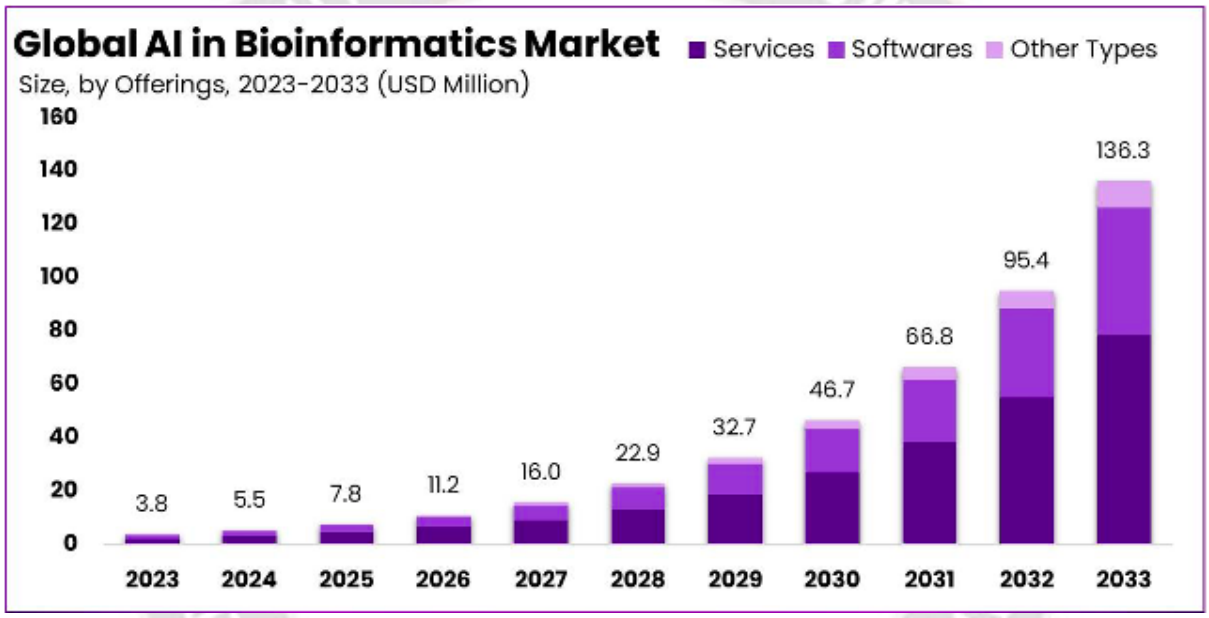
- **Improved Adaptability:** Iterative planning and feedback from Scrum Masters help teams adapt fast. New data and conclusions often change bioinformatics project requirements, making adaptation essential[10].

Impact of AI on Agile Project Management Practices and Outcomes in Bioinformatics :

AI integration into agile project management has several benefits, especially in bioinformatics, where data complexity and volume are major issues.

- **Better Decision-Making:** AI tools help in sprint planning and resource allocation by providing data-driven insights. This optimises project outcomes with more strategic and informed judgments[4].
- **Automated Routine Tasks:** Team members can focus on higher-level analytical work by automating repetitive processes like data pre-treatment with AI. This automation can cut bioinformatics project completion time by 30% [11].
- **Predictive Analytics:** AI-driven predictive analytics can identify project risks and bottlenecks for proactive mitigation. This capability boosts project success by 37% [13].

The AI Bioinformatics market globally is projected in graph 3.1 for the years 2023–2033.



Graph 3.1: Global AI in Bioinformatics market from 2023-2033 ("https://market.us/wp-content/uploads/2024/03/AI-In-Bioinformatics-Market-Growth.jpg")

IV. AI ALGORITHMS IN BIOINFORMATICS AND AGILE TOOLS IN PROJECT MANAGEMENT

A) AI Algorithms in Bioinformatics

Bioinformatics analyses and interprets complex biological data using AI algorithms. AI methods like CNNs, RF, and K-Means Clustering are covered in this section. The computer science method, implementation, mathematical model, and bioinformatics applications of each technique are addressed.

This section covers the following AI algorithms and methods:

1. Convolutional Neural Networks (CNNs):

Algorithm:

CNNs are deep learning algorithms used for image analysis. They are used in bioinformatics for cell imaging and protein structure prediction.

Steps of CNNs:

- **Convolution:** Extract features from input data using convolutional filters.
- **Activation:** To add non-linearity, use an activation function like ReLU.
- **Pooling:** Pooling layers (e.g., max pooling) reduce data spatial dimensions.

International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 9 Issue: 3
Article Received: 25 December 2020 ***Revised:*** 12 January 2021 ***Accepted:*** 20 February 2021

- **Fully Connected Layers:** Use previous layers' neurons in the classification layer.
- **Output:** Make final predictions using learned features.

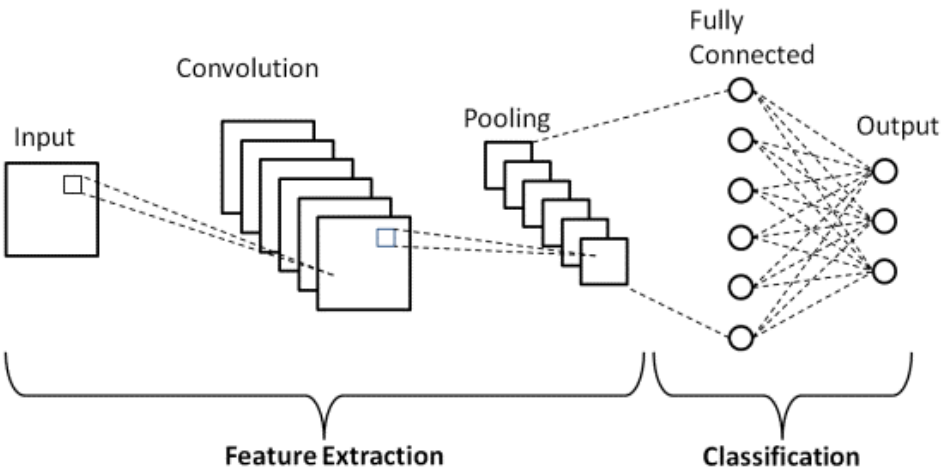


Fig 4.1: Steps of CNNs ("https://d14b9ctw0m6fid.cloudfront.net/ugblog/wp-content/uploads/2020/12/1-4.png")

Mathematical Model:

For a given input X ,a convolutional layer with filter W and bias b produces the output,

$$Y = \sigma(W * X + b)$$

Where, $*$ signifies the convolution operation and σ is the activation function.

Applications:

CNNs are utilized in bioinformatics for image-based applications, including microscope analysis, protein structure prediction, and illness detection in medical pictures [14].

2. Random Forests (RFs):

Algorithm:

RFs classify and regress via ensemble learning. During training, they build several decision trees and output the class mode or tree mean prediction.

Steps of RFs:

- **Bootstrap sampling:** It generates several training data subsets.
- **Tree Construction:** Use random features to build a decision tree for each subset.
- **Aggregation:** Use all tree forecasts to decide.

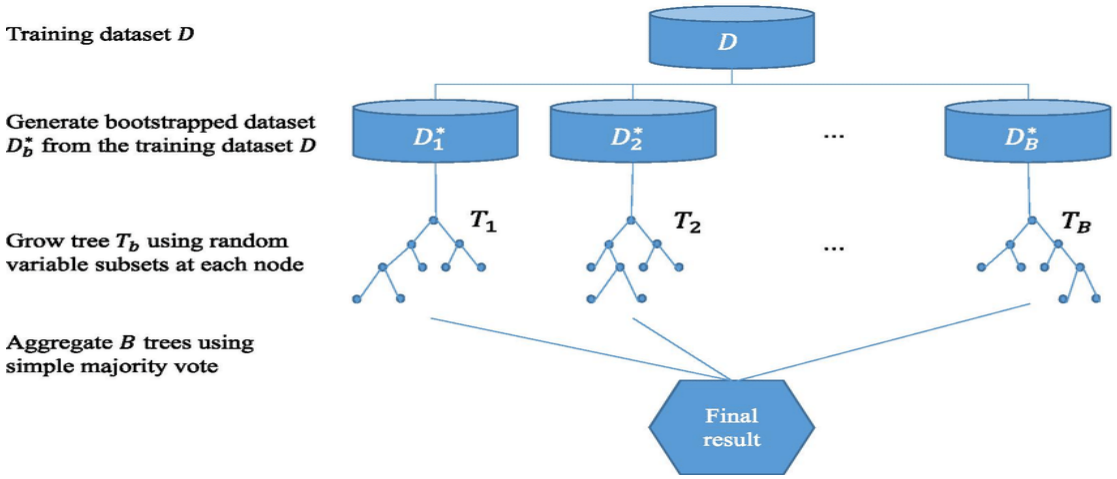


Fig 4.2: Steps of RFs
("https://www.researchgate.net/publication/356441616/figure/fig1/AS:1093173346607105@1637644244185/A-flow-diagram-for-the-random-forest-algorithm-in-the-context-of-classification.png")

International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 9 Issue: 3
Article Received: 25 December 2020 *Revised:* 12 January 2021 *Accepted:* 20 February 2021

Mathematical Model:

For a new instance x , the prediction y' is:

$$y' = \frac{1}{T}\sum_{t=1}^{T} h_t(x)$$

where, T is the number of trees and h_t is the prediction from the $t-th$ tree.

Applications:

Random Forests are utilized in bioinformatics for gene expression analysis, disease classification, and biomarker identification [15].

3. K-Mean Clustering :

Algorithm:

K-Means Clustering is an unsupervised technique that divides data into K feature-similar clusters. The within-cluster sum of squares is reduced.

Steps of K-Mean Clustering

- **Initialization:** Randomly initialize K cluster centroids.
- **Assignment:** Put each data point to the nearest centroid.
- **Update:** Recalculate centroids from assigned data points.
- **Iteration:** Repeat the assignment and update until convergence.

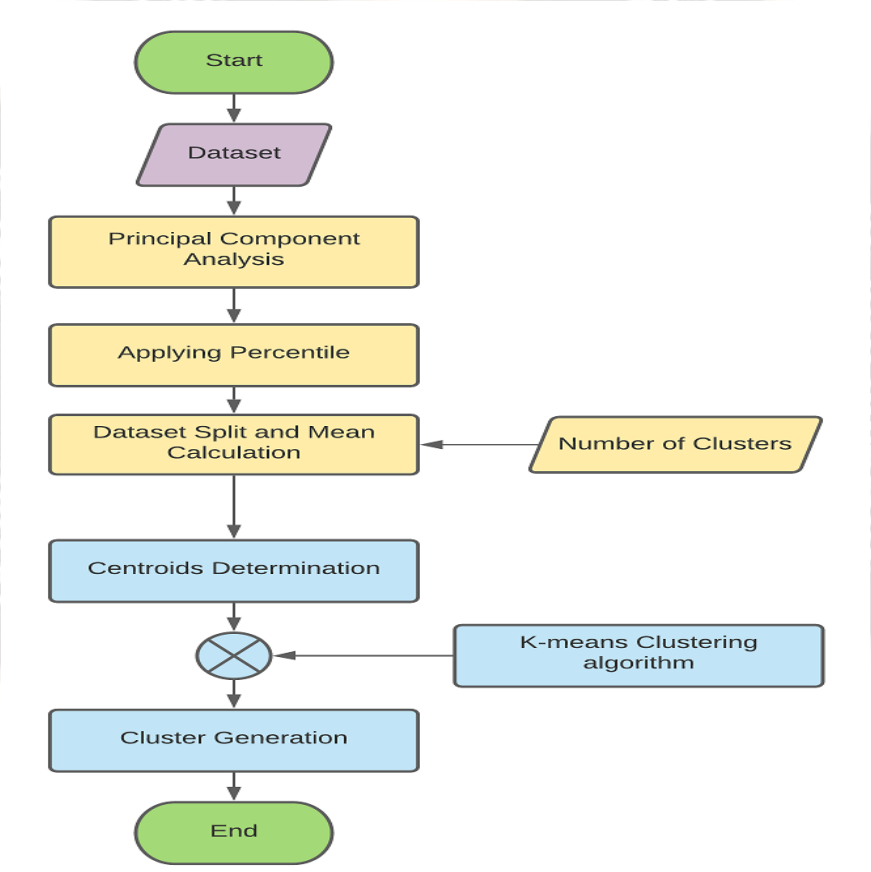


Fig 4.3: Steps of K-Mean Clustering
("https://www.google.com/url?sa=i&url=https%3A%2F%2Ftowardsdatascience.com%2Fefficient-k-means-clustering-algorithm-with-optimum-iteration-and-execution-time-9358a794406c&psig=AOvVaw0Cn3ziQcqiMoUSCe1cGuWw&ust=1716496593219000&source=images&cd=vfe&opi=89978449&ved=0CBIQjRxqFwoTCLC8y6GOooYDFQAAAAAdAAAAABBr")

Mathematical Model:

The objective function to minimize is:

$$J = \sum_{i=1}^{K}\sum_{x\epsilon C_i} \| x - u_i \|^2$$

The set of points in cluster i is denoted by C_i and the centroid of cluster i is represented by μ_i .

Applications:

K-Means is utilized in bioinformatics to cluster gene expression data, group proteins with comparable functions, and segment biological pictures [16].

International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 9 Issue: 3
Article Received: *25 December 2020* ***Revised:*** *12 January 2021* ***Accepted:*** *20 February 2021*

B) Agile Tools and Techniques in Project Management

In the field of bioinformatics, agile methodologies make use of a variety of tools and techniques to effectively manage initiatives. JIRA and Trello, two popular Agile technologies, are compared in this section. Each tool's characteristics, implementation, benefits, and bioinformatics project management applications are discussed.

1. JIRA:

Tool Description : JIRA, an all-encompassing project management application, was created by Atlassian. Real-time collaboration, sprint planning, task monitoring, and backlog management are some of the features it provides. JIRA is extensively utilized in agile software development and is highly configurable.

Applications in Bioinformatics: JIRA is utilized in bioinformatics to manage research assignments, track data analysis workflows, and coordinate team operations[17].

Implementation: Web-based JIRA requires server or cloud configuration. It makes creating projects, boards, and issues easy. Users can configure procedures, add team members, and produce project monitoring reports.

2. TRELLO:

Tool Description : Trello organizes projects into boards, lists, and cards. It suits agile teams because it promotes simplicity and participation. Trello has task cards, checklists, due dates, and integrations.

Applications in Bioinformatics: In bioinformatics, Trello is utilized for controlling research workflows, arranging experiments, and collaborating on data analysis[18].

Implementation: Trello requires account signup and is web- and mobile-friendly. Project boards, task stages (To Do, In Progress, Done), and task cards can be created. Cards can have descriptions, attachments, deadlines, and checklists.

V. COMPARISON OF AI ALGORITHMS IN BIOINFRMATICS AND AGILE TOOLS IN PROJECT MANAGEMENT

Comparison of AI Algorithms in Bioinformatics

The table 4.1 below compares different AI algorithms on the basis of their strengths, weakness and applications.

Algorithm	Strengths	Weaknesses	Applications
Convolutional Neural Networks (CNNs)	Excellent for image analysis; learns complex features	Requires large labelled datasets; computationally intensive	Cell imaging, protein structure prediction, disease detection
Random Forests (RF)	Handles high-dimensional data; interpretable	Prone to overfitting on noisy data; slower for large datasets	Gene expression analysis, disease classification, biomarker identification
K-Means Clustering	Simple to implement; fast convergence	Requires predefined number of clusters; sensitive to initial centroids	Gene expression clustering, protein grouping, image segmentation

Table 5.1: Comparison of AI algorithms in Bioinformatics

Table 4.2 below compares different of AI algorithms on the basis of their performance metrics

Metric	CNN	RF	K-Means
Accuracy	High (depends on data size and quality)	High (with adequate tuning)	Moderate (depends on correct *KK* value)
Computational Efficiency	Low (requires GPUs)	Moderate (parallelizable)	High (fast convergence)
Interpretability	Low (black-box model)	High (decision trees)	Moderate (cluster centroids)
Scalability	Moderate	High	High

Table 5.2: Comparison of Performance Metrics AI algorithms in Bioinformatics

Convolutional neural networks, random forests, and K-means clustering are compared in order to show their individual advantages and uses in bioinformatics. Image analysis tasks are best left to CNNs, classification and regression difficulties

International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 9 Issue: 3
Article Received: *25 December 2020* ***Revised:*** *12 January 2021* ***Accepted:*** *20 February 2021*

to RFs, and clustering jobs to K-Means. When these algorithms are included into bioinformatics processes and agile project management techniques are used, data analysis may be done more accurately and efficiently.

Comparative Analysis of Agile Tools and Techniques in Project Management

A comparative analysis of two project management tools i.e., JIRA and TRELLO are done on the basis of their features in table 4.3.

Feature	JIRA	Trello
Issue Tracking	Comprehensive with customizable fields	Simplified with card-based approach
Agile Boards	Supports Scrum, Kanban, and custom workflows	Supports Kanban-style boards
Collaboration	Real-time collaboration and mention features	Collaborative task assignments
Reporting	Extensive reporting and analytics tools	Basic task metrics and progress tracking
Integrations	Wide range of integrations with other tools	Integrates with popular platforms
Customization	Highly customizable workflows and project setups	Limited customization options
Usability	May have a learning curve for new users	Intuitive and easy to use interface

Table 5.3:Comparative Analysis of JIRA and Trello in Bioinformatics

For bioinformatics agile project management, Trello and JIRA both provide useful tools. Because JIRA offers so many customizing and reporting options, it is appropriate for complicated projects. On the other side, Trello is perfect for smaller teams and simple processes because of its emphasis on visual organization and simplicity. Project complexity, team size, and particular needs in bioinformatics project management will determine which of these technologies is best.

VI. DISSCUSSION

Agile approaches and AI algorithms can improve project management and data analysis in bioinformatics, a fast expanding area. The introduction stressed the importance of Agile techniques in managing big bioinformatics projects and AI algorithms in data-driven insights and decision-making. The following sections covered bioinformatics AI methods such Convolutional Neural Networks (CNNs), Random Forests (RF), and K-Means Clustering, including their computational models, implementation, and applications.

The comparative tables revealed these AI algorithms' strengths, shortcomings, and bioinformatics applications. CNNs had great image analysis accuracy but required a lot of computer power, while RF had interpretability and scalability but might overfit. K-Means Clustering was simpler and faster but used predefined cluster numbers. The comparisons helped choose an algorithm based on project needs and data characteristics.

JIRA and Trello-based Agile bioinformatics project management technologies are also discussed. Each tool's issue tracking, agile boards, communication, reporting, and integrations stood out in the comparison. JIRA's customisation and reporting tools are ideal for complex bioinformatics projects with sophisticated workflows and analytics. Trello's simplicity, visual structure, and ease of use promote collaboration and task visibility for smaller teams and workflows.

Agile approaches, AI algorithms, and bioinformatics project management systems work together to streamline operations, improve team cooperation, and improve decision-making. With AI algorithms for data analysis and Agile project management, bioinformatics teams can solve complex biological problems and make scientific discoveries more efficiently, agilely, and successfully. Technical skills and project management methods must be aligned to traverse bioinformatics research's difficulties.

VII. CONCLUSION AND FUTURE SCOPE

Overall, Agile approaches, AI algorithms, and project management tools have advanced bioinformatics research and project management. The introduction stressed the importance of Agile practices in bioinformatics projects, while the

exploration of AI algorithms like CNNs, RF, and K-Means Clustering revealed their computational models and applications. The comparison tables showed the pros and cons of each method, helping choose one based on project requirements and data characteristics.

JIRA and Trello, Agile bioinformatics project management systems, were also discussed for their particular benefits. JIRA's customization and reporting suit complex bioscience projects, whereas Trello's simplicity and visual organizing suit smaller teams. This combination of technical skills and project management tactics improves bioinformatics workflow, cooperation, and decision-making, helping teams overcome biological hurdles and advance science.

Future work includes integrating AI into Agile frameworks and improving project management tools for biology. This includes creating AI algorithms that can handle larger datasets with improved accuracy and scalability, adapting Agile methodologies to bioinformatics research's dynamic nature, and improving project management tools with collaboration and data visualization. Future bioinformatics project management research should include examine blockchain for data management and machine learning models for predictive analytics. Agile, AI, and project management techniques can advance bioinformatics research and produce significant scientific results in the future.

REFERENCES

[1] Schwaber, K., & Sutherland, J. (2020). The Scrum Guide. Scrum.org.

[2] Libbrecht, M.W. and Noble, W.S., 2015. Machine learning applications in genetics and genomics. *Nature Reviews Genetics*, *16*(6), pp.321-332.

[3] Larranaga, P., Calvo, B., Santana, R., Bielza, C., Galdiano, J., Inza, I., Lozano, J.A., Armananzas, R., Santafé, G., Pérez, A. and Robles, V., 2006. Machine learning in bioinformatics. *Briefings in bioinformatics*, *7*(1), pp.86-112.

[4] Russell, S.J. and Norvig, P., 2016. *Artificial intelligence: a modern approach*. Pearson.

[5] Johnson, C., 2020. Agile and lean concepts for teaching and learning: bringing methodologies from industry to the classroom: edited by David Parsons and Kathryn MacCallum, Singapore, Springer, 2019 edition, 2018, 441 pp.,£ 107.19 (hbk), ISBN-10: 9811327505/ISBN-13: 978-9-81132-750-6.

[6] Rubin, K.S., 2012. *Essential Scrum: A practical guide to the most popular Agile process*. Addison-Wesley.

[7] Beck, K., et al. (2001) The Agile Manifesto. Agile Alliance. http://agilemanifesto.org/

[8] Karlsson, F. and Ågerfalk, P., 2009. Exploring agile values in method configuration. *European journal of information systems*, *18*, pp.300-316.

[9] Stray, V., Sjøberg, D.I. and Dybå, T., 2016. The daily stand-up meeting: A grounded theory study. *Journal of Systems and Software*, *114*, pp.101-124.

[10] Bick, S., Spohrer, K., Hoda, R., Scheerer, A. and Heinzl, A., 2017. Coordination challenges in large-scale software development: a case study of planning misalignment in hybrid settings. *IEEE Transactions on Software Engineering*, *44*(10), pp.932-950.

[11] Hollander, M., Do, T., Will, T. and Helms, V., 2021. Detecting rewiring events in protein-protein interaction networks based on transcriptomic data. *Frontiers in Bioinformatics*, *1*, p.724297.

[12] Feurer, M., Klein, A., Eggensperger, K., Springenberg, J., Blum, M. and Hutter, F., 2015. Efficient and robust automated machine learning. *Advances in neural information processing systems*, *28*.

[13] Project Management Institute (PMI). (2019). Pulse of the Profession: AI Innovators: Cracking the Code on Project Performance.

[14] LeCun, Y., Bengio, Y. and Hinton, G., 2015. Deep learning. *nature*, *521*(7553), pp.436-444.

[15] Breiman, L., 2001. Random forests. *Machine learning*, *45*, pp.5-32.

[16] MacQueen, J., 1967, June. Some methods for classification and analysis of multivariate observations. In *Proceedings of the fifth Berkeley symposium on mathematical statistics and probability* (Vol. 1, No. 14, pp. 281-297).

[17] Atlassian. (n.d.). JIRA Software Features. Retrieved from https://www.atlassian.com/software/jira/features

[18] Trello. (n.d.). Trello Features. Retrieved from https://trello.com/en-US/features