

Prediction of Protein Level in Food using Machine Learning

Submitted in partial fulfillment of the requirements
for the award of
Bachelor of Engineering Degree in Computer Science and Engineering
By

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(DEEMED TO BE UNIVERSITY)
Accredited with Grade "A" by NAAC
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MARCH 2021



SATHYABAMA

INSTITUTE OF SCIENCE AND TECHNOLOGY
(DEEMED TO BE UNIVERSITY)

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BONAFIDE CERTIFICATE

This is to certify that this project report is the bonafide work of **OBULAPURAM ANIL KUMAR** (Reg. No. 37110524) and **PANJALA AKSHITH GOUD** (Reg. No. 37110541) who carried out the project entitled “**Prediction of Protein Level in Food using Machine Learning**” under my supervision from **August 2020** to **March 2021**.

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DECLARATION

I **OBULAPURAM ANIL KUMAR(Reg.no.37110524)** hereby declare that the Professional training Report entitled **“Prediction of Protein Level in Food using Machine Learning”** done by me under the guidance of **Mrs. B. KEERTHI SAMHITA, M.Tech ., (Ph.D).**, is submitted in partial fulfillment of the requirements for the award of Bachelor of Engineering degree in Computer Science and Engineering.

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ACKNOWLEDGEMENT

I am pleased to acknowledge my sincere thanks to **Board of Management of SATHYABAMA** for their kind encouragement in doing this project and for completing it successfully. I am grateful to them.

I convey my thanks to **Dr. T. SASIKALA., M.E., Ph.D.**, Dean, School of Computing and **Dr. S. VIGNESHWARI M.E., Ph.D.**, and **Dr. L. LAKSHMANAN M.E., Ph.D.**,

Head of the Department, Dept. of Computer Science and Engineering for providing me necessary support and details at the right time during the progressive reviews.

I would like to express my sincere and deep sense of gratitude to my Project Guide **Mrs.B.KEERTHI SAMHITA, M.Tech ., (Ph.D).**, for her valuable guidance, suggestions and constant encouragement paved way for the successful completion of my project work.

I wish to express my thanks to all Teaching and Non-teaching staff members of the Department of **Computer Science and Engineering** who were helpful in many ways for the completion of the project.

ABSTRACT

Protein forecasting is the deduction of the 3D proteins that are structural from their acids(amino) sequences, which involves the prediction of its folding and the secondary structure from the cheif sequence. New proteins on discovery are subject to structure prediction. A linear protein structure is derived from the protein in the form of chains which is the primary structure. The chain provides information about arrangement of the amino acids that is helix, strands, loops and turns. There are several algorithms that have been used to predict the structure of the protein. Although plenty of protein sequence data is available online, it was not easy to acquire data that was pretty classified with labels. We scraped information from various websites allowing us to get class labels for our unsupervised data set. Our attempt uses Feature Vectors methodology to generate a transformed view of the protein sequences, which are then used as input to classifiers like Random Forest and Naive Bayesian. With this we are able to differentiate and disparity the precision and accuracy of the predicted sequences. Results of the comparison will provide deep insights in methodologies used for structure prediction in the future. Our research yields the best result using the Random Forest Classifier with an astounding accuracy of 96%.

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LIST OF ABBREVIATIONS

ABBREVIATION	EXPANSION
API	Application program interface
Bg	Back ground
UI	User Interface
GUI	Graphical user interface
ISVM	Improved Support Vector Machine
OpenCV	Open Source Computer Vision
SDK	Software Development Kit

CHAPTER 1

INTRODUCTION

1.1 INTRODUCTION ON PROJECT

Proteins are chains of Amino Acids otherwise known as building blocks. DNA holds the data and Protein accomplish the work. The essential design of enzyme mentions to the grouping of acids called amino in the biological molecules sequences. The required construction is happened along with by biological molecules that are made during the interaction of amino acids biogenesis. The both closures of the biological molecules attached are suggested to as the carboxyl end (C-end) and the amino end (N-end) in illumination of the plan of the liberty grouping on each restriction. The essential pattern of amino acid is managed by the standard connecting to the amino acids. A specific succession of adenosine diphosphates in DNA is interpreted in the direction of mRNA, which is examined by the complex molecular machine in an interaction known as exposition. The positioning of proteins in novolin was established by Frederick Sanger¹, building up that amino acids have distinguishing protein caustic assemblings. The succession of a amino acids is special to that amino acid, and characterizes the design and capacity of the amino acid. The organising of a amino acid can be uttered by strategies, for ex, Edman degradation² or pair mass spectrometry. Generally, be that as it may, it is examined directly from the arrangement of the standard making use of the inherited code. After interpreting the change, for example, disulfide bond arrangement, phosphorylations and glycosylations are normally likewise notion to be a part of the required construction, and cannot be examined from the standard. For example, Novolin consists of 51 proteins in two sequences. One sequence has 31 proteins, and the second one has 20 proteins.

1.2 PURPOSE

Computationally anticipated three-dimensional design of proteins has exhibited the value in numerous territories of biomedicine, going from inexact family medical care measures to exact medication screening. In any case, or almost

40 years the precision of the anticipated models has been directed by the

accessibility of close underlying formats. Progress has as of late been accomplished in refining low-goal structures nearer to the local ones; this has been made conceivable by joining information based data from numerous wellsprings of primary layouts. Tragically, no fundamental advancement in the improvement of procedures for distinguishing distantly homologous formats and for anticipating novel protein structures.

1.3 SOFTWARE REQUIREMENTS

- Operating System - Windows XP
- Language for coding - PYTHON
- IDE - Jupyter Notebook
- Database - EXCEL

1.4 HARDWARE REQUIREMENTS

- System - Windows 8/10
- Speed - 2.4GHZ
- Hard disk - 40GB
- Monitor - 15VGA color
- RAM - 4GB

CHAPTER 2

LITERATURE SURVEY

2.1 ANALYSIS OF THE LITERATURE

Writing overview is the principle advance in programming improvement measure. Prior to expanding the instrument it is essential to choose to measure time, wealth and companions power. At the point when these objectives are fulfilled, by that time the resulting stage is to sort out which working structure and speech are used for evolving the gadget. At the point when the designers start collecting the device the engineers need collection of exterior assistance. This assistance can be gotten from higher engineers, from notes publications or from destinations. The significant piece of the task development area contemplate and entirely read every one of the required essentials for raising up the journey. Prior to raising up the apparatus and the connected planning it is major to answerable and review the amount of time, requirement of assets, labor, wealth, and companion strength. Before constructing the structure the afore mentioned idea are taken into account for developing the suggested system. The critical part of the endeavor progression zone takes the consideration and totally overview every one of the fundamental prerequisites for developing the endeavor. For each endeavor Writing opinion is the fundamental zone in coding enhanced measure. Prior to developing the equipments and the connected arranging it is critical to choose and survey the amount of time, resource essential, work, wealth, and companions strength. At the point when these things are satisfied and totally read, by then the accompanying platform is to choose regarding the item subtleties in the different system, for instance, which kind of working structure the endeavor would be needed and to a great extent the significant writing computer programs are relied upon to proceed with the resulting stage like structure up the mechanical assemblies, and the connected exercises. Here we have taken the overall studies of various makers and noted down the key focal issues as for their work. In this endeavor writing study accepts a common part in get resources from various regions and every one of the associated focuses that are especially significant under this section. The most magnificent perspective

if this is the way where things get all together and urges us to suite our work as indicated by the current data.

2.2 LITERARY REVIEWS

"Mixture Counterfeit Honey bee Province and Molecule Multitude Advancement"

Mirzaei S, T. Sidi, C. Keasar, and S. Crivelli (2016)

Proteins are significant in the organic cycles, and their construction decides if they can work well or not. Since the hypothesis introduced by Anfinsen that proteins space structure is totally dictated by the essential construction came out, it is feasible for us to foresee the design of proteins through their essential design with no examination. To arrive at this objective, the expectation issue can be figured as a streamlining issue that is set to track down the most minimal free energy conformity. In this paper¹, a cross breed Counterfeit Honey bee State (ABC) with Molecule Multitude Enhancement (PSO) Calculation is utilized to tackle this issue. Taking into account that the two calculations have corresponding attributes, consequently by consolidating them together outcomes in better advancement results through this test approach.

"Prediction of protein structural classes using Improved Support Vector Machine (ISVM)" Zhou H., and Skolnick J. (2011)

As a rule, the hole is expanding quickly among the quantity of realized amino acids arrangements and the quantity of familiar amino acids primary structures. To defeat this emergency, it is fundamental to build up a calculated expectation strategy for quick and unequivocally deciding the protein primary class. In light of the anticipated optional design data, the protein amino acid structures are anticipated. To assess the exhibition of the suggested calculation with the current calculations, 4 sets of data , to be specific 25PDB, 1189, D640 and FC699 are utilized. In this work¹ , an enhanced Help Vector Network (ISVM) is suggested to anticipate the amino acids underlying structures. The examination of output shows that enhanced Help Vector Network (ISVM) forecasts high precise amino acid underlying structure than the current calculations. The current calculations to be specific Help Vector Machine (SVM), Nave Bayes and the proposed Improved Help Vector Network

(ISVM) calculations are contrasted with foresee the amino acid primary structures. From the outcomes delivered, it is construed that the ISVM calculation gives preferable

outcomes over the current calculations.

“Parallel Ant Colony Optimization using the HP Lattice Model” Khoury G. et al., (2014)

The Protein Collapsing Issue considers the manner by which a amino acid – a sequence of proteins - will 'overlay' to the normal state. Foreseeing the manner by which different amino acids overlay can be central in creating medicines of infections like Alzheimer's and Cystic Fibrosis. Traditional answers for computing the nal conformity of a amino acids classes are asset concentrated. The (HP) strategy is one method of improving on the issue. We present a story strategy for taking care of the HP protein collapsing issue in both two and three measurements utilizing Insect Province Enhancements and an appropriated programming paradigm¹ . Tests Across few processors show that the numerous province disseminated ACO (MACO) approach is adaptable and outflanks. single state executions. The Hydrophobic- Hydrophilic (HP) grid was created to improve on the issue while keeping up social importance. As of not long ago the 3D HP model has been to a great extent overlooked for the two dimensional HP model because of the straightforwardness of the inquiry area and simple perception. The worked on HP structures have been demonstrated to be NP-Finished in this manner giving an ideal stage to assessing and enhancing interested calculations that are going to help succeeding improvement of extended amino acid collapsing issues. A significant part of the past work in this field zeroed in on creating and executing answers for 2D protein collapsing without thinking about 3D executions. The paper proposes a calculation that can settle the 3D HP protein collapsing issue by stretching out the answer for the 2D HP issue.

CHAPTER 3

AIM AND SCOPE OF THE PRESENT INVESTIGATION

3.1 AIM

The aim of the project is to let people know about their food calories, proteins, Carbohydrates, Fats.

3.2 OBJECTIVES

We want to aid in the development of medical science. Drug development in particular requires knowledge of the binding sites of the candidate compounds, a well predicted structure helps in the computational screening and optimizing candidate compounds. Identifying the mechanism by which a protein functions and how it folds is of great curiosity for researchers and students alike. Taking this into account, we look to present a case study which will provide insights on the most accurate algorithm for structure prediction using feature vectors.

3.3 SCOPE OF THE PRESENT INVESTIGATION

Computationally anticipated three-dimensional construction of proteins has exhibited the value in numerous zones of biomedicine, going from surmised family medical care measures to exact medication screening. Notwithstanding, or almost 40 years the exactness of the anticipated models has been directed by the accessibility of close primary formats. Progress has as of late been accomplished in refining low- goal structures nearer to the local ones; this has been made conceivable by joining information based data from various wellsprings of underlying layouts. Shockingly, no fundamental advancement in the improvement of strategies for identifying distantly homologous formats and for anticipating novel protein structures.

CHAPTER 4

EXPERIMENTAL OR MATERIALS AND METHODS

ALGORITHMS USED

4.1 EXISTING SYSTEM

A longstanding issue in set up scientists is the examination of amino acids. Amino acids, that are the design squares of presence, are made out of related proteins and cover into 3D developments that chooses own abilities. Data on the developments is basic for the meaning of found medications, the examination of diseases, and nearby amino acids planning. Choosing the 3D developments of the amino acids along testing is expensive and drawn-out. On the other hand we can use a PC to make huge number of likely 3D developments for each amino corrosive and a while later sort out which one among the assumptions is the wonderful.

4.2 SYSTEM CAPABILITIES

The information arrangement is the association between the information structure and the customer. It incorporates the making assurance and procedures for data game plan and those methods are critical to put trade data in to a usable design for taking care of can be cultivated by inspecting the PC to scrutinize data from a made or printed file or it can occur by having people entering the data clearly into the system. The arrangement of data revolves around controlling the proportion of data required, controlling the mix-ups, keeping an essential separation from delay, evading extra methods and keeping the association direct. The data is arranged in such a way so it outfits security and convenience with holding the insurance. Data Arrangement considered the going with things:

What information ought to be given as info?

How the information ought to be orchestrated or coded?

The discourse to direct the working faculty in giving info.

Strategies for getting ready information approvals and steps to follow
when blunder happen

A standard yield is single, which gathers the necessities of the one side agent and presents the information unmistakably. In any structure significance of preparing are divided to the agents and to other framework along surrender. In relent plan it is set on how the information is to be dislodged for guaranteed need and next the printed version relent. It is the highly important and straight source information to the agent. Proficient and insightful relent specifications increases the structural connection to assist agent dynamic.

The relent kind of a information structure have to achieve minimum one of the going with targets. Target information about previous activities, present situation or estimation of the

Future.

Wave specific instances, aperture, problems, or attentive.

Activate an event.

Affirm a project.

4.3 SYSTEM FUNCTIONALITIES

4.3.1 FUNCTIONAL REQUIREMENTS

It is a specialized determination prerequisite for the product items. It is the initial phase in the necessity examination measure which records the prerequisites of specific programming frameworks including useful, execution and security necessities. The capacity of the framework relies chiefly upon the quality equipment used to run the product with given usefulness.

- **Usability**

It indicates how simple the framework should be use. It is not difficult to ask inquiries in any organization which is short or long, watchman stemming calculation animates the ideal reaction for client.

- **Robustness**

It alludes to a program that performs well under common conditions as well as under abnormal conditions. It is the capacity of the client to adapt to mistakes for unimportant questions during execution.

- **Security**

The condition of giving ensured admittance to asset is security. The framework gives great security and unapproved clients can't get to the framework there by giving high security.

- **Reliability**

It is the likelihood of how regularly the result comes up little. The prediction is regularly transmit in MTBF (Mean Time Between Disappointments). The prerequisite is required to guarantee that the cycles work accurately and totally without being cut off. It can deal with any heap and endure and endure and surprisingly fit for working around any disappointment.

- **Compatibility**

It is upheld by variant over all internet browsers. Utilizing any web workers like localhost makes the framework ongoing experience.

- **Flexibility**

The adaptability of the undertaking is given so that is can run on various conditions being executed by various clients.

- **Safety**

Security is an action taken to forestall inconvenience. Each inquiry is prepared in a tied down way without letting others to know one's very own data.

4.3.2. NON- FUNCTIONAL REQUIREMENTS

- **Portability**

It is the convenience of similar programming in various conditions. The venture can be run in any working framework.

- **Performance**

These prerequisites decide the assets wanted,space stretch, output and all that manages the exhibition of the framework.

- **Accuracy**

The aftereffect of the mentioning inquiry is exceptionally exact and high velocity of recovering data. The level of safety given by the framework is high and powerful.

- **Maintainability**

Undertaking is basic as additional updates can be handily managed without influencing its soundness. Practicality fundamentally characterizes that that it is so

natural to keep up the framework. It implies that that it is so natural to keep up the framework, dissect, change and test the application. Viability of this task is basic as

additional updates can be handily managed without influencing its strength.

4.4 REQUIREMENT SPECIFICATION

This proposed programming runs successfully on a figuring framework that has the base prerequisites. Undertaking all the gear necessities are not fulfilled yet rather exist in their frame works organization between the client's machines as of now. So the principle need is to present proper gear for the item.

The prerequisites are part into two classes, in particular:

Software Requirements

- Operating System - Windows XP
- Coding language - PYTHON
- IDE - Jupyter Notebook
- Database - EXCEL

Hardware Requirements

- System - Windows 8/10
- Speed - 2.4GHZ
- Hard disk - 40GB
- Monitor - 15VGA color
- RAM - 4GB

4.5 MODULES

Collection and Analysis of Data

Collection and Analysis of Data using Selenium for extracting protein data from websites by processing the HTML Web Page and extracting data for manipulation to a local storage. Once the protein sequences are stored locally, the application can run without an internet connection. Protein Data Banks¹ contain millions of sequences and the whole process was parallelised using Java and multithreading

to increase computational performance. The sequence data that is collected from

the internet had a mix of protein and non-protein data (such as DNA and RNA) which was filtered and cleansed for our requirement.

Design and Development of Feature Vector

Design and Development of Feature Vector which is a measurable entity or characteristic that is used to describe an attribute or feature of the objects. Selection of feature vectors is key to improving the performance of the predictor algorithm, for structure prediction the features selected need to have direct correlation to the three dimensional structure of the protein. The four feature vectors most suitable for us are Hydrophobicity, Polarizability, Polarity and Van der Waals Volume. These features are combined in a matrix to improve the efficiency of the vector.

Parallel programming

Parallel programming Structure prediction is a computationally expensive and time consuming process. In order to overcome this, we designed a parallel programming predictor by sending sequences to multiple classifiers at once, this increases the overall performance and usability of the application as the users can compare the results returned by the classifiers simultaneously. Further, the data collection process was done parallelly by scraping multiple websites at once.

Design of UI

Design of UI that provides an interactive interface to run the sequence search either parallel or in sequence, based on the users requirements. The UI displays the feature vector along with the predicted structures. We kept the UI minimalistic and straight forward to aid in convenience to the users who may comprise of research students or scientists.

4.6. DESCRIPTION OF DIAGRAM

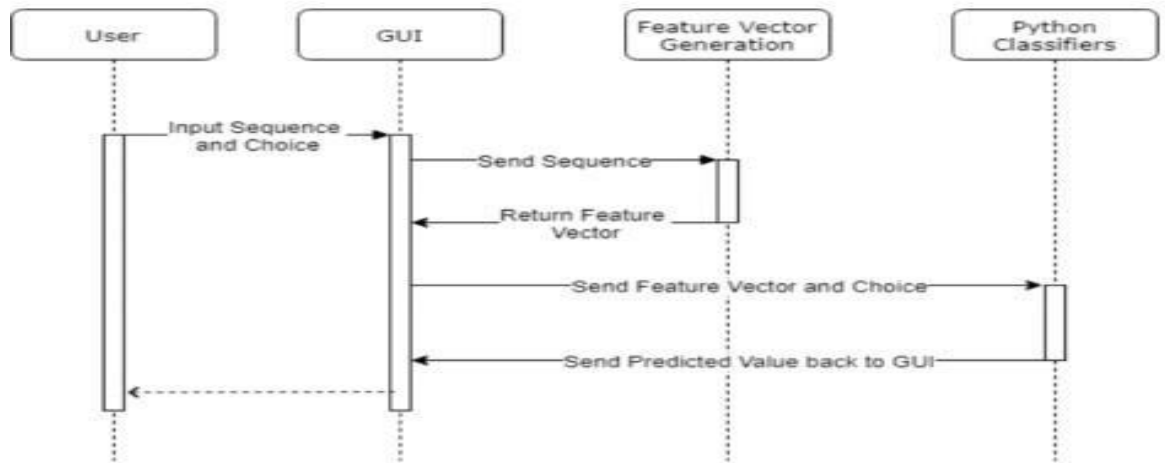


Fig 4.6: BLOCK DIAGRAM

In Fig 4.1 of the block is examined in this position and strategic agreement is modern with an exceptionally wide positioning for the undertaking and some quotes. During structure enquiry of the suggested structure is made. This is to warranty that the suggested structure isn't a weight to the company. For practicality inspected understanding, some understanding of the notable requirements for the structure is basic.

Three key contemplations associated with the investigation are

◆ ECONOMICAL FEASIBILITY

This examination is done to check the money related impact that the system will have on the affiliation. The proportion of resource that the association can fill the inventive work of the system is limited. The utilizations ought to be upheld. Thusly the made structure additionally inside the spending plan and this was cultivated considering the way that by far most of the advancements used are transparently available. Simply the changed things should be purchased.

◆ TECHNICAL FEASIBILITY

This assessment is finished to check the specific feasibility, that is, the particular necessities of the system. Any structure made ought not have a prominence on the open particular resources. This will incite high demands on the open particular resources. This will incite high demands being put on the client. The made system ought to have a modest essential, as unimportant or invalid changes are required for completing this structure.

◆ SOCIAL FEASIBILITY

The piece of study is to check the level of affirmation of the structure by the customer. This joins the route toward setting up the customer to use the structure successfully. The customer ought not feel undermined by the system, rather ought to recognize it as a need. The level of affirmation by the customers solely depends upon the strategies that are used to show the customer the system and to make him familiar with it. His level of sureness ought to be raised so he is in like manner prepared to make some important investigation, which is welcomed, as he is the last customer of the system.

4.7 ARCHITECTURAL DESIGN

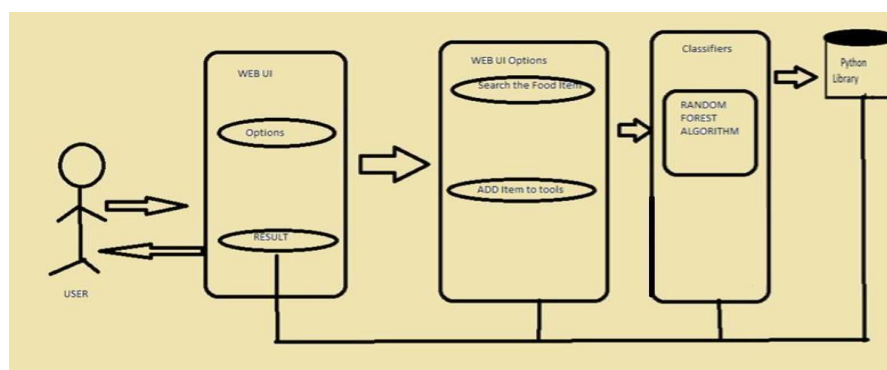


Fig 4.7: Architectural Diagram

4.8 USE CASES

A use case graph in the Unified Modeling Language (UML) is a sort of directed diagram described by and produced using a Use case examination. Its inspiration is to present a graphical diagram of the handiness given by a system to the extent performers, their targets (tended to as use cases), and any conditions between those usage cases. The standard inspiration driving a usage case layout is to show what system limits are performed for which performer. Occupations of the performers in the structure can be depicted.

RESULTS AND DISCUSSION

Find out how many calories you consume

Search Food Database

My Totals:

Page 1

Total Calories: 0

Created by Anil & Akshith

Fig5.1 Main Page

This is the Main opening page where we can search the food item. (Fig5.1)

Find out how many calories you consume

dosa

My Totals:

	Dosa 1 serving 168 calories	

Page 1

Total Calories: 168



Serving size: **1** medium dosa
Calories (1 serving): **168**
Calories (100 gr): **174**

Dosa

Amount of Servings:

Fat: **4** grams
Carbohydrates: **29** grams
Protein: **4** grams

Created by Anil & Akshith

Fig5.2 Dosa protein details

Here we can see the image of dosa and its fats, carbohydrates, proteins and finally calories of the food item. (Fig5.2)

Find out how many calories you consume

My Totals:

	Dosa 1 serving 168 calories	
	Milk 1 serving 125 calories	

Page 1

Total Calories: 293



Milk

Amount of Servings:

-
1
+

Add to My Totals

Fat: **5** grams
Carbohydrates: **12** grams
Protein: **9** grams



Serving size: **1 cup**
Calories (1 serving): **125**
Calories (100 gr): **51**

Created by Anil & Akshith

Fig5.3 Milk Protein details

Here we can see the image of milk and its fats, carbohydrates, proteins and finally calories of the food item. (Fig 5.3)

Find out how many calories you consume

My Totals:

	Dosa 1 serving 168 calories	
	Milk 1 serving 125 calories	
	Chicken 1 serving 187 calories	
	Egg 1 serving 72 calories	

Page 1

Total Calories: 552



Egg

Amount of Servings:

-
1
+

Add to My Totals

Fat: **5** grams
Carbohydrates: **0** gram
Protein: **6** grams



Serving size: **1 large**
Calories (1 serving): **72**
Calories (100 gr): **144**

Created by Anil & Akshith

Fig5.4 Egg Protein details

Here we can see the image of eggs and its fats, carbohydrates, proteins and finally calories of the food item. (Fig5.4)

Find out how many calories you consume



Dosa

1 serving

168 calories



Milk

1 serving

125 calories



Chicken

1 serving

187 calories



Egg

1 serving

72 calories



Kiwi

1 serving

42 calories

Page 1

Total Calories: 594



Serving size: 1 fruit (2" dia)

Calories (1 serving): 42

Calories (100 gr): 61

Kiwi

Amount of Servings:

-

1

+

Add to My Totals

Fat: 0 gram

Carbohydrates: 10 grams

Protein: 1 gram

Fig5.5 Kiwi Protein details

Find out how many calories you consume

My Totals:



Cashew
1 serving
9 calories



Page 1

Page 2

Total Calories: 603



Serving size: 1 cashew
Calories (1 serving): 9
Calories (100 gr): 573

Cashew

Amount of Servings:

-

1

+

Add to My Totals

Fat: 1 gram
Carbohydrates: 1 gram
Protein: 0 gram

Fig5.6 Cashew Protein details

Here we can see the image of cashew and its fats, carbohydrates, proteins and finally calories of the food item. (Fig5.6)

Find out how many calories you consume



Cashew
1 serving
9 calories





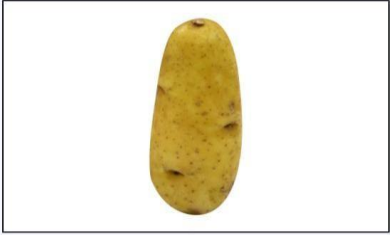
Potato
1 serving
161 calories



Page 1

Page 2

Total Calories: 764



Serving size: 1 potato medium
Calories (1 serving): **161**
Calories (100 gr): **93**

Potato

Amount of Servings:

-

1

+

Add to My Totals

Fat: 0 gram
Carbohydrates: 37 grams
Protein: 4 grams

Created by Anil & Akshith

Fig5.7 Potato Protein details

Here we can see the image of potato and its fats, carbohydrates, proteins and finally calories of the food item. (Fig5.7)

CHAPTER 6

CONCLUSION AND FUTURE WORK

CONCLUSION

We have built a ML model which predicts the two dimensional structure of the protein from their amino acid sequences. Deciding the three-dimensional construction of protein atoms is an essential concentration for some parts of present day organic examination. Our model takes the primary protein sequence as input and outputs the three-dimensional structure to which the protein folds. This can be used in various Drug development which in particular requires knowledge of the binding sites of the candidate compounds, a well- predicted structure helps in the computational screening and optimizing candidate compound. The unsupervised dataset to train our Machine Learning model is a straight sequence of proteins which forms the main framework of the amino acids. We extracted information from various websites allowing us to get class labels for our unsupervised data set. We have generated a unique Feature Vectors for each protein sequences based on Polarity, Hydrophobicity, Polarizability and Van der Waals Volume. We then used various classification models which are used to analyze and predict class labels for each entered sequence. Our initial approach of using Nave Bayesian classifier yielded an accuracy of approximately 47%.

FUTURE WORK

The secondary structure of the protein gives a good indication of what the protein is majorly made up off. We've developed a system with three classifiers that predict the secondary structure of protein and gives the bioinformaticians a one stop shop and access to different methods in predicting the actual structure that a chain of proteins would form. The next framework is essential along with angles that the amino acids make with each other to give the final tertiary structure of the protein. This third framework is the naturally occuring structure of the amino acid in nature. These various structures depend on the amino acids that form these chains and the twists and turns occur due to the interactions between these acids. The tertiary structure of proteins is an important field is the drug making industry. Pharmacists and bioinformaticians study

these structures and collaborate in making these drugs. Hence its extremely important to know minute details in these structures as minimal changes make a huge difference in the

structure. By getting the amino acid chains and passing it to the classifiers which have been trained on huge datasets the accuracy of certain classifiers has been found out to give better accuracy as compared to the others. Addition of other classifiers as well as implementation of the prediction of the tertiary structure of proteins in this system can make it a comprehensive tool for bioinformaticians to predict the structures of proteins from their amino acids sequences and compare results of various machine learning algorithms for the same sequence. The smallest of details can be added to classifiers to make them take into consideration all the factors that would result in a real world structure of the protein. Physical devices need not be used and precious time need not be wasted on identifying the structure of protein which is all taken care by the system trained on large datasets and working on a system running several machine learning algorithms simultaneously to make the human effort in prediction minimal.

REFERENCES

- [1] Mirzaei S, T. Sidi, C. Keasar, and S.Crivelli (2016), Absolutely Primary Protein Scoring Capacities Utilizing Backing Vector Machine and Gathering Learning, IEEE/ACM Exchanges.
- [2]Zhou H., and Skolnick J. (2011), GOAP: a Generalized Orientation Dependent, All-Atom Statistical Potential for Protein Structure Prediction, Biophysical Journal, vol. 101, no. 8, pp. 2043- 2052.
- [2]Zhou H., and Skolnick J. (2011), GOAP: a Summed up Direction Needy, All-Iota Measurable Potential for Protein Construction Forecast, Biophysical Diary, vol. 101, no. 8, pp. 2043-2052.
- [3]Khoury G. et al., (2014), We Overlap: A Coopetition for Protein Construction Expectation. Proteins: Design, Capacity, and Bioinformatics; 82(9): 1850-1868, doi: 10.1002/prot.24538.
- [4]Faraggi E. also, Kloczkowski A. (2014), A worldwide AI based scoring capacity for protein structure expectation, Proteins: Design, Capacity, and Bioinformatics, vol. 82, no. 5, pp. 752-759.
- [5] Computational Science and Bioinformatics, Volume: PP Issue: 99. DOI: 10.1109/TCBB.2016.2602269.
- [6] Pollastri, Gianluca, et al., (2011), Improving the expectation of protein auxiliary design in three and eight classes utilizing intermittent neural organizations and profiles." Proteins: Construction, Capacity, and Bioinformatics 47.2: 228-235.
- [7] Zaremba W. et al. (2014), Intermittent Neural Organization Regularization, arXiv preprint arXiv:1409.2329.
- [8] Keasar C et al., (2017). "An Evaluation of WeFold: A System of Global Collective Pipelines for Protein Construction Forecast." submitted to Logical Reports.
- [9] A.C.M. May. Toward more significant various leveled characterization of amino acids scoring capacities. Protein Designing, 12:707-712, 2011.
- [10] Marco Tulio Ribeiro Sameer Singh Carlos Guestrin 2016, Prologue to Nearby Interpretable Model-Rationalist Clarifications (LIME) A procedure to clarify the machine learning.

APPENDIX

A. PLAGIARISM REPORT

akob3070@gmail.com.pdf			
ORIGINALITY REPORT			
9%	1%	8%	2%
SIMILARITY INDEX	INTERNET SOURCES	PUBLICATIONS	STUDENT PAPERS
PRIMARY SOURCES			
1	Bogdan Czejdo, Sambit Bhattacharya, Catherine Spooner. "Improvement of Protein Model Scoring Using Grouping and Interpreter for Machine Learning", 2019 IEEE 9th Annual Computing and Communication Workshop and Conference (CCWC), 2019 Publication		5%
2	Submitted to Chino Valley Unified School District Student Paper		1%
3	Submitted to Ain Shams University Student Paper		1%
4	"Hybrid Evolutionary Algorithms", Springer Science and Business Media LLC, 2007 Publication		1%
5	Daniel Chu, Albert Zomaya. "Chapter 9 Parallel Ant Colony Optimization for 3D Protein Structure Prediction using the HP Lattice Model", Springer Science and Business Media LLC, 2006 Publication		1%

B. JOURNAL PAPER

FOOD PROTEIN LEVEL PREDICTION

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ABSTRACT- Currently, The prediction of protein structures involves the prediction of their folding and the secondary structure from their primary sequence, which deduces a protein's three-dimensional amino acid structure sequence. New proteins on discovery are subject to structure prediction. A linear protein structure is derived from the protein in the form of chains which is the primary structure. The chain provides information about the arrangement of the amino acids that is helix, strands, loops and turns. To predict the structure of the protein, several algorithms were used. Although plenty of protein sequence data is available online, it was not easy to acquire data that was pretty classified with labels. We scraped information from various websites allowing us to get class labels for our unsupervised data set. Our attempt uses Feature Vectors methodology to generate a transformed view of the protein sequences, which are then used as input to classifiers like Random Forest and Naive Bayesian. With this, we can compare and contrast the precision and accuracy of the predicted sequences. Results of the comparison will provide deep insights into methodologies used for structure prediction in the future. The Random Forest Classifier, which we used in our study, generated the best results, with a remarkable accuracy of 96%.

Keywords: - Machine Learning, Amino acids, Random Forest, Bayes Classifier.

1.INTRODUCTION:

Proteins consists of linkage of amino acids, which are the basic structures of life. DNA holds the information and Protein do the work. The original protein refers to the polypeptide protein sequence. The protein chain in the polypeptide sequence is known as the original structure of a protein. Peptide bonding during protein biosynthesis mainly holds the structure together. The both edges of the polypeptide links are known as the carboxyl terminus (C-termus) and the amino endus (N-terminus), based on the free group nature of each end. The original protein format is described by the protein-related gene. The ribosome reads a certain nucleotide sequence in DNA into mRNA during a translation process.

Frederick The protein sequence is unique and defines the protein's structure and function. There are 31 amino acids in one chain and 20 amino acids in the other chain.

1. LITERATURE SURVEY:

[1] Hybrid Artificial Bee Colony and Particle Swarm Optimization

In biological processes, proteins are crucial and their format describes them or not they working properly. Since Anfinsen's theory that the protein structure is wholly influenced by the primary structure has been developed, we can forecast the format of proteins without experimentation by its primary format. The forecasting problem is formulated in order to achieve this objective to identify the lowest free energy concentration as an optimization problem. The Hybrid Particle Swarm Optimization (PSO) Algorithm is used in this paper¹ to address the issue with the Hybrid Artificial Bee Colony (ABC). Taking into consideration that the two algorithms have supporting properties, hence by combining them simultaneously results in better optimization results through this experimental approach.

[2] Protein structural class prediction of the Vector Machine Improved Support (ISVM)

The difference between the amount of familiar succession of protections and the amount of familiar classes of protein structures generally expands rapidly. In order to overcome this crisis, a computational predictive method is essential for the rapid and precise determination of structural protein classes. The protein classes that are structural are forecasted on the basis of the secondary structure information. Four datasets – 25PDB, 1189, D640 and FC699 – evaluate algorithm's performance using existing algorithms. This article aims at predicting an Enhanced Support Vector Machine structural protein class (ISVM). Compared with current algorithms, improved support vector network forecasts a high precise structural class of proteins. The differentiation of output demonstrates that increased vector support forecasts a high precise structural class of proteins than current algorithms. The comparison of results demonstrates that improved vector support predicts a more accurate structural protein class than current algorithms. In comparison with the protein structure, the algorithms that already exist are Support Vector Network (SVM), Naive Bayes and the proposed Enhanced Support Vector Network (ISVM). The results are shown to be better results than the current algorithms with the ISVM algorithm.

[3] Parallel Ant Colony Optimization using the HP Lattice Model

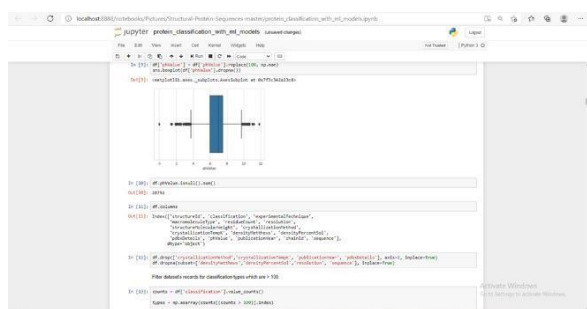
The problem of expanding protein examines the way a protein – an amino acid chain – 'folds' into its natural state. The problem of protein folding examines the way a protein – an amino acid chain – 'folds' into its natural state. Predict how various protein falls in the development of diseases like

Alzheimer's and Cystic Fibrosis treatments can be fundamental. Resource-intensive traditional calculation solutions for the final configuration of the protein structure. One way to simplify the

problem is the hydrophobic hydrophilic (HP) method. With Ant Colony Optimizations and a distributed programming paradigm, we present the novel method to address the HP protein folding problem in two or three dimensions¹. Testing. Across a few processors, the ACO (MACO) distributed by multiple colonies is scalable and outperforms. Implementation of the single colony. In order to simplify the problem while maintaining the behaviorally, the hydrophobic-hydrophilic (HP) net was designed. Until recently the 3D HP model has been largely ignored in favor of the 2D HP model due to the simplicity of the search space and easy visualization. The simplified HP models are NP-complete, offering an ideal platform to evaluate and improve heuristic-based algorithms which help develop expanded protein folding problems. Much of the work in this field was done in the past to develop and implement 2D protein folding solutions without considering 3D applications. The paper offers a solution algorithm for the problem of folding 3D HP protein in order to extend the solution to the 2D HP issue.

1.1 SCOPE OF THE PROJECT:

We would like to help develop medical science in this paper. In particular, drug development requires knowledge of the candidate compounds' binding sites, a well-predicted structure helps to screen computation and optimize the candidate compounds. It is very curious for both researchers and students to recognize the mechanism through which a protein functions and how it folds. In this respect, we are looking for a case study that provides information on the most accurate structure prediction algorithm using function vectors.



1.2 EXISTING SYSTEM:

A longstanding issue in established researchers is the investigation of proteins. Proteins, The structure blocks for life comprise of the amino acids that are associated and blur into three-dimensional designs that decide their capacities. Information on these constructions is vital for the plan of new drugs, the investigation of infections, and in the field of protein designing.

Experimentation is expensive and tedious to decide the three-dimensional construction of such proteins.. Then again, we can utilize a PC to produce hundreds or thousands of likely three-

dimensional designs for every protein and afterward figure out which of the forecasts are the awesome.

2.3 PROPOSED SYSTEM:

The primary protein sequences are accepted one at a time by the user. This process can be automated by using a script to process multiple sequences. Its application requires the user to choose which classifier they prefer to use for their analyses Naive Bayes, Support Vector Machines, or Random Forest. Feature vectors are generated from the entered sequence and then evaluated for each entered sequence to predict class labels. The protein sequences vary in length and can be categorized based on various physical and stereochemical properties, these properties determine the feature vector generation. In the application, polarity, hydrophobicity, polarity and volume of Van der Waals are the attributes used to describe the sequence. Our application can return the predicted labels of multiple classifiers at once. This helps the user compare and understand the best algorithm to be used for prediction. Our research yields the best result using the Random Forest Classifier with an astounding accuracy of 96%.

2. SYSTEM ARCHITECTURE:

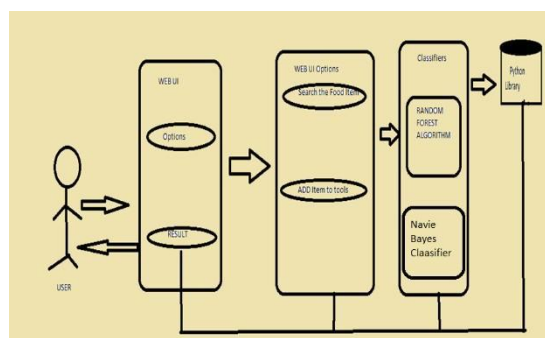
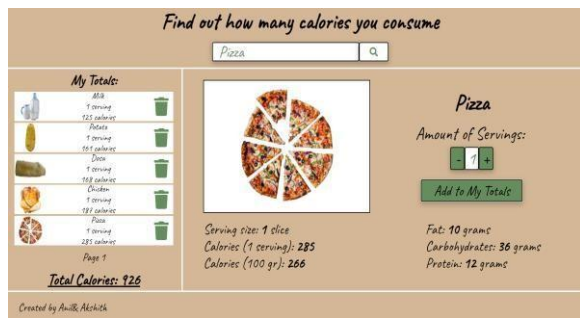


Fig 2. System Architecture

3. MODULE DESCRIPTION:

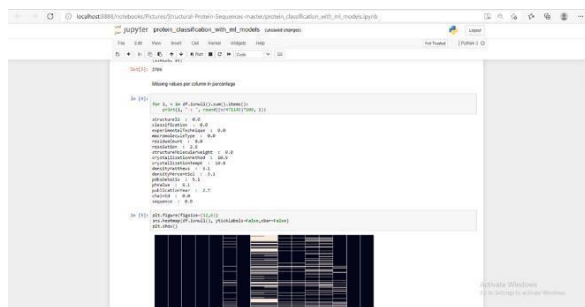
Project Modules:

- Collection and Analysis of Data.
- Design and Development of Feature Vector.
- Parallel Programming.
- Design of UI.



I. Collection and Analysis of Data:

Data collection and analysis using Selenium for website extraction by processing the HTML Web page and extracting data for local storage handling. The application can run without an Internet connection when the protein sequences are stored locally. Protein Data Banks¹ contains millions of sequences and the entire process was combined to increase computer performance with Java and multithreading. A mix of protein and non-protein data (such as DNA and RNA) were available to collect sequence data from the internet and have been filtered and cleaned to meet our needs.



II. Design and Development of Feature Vector:

Design and development of a feature vector, a measurable entity or feature used to describe an object attribute or feature. The selection of features is essential to improve the performance of the predictor algorithm, and the selected features must have a direct correlation with the three-dimensional protein structure for prediction of structures. Hydrophobicity, polarity and Van der Waals Evolution volume are the four best characteristics. The features in a matrix are combined to improve the vector's efficiency.

III. Parallel programming

Parallel programming Structure prediction is a computationally expensive and time-consuming process. In order to overcome this, we designed a parallel programming predictor by sending sequences to multiple classifiers at once, this increases the overall performance and usability of the

application as the users can compare the results returned by the classifiers simultaneously. Further, the data collection process was done parallelly by scraping multiple websites at once.

IV. Design of UI :

In this Module, the Receiver can find collusion occurring or not using calculating a distance.



4. CONCLUSION:

We created a model for machine learning, which predicts the two-dimensional protein structure from its amino acid sequences. The three-dimensional structure of protein molecules is a major focus in many aspects of modern biological research. Our model takes the primary protein sequence as inputs and inputs the three-dimensional structure into which the protein folds. This can be used in various drugs, especially for the knowledge of candidate compound binding sites, and an advanced structure that helps to screen and optimise the candidate compound. The unchecked data set for the development of our machine learning model is a linear amino acid chain which forms the protein's primary structure. In order to get class marks of our unattended data set, we extracted information from different websites. For each protein sequence, we have produced unique feature vectors based on polarity, hydrophobicity, polarizability and volume of the van der Waals. We then used various classification models which are used to analyze and predict class labels for each entered sequence. Our initial approach of using a Naive Bayesian classifier yielded an accuracy of approximately 47%.

REFERENCES:

- [1] Alberts B. et al. (2012), Protein Structure and Construction, Cell Atomic Science; Fourth Release. New York and London: Study of Festoon. ISBN 0-8153-3218-1..
- [2] Mirzaei S, T Sidi, S. Crivelli and Keasar (2016) Utilizing Vector Machine Backing and Gathering Learning Capacities, IEEE/ACM Exchanges. Underlying Protein Scoring Capacities.
- [3] Zhou H., and Skolnick J. (2011), GOAP: a Protein Construction Expectation All-Iota Measurable Likely Accessible, Biophysical Diary, vol. 101, no. 8, pp. 2043-2052.

[4] Khoury G. et al., (2014), We Overlap: A Coopetition for the Forecast of Protein Design. *Proteins: Bioinformatics and construction*; 82(9): 1850-1868; doi: 101002/prot.24538.

- [5] A Worldwide Protein Construction Scoring Capacity for AI, Protein Organizing and Bioinfo-upgrading, vol. 82, no. 5, pp. 752-759. Faraggi E. also, Klotzkowski A. (2013).
- [6] Computational Science and Bioinformatics, Volume: PP Issue: 99. DOI: 10.1109/TCBB.2016.2602269.
- [7] Zaremba W. et al. (2014), Intermittent Neural Organization Regularization, arXiv preprint arXiv:1409.2329.
- [8] C et al. Keasar (2017). Submitted to Logical Reports. "An assessment of we crease: a worldwide shared pipelines system for foreseeing protein structures."
- [9] Tulio Ribeiro, Marco Sameer Singh Prologue to Neighborhood Interpretable Model-Skeptic Clarifications, via Carlos Guestrin, 2016. (LIME) A strategy for clarifying any AI classifier's expectations.
- [10] Alberts B. et al. (2011), The Shape and Construction of Proteins, Cell sub-atomic science; fourth version. New York and London: Study of Wreath. ISBN 0-8153-3218-1.
- [11] A.C.M. May. Towards a more significant various leveled characterization of the rating elements of amino acids. Protein Designing, 12:077-712, 2011.

C. Source Code:

Front end:

```
<!DOCTYPE html>
```

```
<html lang="en">
```

```
<head>
```

```
<meta charset="UTF-8">
```

```
<meta name="viewport" content="width=device-width, initial-scale=1.0">
```

```
<meta http-equiv="X-UA-Compatible" content="ie=edge">
```

```
<title>Food Protein Calculator</title>
```

```
<link rel="stylesheet" href="css/normalize.css">
```

```
<link rel="stylesheet" href="css/styles.css">
```

```
<link href="https://fonts.googleapis.com/css?family=Caveat&display=swap"
rel="stylesheet">
```

```
<link rel="stylesheet" href="css/font-awesome-animation.min.css">
```

```
<script
```

```
src="https://kit.fontawesome.com/19e2f65e12.js"
```

```
crossorigin="anonymous"></script>
```

```
</head>
```

```
<body class="body">
```

```
<article class="article">
```

```
<div class="alert-box-max-items alert-box alert-box_hidden">
```

```
<span class="alert-box-max-items-text alert-box-text">You have reached the
maximum amount of items in "My Totals".</span>
```

```
<span class="alert-box-max-items-close alert-box-close">  
  <button class="alert-box-max-items-close_button  
alert-box- close_button">&times;</button>
```


</div>

<div class="alert-box-wrong-query alert-box alert-box_hidden">
 There is no such food item.
Please type a correct food item.

 <button class="alert-box-wrong-query-close_button
alert-box- close_button">×</button>

</div>

<header class="header">
 <h1 class="header-text">Find out how many calories you consume</h1>
 <form name="header-form" method="get" class="header-form">
 <div><input class="header-form__input input" type="text" placeholder="Search
Food Database"></div>
 <div class="header-form_icon icon"><i class="fas fa-search fa-1x faa-pulse
animated-hover"></i></div>
 </form>
</header>

<article class="container">

<section class="container-aside">

<div class="my-totals">
 <h2 class="my-totals_text">My Totals:</h2>
</div>

<div class="food-items">

<div class="food-items_page-1 food-itemspage-1-4 food-itemspage-1-4_visible

food-items_page-1-4_active">

```
<div class="food-item-1 food-item-1-20 food-item-1-20_visible">
  <figure class="food-item-1-picture-container food-item-1-20-picture-container">
    <img class="food-item-1-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
  </figure>
  <div class="food-item-1-text-container food-item-1-20-text-container
food-item-1- 20-text-container_hidden">
    <div class="food-item-1-text-container-title"></div>
    <div class="food-item-1-text-container-servings">
      <span class="food-item-1-text-container-servings__value"></span>
      <span class="food-item-1-text-container-servings__text"></span>
    </div>
    <div class="food-item-1-text-container-calories">
      <span class="food-item-1-text-container-calories__value"></span>
      <span class="food-item-1-text-container-calories__text">calories</span>
    </div>
  </div>
  <div class="food-item-1-bin food-item-1-20-bin food-item-1-20-bin_hidden">
    <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
  </div>
</div>
```

```
<div class="food-item-2 food-item-1-20 food-item-1-20_visible">
  <figure class="food-item-2-picture-container food-item-1-20-picture-container">
    <img class="food-item-2-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
  </figure>
  <div class="food-item-2-text-container food-item-1-20-text-container
food-item-1- 20-text-container_hidden">
    <div class="food-item-2-text-container-title"></div>
    <div class="food-item-2-text-container-servings">
```



```

        <span class="food-item-2-text-container-servings__text"></span>
    </div>
    <div class="food-item-2-text-container-calories">
        <span class="food-item-2-text-container-calories__value"></span>
        <span class="food-item-2-text-container-calories__text">calories</span>
    </div>
</div>
<div class="food-item-2-bin food-item-1-20-bin food-item-1-20-bin_hidden">
    <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
</div>
</div>

<div class="food-item-3 food-item-1-20 food-item-1-20_visible">
    <figure class="food-item-3-picture-container food-item-1-20-picture-container">
        <img class="food-item-3-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
    </figure>
    <div class="food-item-3-text-container food-item-1-20-text-container
food-item-1-20-text-container_hidden">
        <div class="food-item-3-text-container-title"></div>
        <div class="food-item-3-text-container-servings">
            <span class="food-item-3-text-container-servings__value"></span>
            <span class="food-item-3-text-container-servings__text"></span>
        </div>
        <div class="food-item-3-text-container-calories">
            <span class="food-item-3-text-container-calories__value"></span>
            <span class="food-item-3-text-container-calories__text">calories</span>
        </div>
    </div>
    <div class="food-item-3-bin food-item-1-20-bin food-item-1-20-bin_hidden">
        <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>

```

</div>

</div>

```
<div class="food-item-4 food-item-1-20 food-item-1-20_visible">
  <figure class="food-item-4-picture-container food-item-1-20-picture-container">
    <img class="food-item-4-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
  </figure>
  <div class="food-item-4-text-container food-item-1-20-text-container
food-item-1-20-text-container_hidden">
    <div class="food-item-4-text-container-title"></div>
    <div class="food-item-4-text-container-servings">
      <span class="food-item-4-text-container-servings__value"></span>
      <span class="food-item-4-text-container-servings__text"></span>
    </div>
    <div class="food-item-4-text-container-calories">
      <span class="food-item-4-text-container-calories__value"></span>
      <span class="food-item-4-text-container-calories__text">calories</span>
    </div>
  </div>
  <div class="food-item-4-bin food-item-1-20-bin food-item-1-20-bin_hidden">
    <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
  </div>
</div>
```

```
<div class="food-item-5 food-item-1-20 food-item-1-20_visible">
  <figure class="food-item-5-picture-container food-item-1-20-picture-container">
    <img class="food-item-5-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
  </figure>
  <div class="food-item-5-text-contaisner food-item-1-20-text-container
food-item-1-20-text-container_hidden">
    <div class="food-item-5-text-container-title"></div>
```

<div class="food-item-5-text-container-servings">

```

        <span class="food-item-5-text-container-servings__value"></span>
        <span class="food-item-5-text-container-servings__text"></span>
    </div>
    <div class="food-item-5-text-container-calories">
        <span class="food-item-5-text-container-calories__value"></span>
        <span class="food-item-5-text-container-calories__text">calories</span>
    </div>
</div>
<div class="food-item-5-bin food-item-1-20-bin food-item-1-20-bin_hidden">
    <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
    </div>
</div>

</div>

<div class="food-items_page-2 food-itemspage-1-4 food-items_page-1-4_none">

    <div class="food-item-6 food-item-1-20">
        <figure class="food-item-6-picture-container food-item-1-20-picture-container">
            <img class="food-item-6-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
        </figure>
        <div class="food-item-6-text-container food-item-1-20-text-container
food-item-1-20-text-container_hidden">
            <div class="food-item-6-text-container-title"></div>
            <div class="food-item-6-text-container-servings">
                <span class="food-item-6-text-container-servings__value"></span>
                <span class="food-item-6-text-container-servings__text"></span>
            </div>
            <div class="food-item-6-text-container-calories">
                <span class="food-item-6-text-container-calories__value"></span>
                <span class="food-item-6-text-container-calories__text">calories</span>
            </div>
        </div>
    </div>

```

</div>

```

    </div>
    <div class="food-item-6-bin food-item-1-20-bin food-item-1-20-bin_hidden">
        <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
    </div>
</div>

<div class="food-item-7 food-item-1-20">
    <figure class="food-item-7-picture-container food-item-1-20-picture-container">
        <img class="food-item-7-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
    </figure>
    <div class="food-item-7-text-container food-item-1-20-text-container
food-item-1-20-text-container_hidden">
        <div class="food-item-7-text-container-title"></div>
        <div class="food-item-7-text-container-servings">
            <span class="food-item-7-text-container-servings__value"></span>
            <span class="food-item-7-text-container-servings__text"></span>
        </div>
        <div class="food-item-7-text-container-calories">
            <span class="food-item-7-text-container-calories__value"></span>
            <span class="food-item-7-text-container-calories__text">calories</span>
        </div>
    </div>
    <div class="food-item-7-bin food-item-1-20-bin food-item-1-20-bin_hidden">
        <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
    </div>
</div>

<div class="food-item-8 food-item-1-20">
    <figure class="food-item-8-picture-container food-item-1-20-picture-container">
        <img class="food-item-8-picture food-item-1-20-picture food-item-1-20-

```

picture_hidden" src="" alt="">

```

</figure>
<div class="food-item-8-text-container food-item-1-20-text-container
food-item-1- 20-text-container_hidden">
  <div class="food-item-8-text-container-title"></div>
  <div class="food-item-8-text-container-servings">
    <span class="food-item-8-text-container-servings__value"></span>
    <span class="food-item-8-text-container-servings__text"></span>
  </div>
  <div class="food-item-8-text-container-calories">
    <span class="food-item-8-text-container-calories__value"></span>
    <span class="food-item-8-text-container-calories__text">calories</span>
  </div>
</div>
<div class="food-item-8-bin food-item-1-20-bin food-item-1-20-bin_hidden">
  <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
</div>
</div>

<div class="food-item-9 food-item-1-20">
  <figure class="food-item-9-picture-container food-item-1-20-picture-container">
    <img class="food-item-9-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
  </figure>
  <div class="food-item-9-text-container food-item-1-20-text-container
food-item-1- 20-text-container_hidden">
    <div class="food-item-9-text-container-title"></div>
    <div class="food-item-9-text-container-servings">
      <span class="food-item-9-text-container-servings__value"></span>
      <span class="food-item-9-text-container-servings__text"></span>
    </div>
    <div class="food-item-9-text-container-calories">
      <span class="food-item-9-text-container-calories__value"></span>

```

calories

```

        </div>
    </div>
    <div class="food-item-9-bin food-item-1-20-bin food-item-1-20-bin_hidden">
        <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
    </div>
</div>

<div class="food-item-10 food-item-1-20">
    <figure class="food-item-10-picture-container food-item-1-20-picture-container">
        <img class="food-item-10-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
    </figure>
    <div class="food-item-10-text-container food-item-1-20-text-container food-item-
1-20-text-container_hidden">
        <div class="food-item-10-text-container-title"></div>
        <div class="food-item-10-text-container-servings">
            <span class="food-item-10-text-container-servings_value"></span>
            <span class="food-item-10-text-container-servings_text"></span>
        </div>
        <div class="food-item-10-text-container-calories">
            <span class="food-item-10-text-container-calories__value"></span>
            <span class="food-item-10-text-container-calories_text">calories</span>
        </div>
    </div>
    <div class="food-item-10-bin food-item-1-20-bin food-item-1-20-bin_hidden">
        <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
    </div>
</div>

```

<div class="food-items_page-3 food-itemspage-1-4 food-items_page-1-4_none">

```

<div class="food-item-11 food-item-1-20">
  <figure class="food-item-11-picture-container food-item-1-20-picture-container">
    <img class="food-item-11-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
  </figure>
  <div class="food-item-11-text-container food-item-1-20-text-container food-item-
1-20-text-container_hidden">
    <div class="food-item-11-text-container-title"></div>
    <div class="food-item-11-text-container-servings">
      <span class="food-item-11-text-container-servings_value"></span>
      <span class="food-item-11-text-container-servings_text"></span>
    </div>
    <div class="food-item-11-text-container-calories">
      <span class="food-item-11-text-container-calories__value"></span>
      <span class="food-item-11-text-container-calories_text">calories</span>
    </div>
  </div>
  <div class="food-item-11-bin food-item-1-20-bin food-item-1-20-bin_hidden">
    <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
  </div>
</div>

```

```

<div class="food-item-12 food-item-1-20">
  <figure class="food-item-12-picture-container food-item-1-20-picture-container">
    <img class="food-item-12-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
  </figure>
  <div class="food-item-12-text-container food-item-1-20-text-container food-item-
1-20-text-container_hidden">
    <div class="food-item-12-text-container-title"></div>
    <div class="food-item-12-text-container-servings">

```



```

        <span class="food-item-12-text-container-servings_text"></span>
    </div>
    <div class="food-item-12-text-container-calories">
        <span class="food-item-12-text-container-calories__value"></span>
        <span class="food-item-12-text-container-calories_text">calories</span>
    </div>
</div>
<div class="food-item-12-bin food-item-1-20-bin food-item-1-20-bin_hidden">
    <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
</div>
</div>

<div class="food-item-13 food-item-1-20">
    <figure class="food-item-13-picture-container food-item-1-20-picture-container">
        <img class="food-item-13-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
    </figure>
    <div class="food-item-13-text-container food-item-1-20-text-container food-item-
1-20-text-container_hidden">
        <div class="food-item-13-text-container-title"></div>
        <div class="food-item-13-text-container-servings">
            <span class="food-item-13-text-container-servings_value"></span>
            <span class="food-item-13-text-container-servings_text"></span>
        </div>
        <div class="food-item-13-text-container-calories">
            <span class="food-item-13-text-container-calories__value"></span>
            <span class="food-item-13-text-container-calories_text">calories</span>
        </div>
    </div>
    <div class="food-item-13-bin food-item-1-20-bin food-item-1-20-bin_hidden">
        <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>

```

</div>

</div>

```
<div class="food-item-14 food-item-1-20">
  <figure class="food-item-14-picture-container food-item-1-20-picture-container">
    <img class="food-item-14-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
  </figure>
  <div class="food-item-14-text-container food-item-1-20-text-container food-item-
1-20-text-container_hidden">
    <div class="food-item-14-text-container-title"></div>
    <div class="food-item-14-text-container-servings">
      <span class="food-item-14-text-container-servings_value"></span>
      <span class="food-item-14-text-container-servings_text"></span>
    </div>
    <div class="food-item-14-text-container-calories">
      <span class="food-item-14-text-container-calories__value"></span>
      <span class="food-item-14-text-container-calories_text">calories</span>
    </div>
  </div>
  <div class="food-item-14-bin food-item-1-20-bin food-item-1-20-bin_hidden">
    <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
  </div>
</div>
```

```
<div class="food-item-15 food-item-1-20">
  <figure class="food-item-15-picture-container food-item-1-20-picture-container">
    <img class="food-item-15-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
  </figure>
  <div class="food-item-15-text-container food-item-1-20-text-container food-item-
1-20-text-container_hidden">
    <div class="food-item-15-text-container-title"></div>
```

<div class="food-item-15-text-container-servings">

```

        <span class="food-item-15-text-container-servings_value"></span>
        <span class="food-item-15-text-container-servings_text"></span>
    </div>
    <div class="food-item-15-text-container-calories">
        <span class="food-item-15-text-container-calories__value"></span>
        <span class="food-item-15-text-container-calories_text">calories</span>
    </div>
</div>
<div class="food-item-15-bin food-item-1-20-bin food-item-1-20-bin_hidden">
    <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
    </div>
</div>

</div>

<div class="food-items_page-4 food-itemspage-1-4 food-items_page-1-4_none">

    <div class="food-item-16 food-item-1-20">
        <figure class="food-item-16-picture-container food-item-1-20-picture-container">
            <img class="food-item-16-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
        </figure>
        <div class="food-item-16-text-container food-item-1-20-text-container food-item-
1-20-text-container_hidden">
            <div class="food-item-16-text-container-title"></div>
            <div class="food-item-16-text-container-servings">
                <span class="food-item-16-text-container-servings_value"></span>
                <span class="food-item-16-text-container-servings_text"></span>
            </div>
            <div class="food-item-16-text-container-calories">
                <span class="food-item-16-text-container-calories__value"></span>
                <span class="food-item-16-text-container-calories_text">calories</span>

```

</div>

```

    </div>
    <div class="food-item-16-bin food-item-1-20-bin food-item-1-20-bin_hidden">
        <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
    </div>
</div>

<div class="food-item-17 food-item-1-20">
    <figure class="food-item-17-picture-container food-item-1-20-picture-container">
        <img class="food-item-17-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
    </figure>
    <div class="food-item-17-text-container food-item-1-20-text-container food-item-
1-20-text-container_hidden">
        <div class="food-item-17-text-container-title"></div>
        <div class="food-item-17-text-container-servings">
            <span class="food-item-17-text-container-servings_value"></span>
            <span class="food-item-17-text-container-servings_text"></span>
        </div>
        <div class="food-item-17-text-container-calories">
            <span class="food-item-17-text-container-calories__value"></span>
            <span class="food-item-17-text-container-calories_text">calories</span>
        </div>
    </div>
    <div class="food-item-17-bin food-item-1-20-bin food-item-1-20-bin_hidden">
        <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
    </div>
</div>

<div class="food-item-18 food-item-1-20">
    <figure class="food-item-18-picture-container food-item-1-20-picture-container">
        <img class="food-item-18-picture food-item-1-20-picture food-item-1-20-

```

picture_hidden" src="" alt="">

```

</figure>
<div class="food-item-18-text-container food-item-1-20-text-container food-item-
1-20-text-container_hidden">
  <div class="food-item-18-text-container-title"></div>
  <div class="food-item-18-text-container-servings">
    <span class="food-item-18-text-container-servings_value"></span>
    <span class="food-item-18-text-container-servings_text"></span>
  </div>
  <div class="food-item-18-text-container-calories">
    <span class="food-item-18-text-container-calories__value"></span>
    <span class="food-item-18-text-container-calories_text">calories</span>
  </div>
</div>
<div class="food-item-18-bin food-item-1-20-bin food-item-1-20-bin_hidden">
  <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
</div>
</div>

<div class="food-item-19 food-item-1-20">
  <figure class="food-item-19-picture-container food-item-1-20-picture-container">
    <img class="food-item-19-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
  </figure>
  <div class="food-item-19-text-container food-item-1-20-text-container food-item-
1-20-text-container_hidden">
    <div class="food-item-19-text-container-title"></div>
    <div class="food-item-19-text-container-servings">
      <span class="food-item-19-text-container-servings_value"></span>
      <span class="food-item-19-text-container-servings_text"></span>
    </div>
    <div class="food-item-19-text-container-calories">
      <span class="food-item-19-text-container-calories__value"></span>

```

calories

```

        </div>
    </div>
    <div class="food-item-19-bin food-item-1-20-bin food-item-1-20-bin_hidden">
        <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
    </div>
</div>

<div class="food-item-20 food-item-1-20">
    <figure class="food-item-20-picture-container food-item-1-20-picture-container">
        <img class="food-item-20-picture food-item-1-20-picture food-item-1-20-
picture_hidden" src="" alt="">
    </figure>
    <div class="food-item-20-text-container food-item-1-20-text-container food-item-
1-20-text-container_hidden">
        <div class="food-item-20-text-container-title"></div>
        <div class="food-item-20-text-container-servings">
            <span class="food-item-20-text-container-servings_value"></span>
            <span class="food-item-20-text-container-servings_text"></span>
        </div>
        <div class="food-item-20-text-container-calories">
            <span class="food-item-20-text-container-calories__value"></span>
            <span class="food-item-20-text-container-calories_text">calories</span>
        </div>
    </div>
    <div class="food-item-20-bin food-item-1-20-bin food-item-1-20-bin_hidden">
        <i class="fas fa-trash fa-2x faa-shake animated-hover faa-slow
icon_color"></i>
    </div>
</div>

```

<div class="fake-page food-items_page-5 food-itemspage-1-4 food-items_page-1-

4_none">

<div class="food-item-21 food-item-1-20">

<div class="food-item-21-text-container food-item-1-20-text-container food-item-1-20-text-container_hidden"></div>

</div>

</div>

</div>

<div class="food-pagination">

<button class="food-pagination-left-button faa-horizontal faa-slow button">

<div class="food-pagination-left-button__value">Page 0</div>

</button>

<div class="food-pagination-text">

<div>Page </div>

<div class="food-pagination-text_value">0</div>

</div>

<button class="food-pagination-right-button faa-horizontal faa-slow button">

<div class="food-pagination-right-button_value">Page 0</div>

</button>

</div>

<div class="total-calories">

<h3 class="total-calories__text">Total Calories: </h3>

<h3 class="total-calories__value">0</h3>

</div>

</section>

<section class="container-main">

<div class="details details_hidden">

<div class="details-first-row">

```
<figure class="details-first-row-first-column">
  <img class="details-first-row-first-column_picture" src="" alt="">
</figure>
```

```
<div class="details-first-row-second-column">
  <h2 class="details-first-row-second-column-title">Apple</h2>
  <div class="details-first-row-second-column-serving">
    <span class="details-first-row-second-column-serving-text">Amount
of Servings:&nbsp;</span>
    <div class="details-first-row-second-column-serving-buttons">
      <button class="details-first-row-second-column-serving-buttons minus
button">-</button>
      <input class="details-first-row-second-column-serving-buttons  input
input" type="text" readonly pattern="^[0-9]+$" value="1">
      <button class="details-first-row-second-column-serving-buttons plus
button">+</button>
    </div>
  </div>
  <div class="details-first-row-second-column-add-to-totals">
    <button class="details-first-row-second-column-add-to-totals button
button">Add to My Totals</button>
  </div>
</div>
```

```
<div class="details-second-row">
```

```
<div class="details-second-row-first-column">
  <div class="details-second-row-first-column-serving-size">
    <span>Serving size:</span>
    <span>&nbsp;</span>
```

1

```

        <span>&nbsp;</span>
        <span
class="details-second-row-first-column-serving- size
unit">piece</span>
    </div>
    <div class="details-second-row-first-column-calories-amount-in-pieces">
        <span>Calories (</span>
        <span class="details-second-row-first-column-calories-amount-in-
pieces_servings-value">1</span>
        <span>&nbsp;</span>
        <span class="details-second-row-first-column-calories-amount-in-
pieces_servings-text">serving</span>
        <span>):&nbsp;</span>
        <span class="details-second-row-first-column-calories-amount-in-
pieces_value">0</span>
    </div>
    <div class="details-second-row-first-column-calories-amount-in-grams">
        <span>Calories (</span>
        <span
class="details-second-row-first-column-calories-amount-in- grams_____
grams-value">100</span>
        <span>&nbsp;<span>gr):&nbsp;</span>
        <span
class="details-second-row-first-column-calories-amount-in- grams_____
value">0</span>
    </div>
</div>

    <div class="details-second-row-second-column">
        <div class="details-second-row-second-column-fat">
            <span>Fat:&nbsp;</span>
            <span class="details-second-row-second-column-fat__value">0</span>
            <span>&nbsp;</span>
        </div>
    </div>

```

grams

</div>

<div class="details-second-row-second-column-carbohydrates">

Carbohydrates:

```
        <span
class="details-second-row-second-column- carbohydrates
value">0</span>
        <span>&nbsp;</span>
        <span
class="details-second-row-second-column- carbohydrates
text">grams</span>
    </div>
    <div class="details-second-row-second-column-protein">
        <span>Protein:&nbsp;</span>
        <span class="details-second-row-second-column-protein value">0</span>
        <span>&nbsp;</span>
        <span
class="details-second-row-second-column- protein_
text">grams</span>
    </div>
</div>

</div>

</div>

</section>

</article>

<footer class="footer">
    <div class="footer_text-1">Created by Anil & Akshith</div>
    <div class="footer_text-2"></div>
</footer>

</article>
```

```
<script type="text/javascript" src="js/bundle.js"></script></body>
```

```
</html>
```