

Healthcare Analytics Using Machine Learning

Hemkar Goswami, Darsh Sharma

Students, Dept. of Computer Science and Engineering(SCOPE), VIT University, Tamil Nadu, India

Abstract - AI seeks to place the doctor in our pocket. Among other things, AI has applications in disease prediction, cost reduction, efficiency improvements, automating manual tasks, and promoting us to alter our health. As data volume and variety increases, the capabilities of AI models will become more precise, more probing, and also more contentious. Machine learning, a sub-set of artificial intelligence (AI), has taken the world by storm. Within the healthcare domain, it is possible to see how machine learning can make manual processes easier, providing benefits for patients, providers, and pharmaceutical companies alike. Google, for example, has developed a machine learning algorithm that can identify cancerous tumors on mammograms. Similarly, Stanford University has developed a deep learning algorithm to identify skin cancer. Machine Learning for Health care is packed with new approaches and methodologies for creating powerful solutions for healthcare analytics. This project will teach you how to implement key machine learning algorithms and walk you through their use cases by employing a range of libraries from the Python ecosystem.

Key Words: Neural Networks ,Deep learning, Machine Learning, Health prediction, Classification

1.INTRODUCTION

Discussion of the utilization of AI in medicine coincides with the arrival AI within the era . This is not surprising as AI systems initially shall replicate the functioning of the human brain . In 1970, William B Schwartz, a physician interested in the use of computing science in medicine, published an influential paper in the New England Journal of Medicine titled 'Medicine and the computer: the promise and problems of change' . In the paper he argued 'Computing science will probably exert its major effects by augmenting and, in some cases, largely replacing the intellectual functions of the physician'. By the 1970s there was a realisation that conventional computing techniques are unsuitable for solving complex medical phenomenon . A more sophisticated computational model that simulated human cognitive processes, that's AI models, was required for clinical problem solving. Early efforts to use AI in medicine consisted of fixing rules- based systems to assist with medical reasoning. However, serious clinical problems are too complex to lend them to simple rules-based problem solving techniques. Problem solving in medicine then progressed to construction of computer programs supported models of diseases. It was not just with the field of general medicine, that AI was being explored to assist with problem solving. In 1976, the Scottish surgeon Gunn used

computational analysis to diagnose acute abdominal pain . This was achieved through clinical audits of structured case notes through computers, whereby diagnosis through this route proved to be about 10% more accurate than the conventional route. By the 1980s, AI research communities were established across the world but especially in learning centres in the US . This development helped in expansion of the utilization of novel and innovative AI approaches to medical diagnoses. Much of this push was because medicine was a perfect laboratory for these AI applications. A significant number of AI applications in medicine at this stage were supported the expert system methodology . By the end of the 1990s, research in medical AI had started to use new techniques like machine learning and artificial neural networks to aid clinical decision- making.

1.1. Work already done

ANN processing utilizes a parallel sort of processing analogous to the brain . In ANNs, the processing elements, otherwise called as neurons, process data simultaneously while communicating with one another . The processing elements are arranged in layers and therefore the layers, in turn, are connected to every other. The links between the processing elements are related to a numerical link. The memory and adaptation of ANNs are adjusted by changing the link, which results in the amplification of the consequences of afferent connection to every processing element. As a result of this architecture, ANNs are often trained to find out from experience, analyses non-linear data and manage inexact information. These abilities have led to ANN techniques being one among the foremost popularly utilized AI techniques in medicine. ANNs additionally to diagnosis are used for radiology and histopathology analysis. In radiology, gamma camera, CT, ultra- sound and MRI all create digital images, which may be manipulated by ANNs and used as inputs. The digitized inputs are then transmitted through the hidden and output layers to supply desired outputs (see Figure 2). Using the Back- propagation approach, a learning algorithm, ANNs have successfully identified orthopedic trauma from radiographs . When ANNs and radiologists interpret an equivalent radiological images separately, research has identified good diagnostic agreement . ANNs have also been used for analysis of cytological and histological specimens too . for instance , ANNs has been used to screen abnormal cells from slide images for hematology and cervical cytology. Further, ANNs have also been used to interpret ECGs and EEGs through waveform analysis. For this to occur, a multi-layered neural network is trained with waveform data from both people

with the disease and without. Evaluation of the waveform interpretations by ANNs has identified excellent pattern approximation and classification abilities and comparable in interpretation to clinicians.

Data Mining acts because the foundation for machine learning. data processing is that the process for identifying previously unknown patterns and trends in large databases then utilizing an equivalent to make predictive models. data processing involves multiple iterative steps that has retrieval of knowledge sets from data warehouses or operational databases, cleaning of knowledge to get rid of discrepancies, analysis of knowledge sets to spot patterns that represent relationships amongst the info, validation of the patterns with new data sets and culminating in knowledge extraction. Use of knowledge mining has become hugely popular in healthcare largely due to the generation of knowledge too voluminous and sophisticated to be processed by conventional computational techniques. The potential application of knowledge mining in healthcare are often huge but practically data processing has been utilized in evaluating the effectiveness of medical treatments, analyse epidemiological data to spot disease outbreaks and act as an early warning system, analyse hospital records to spot acute medical conditions and help with interventions, quality assessment of medical interventions and predicting survival time for chronic disease and cancer patients. data processing medical data faces two main issues: heterogeneity of knowledge sometimes with incomplete recording or filing of knowledge and complexity of the requested outputs. symbolic logic, which I discussed in an earlier section, with its proficiency to represent assorted data, strength in adapting to vary within the user environment and its distinctive expressiveness can support data processing in addressing these issues. Thus data processing utilizing symbolic logic has been used for a variety of situations in healthcare including prediction of the prognosis of cancer and assessing the satisfaction of clinicians for patient information management systems.

While the appliance of AI in delivery of health-care has very promising potential, challenges- both technical and ethical exist. AI research is largely led and driven by computer scientists without medical training and it has been commented that this has led to a very technologically focused and problem oriented approach within the application of AI in health care delivery. Contemporary health care delivery models are very hooked in to human reasoning, patient-clinician communication and establishing professional relationships with patients to make sure compliance. These aspects are something AI cannot replace easily. Use of robotic assistants in healthcare has raised issues about the mechanization of care in vulnerable situations where human interaction and intervention is probably more appealing. There is also the reluctance of doctors in adopting AI technologies that they envisage will eventually replace them. Yet there's no qualm in them using

technologies that automate and speed up laboratory diagnostic process. This has led to some suggesting a model of co-habitation. This is a model that accommodates both the AI and human elements in health care delivery and anticipates the inevitable automatization of significant components of medical tasks.

2. METHODOLOGY

We have built five end-to-end projects to evaluate the efficiency of Artificial Intelligence (AI) applications for carrying out simple-to-complex healthcare analytics tasks. With each task, you will gain new insights, which will then help you handle healthcare data efficiently. As you make your way through the project, will use ML to detect cancer in a set of patients using support vector machines (SVMs) and k-Nearest neighbors (KNN) models. We developed a deep neural network in Keras to predict the onset of diabetes in a huge data set of patients. We also developed a code to predict heart diseases using neural networks. The various components of the research are-

- 1) Diabetes Detection
- 2) Breast Cancer Detection
- 3) Screening for Autism
- 4) DNA Classification
- 5) Heart Disease Detection

1) Breast Cancer Detection:

700 cells within the dataset. this may include factors like clump thickness, marginal adhesion, repository. We named the columns (or features), then put them into a pandas Data Frame. we preprocessed our data and removed the ID column. we also explored the info, in order that we might know more about it. we used the describe function, which gave us features like the mean, the utmost, the minimum, and therefore the different quartiles. we also created some histograms (so that we could understand the distributions of the various features) and a scatterplot matrix (so that we could search for linear relationships between the variables). Then we split the dataset up into a training set and a testing validation set. we implemented some testing parameters, built a KNN classifier and an SVC, and compared their results employing a classification report. This consisted of features like accuracy, overall accuracy, precision, recall, F1 score, and support. Finally, we built our own cell and explored what it'd fancy actually get a malignant or benign classification.

2) Autism Screening :

A prior knowledge of neurodevelopmental disorders can improve treatment and significantly decrease associated healthcare costs. In this topic, we will use supervised learning to diagnose Autistic Spectrum Disorder (ASD) based on behavioral features and individual characteristics. More specifically, we will build and deploy a neural network using the Keras API. The dataset that we will be using for this chapter is the Autistic Spectrum Disorder Screening Data for

Children Dataset provided by the UCI Machine Learning Repository, which can be found here: <https://archive.ics.uci.edu/ml/datasets/Autistic+Spectrum+Disorder+Screening+Data+for+Children++>. This dataset contains records of 292 patients or children that have been screened for autism. This contains details about their age, ethnicity, and familial history of autism. we will be using this dataset to predict whether these patients actually have autism.

3) Diabetes detection:

Import the Pima Indians diabetes dataset, which contains the small print of about 750 patients. we did some preprocessing techniques after which we built a deep neural network in Keras and that we found the optimal hyperparameters using the scikit-learn grid search. We also learned the way to optimize a network by tuning the hyperparameters. Note that the results that we buy won't be an equivalent but as long as i buy similar predictions, we can consider our model a hit . once you start training on new data, or if you're trying to affect a special problem with a special dataset, you will need to undergo this process again.

4) DNA classification:

We will explore the planet of bioinformatics. we will be able to use Markov models, k-nearest neighbors algorithms, support vector machines, and other common classifiers, to classify short E. coli DNA sequences. For this project, will use a dataset from the UCI machine learning repository that has 106 DNA sequences, with 57 sequential nucleotides each. We learnt the way to import data from the UCI repository, convert text input to numerical data, build and train classification algorithms, and compare and contrast classification machine learning algorithms. Then it was ready to predict whether or not a brief sequence of E.coli bacteria DNA was a promoter or a non-promoter with 96% accuracy.

5) Heart disease prediction:

The dataset we will use is that the heart condition dataset from the UCI repository. You'll download this from archive.ics.uci.edu/ml/machine-learning-databases/heart-disease/. it's exactly 303 patients collected from the Cleveland Clinic Foundation. One of the ways to handle missing data, whether in healthcare applications or not, is to urge obviate the rows or instances that have missing attributes. we then learned the way to describe the info and print out histograms so we do know what we will be working with by doing a train/test split with model selection from sklearn. Furthermore, we also learned the way to convert one-hot encoded vectors for a categorical classification, by defining simple neural networks using Keras. Then we check out sorts of activation function, like softmax, for categorical classifications with categorical_crossentropy. In contrast, once we need to the binary classification, we used a sigmoid activation function and a binary_crossentropy loss. we also checked out training that data and the way to suit our model to the training data. we did that for both categorical and binary problems. Then, we finally checked out the way to do a classification report and accuracy score for our results.

3. RESULT OVERVIEW

In this project, we explored how to implement machine learning to analyze various healthcare issues. In breast cancer detection, we used machine learning to detect cancer in a set of patients using the SVM and KNN models. In the diabetes detection , we created a deep neural network in Keras to predict the onset of diabetes on a huge dataset of patients. In the DNA classification topic, we predicted whether or not a short sequence of E.coli bacteria DNA was a promoter or a non-promoter, and we used some common classifiers to classify short E. coli DNA sequences. We predicted heart disease using neural networks. we were able to predict autism in patients with about 90% accuracy. We also learned how to deal with categorical data; a lot of health applications are going to have categorical data and one way to address this is by using one-hot encoded vectors. Furthermore, we learned how to reduce overfitting using dropout regularization. Consequently, we can now see how machine learning in this day and age is revolutionizing the process of detecting the numerous diseases that are prevalent in the field of healthcare.

Autism detection:

```
In [19]: # generate classification report using predictions for categorical model
from sklearn.metrics import classification_report, accuracy_score

predictions = model.predict_classes(X_test)
predictions

Out[19]: array([1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 1, 0, 0, 1, 1, 1, 0, 1, 1, 0, 1,
1, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 1, 0, 1, 0, 1, 0,
1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 1, 0, 0], dtype=int64)

In [20]: print("Results for Categorical Model")
print(accuracy_score(Y_test[['YES']], predictions))
print(classification_report(Y_test[['YES']], predictions))

Results for Categorical Model
0.961816949152542
          precision    recall  f1-score   support

     0       0.97       0.97       0.97        36
     1       0.96       0.96       0.96        23

 avg / total       0.97       0.97       0.97        59
```

Diabetes onset detection:

```
Best: 0.790816335198, using {'neuron1': 16, 'neuron2': 2}
0.7882653114 (0.0404308487858) with: {'neuron1': 4, 'neuron2': 2}
0.785714291644 (0.0432823764463) with: {'neuron1': 4, 'neuron2': 4}
0.7857142980124 (0.0573177537384) with: {'neuron1': 4, 'neuron2': 8}
0.788265314181 (0.0300745493047) with: {'neuron1': 8, 'neuron2': 2}
0.7857142980124 (0.0337785679152) with: {'neuron1': 8, 'neuron2': 4}
0.785714293165 (0.0317644706476) with: {'neuron1': 8, 'neuron2': 8}
0.790816335198 (0.0301926398124) with: {'neuron1': 16, 'neuron2': 2}
0.790816330638 (0.051329267344) with: {'neuron1': 16, 'neuron2': 4}
0.785714293165 (0.0403287378951) with: {'neuron1': 16, 'neuron2': 8}

In [27]: # generate predictions with optimal hyperparameters
y_pred = grid.predict(X_standardized)

In [28]: print(y_pred.shape)
(392L, 1L)

In [29]: print(y_pred[:5])
[[0]
 [1]
 [0]
 [1]
 [1]]

In [30]: # Generate a classification report
from sklearn.metrics import classification_report, accuracy_score
print(accuracy_score(Y, y_pred))
print(classification_report(Y, y_pred))

0.7806122448979592
          precision    recall  f1-score   support

     0       0.81       0.89       0.84        262
     1       0.71       0.57       0.63        130

 avg / total       0.77       0.78       0.77        392
```

Breast Cancer detection:

```

KNN
0.9428571428571428
precision recall f1-score support
  0      1.00      0.96      0.95      83
  1      0.95      0.91      0.93      57
avg / total      0.94      0.94      0.94      140

SVM
0.9571428571428572
precision recall f1-score support
  0      1.00      0.93      0.96      83
  1      0.90      1.00      0.95      57
avg / total      0.96      0.96      0.96      140

In [31]: clf = SVC()
         clf.fit(X_train, y_train)
         accuracy = clf.score(X_test, y_test)
         print(accuracy)

example_measures = np.array([[4,2,1,1,1,2,3,2,1]])
example_measures = example_measures.reshape(len(example_measures), -1)
prediction = clf.predict(example_measures)
print(prediction)
0.9571428571428572
[2]
    
```

Naive Bayes
0.9259259259259259

	precision	recall	f1-score	support
0	1.00	0.88	0.94	17
1	0.83	1.00	0.91	10
avg / total	0.94	0.93	0.93	27

Nearest Neighbors
0.7777777777777778

	precision	recall	f1-score	support
0	1.00	0.65	0.79	17
1	0.62	1.00	0.77	10
avg / total	0.86	0.78	0.78	27

Gaussian Process
0.8888888888888888

	precision	recall	f1-score	support
0	1.00	0.82	0.90	17
1	0.77	1.00	0.87	10
avg / total	0.91	0.89	0.89	27

Decision Tree
0.7777777777777778

	precision	recall	f1-score	support
0	1.00	0.65	0.79	17
1	0.62	1.00	0.77	10
avg / total	0.86	0.78	0.78	27

Heart disease prediction:

```

In [116]: # generate classification report using predictions for categorical model
         from sklearn.metrics import classification_report, accuracy_score
         categorical_pred = np.argmax(model.predict(X_test), axis=1)
         print('Results for Categorical Model')
         print(accuracy_score(y_test, categorical_pred))
         print(classification_report(y_test, categorical_pred))

Results for Categorical Model
0.6166666666666667
precision recall f1-score support
  0      0.73      0.90      0.81      30
  1      0.14      0.09      0.11      11
  2      0.38      0.38      0.38      8
  3      0.75      0.60      0.67      10
  4      0.00      0.00      0.00      1
avg / total      0.57      0.62      0.58      60

In [117]: # generate classification report using predictions for binary model
         binary_pred = np.round(binary_model.predict(X_test)).astype(int)
         print('Results for Binary Model')
         print(accuracy_score(y_test_binary, binary_pred))
         print(classification_report(y_test_binary, binary_pred))

Results for Binary Model
0.8
precision recall f1-score support
  0      0.75      0.90      0.82      30
  1      0.88      0.70      0.78      30
avg / total      0.81      0.80      0.80      60
    
```

SVM Linear
0.9629629629629629

	precision	recall	f1-score	support
0	1.00	0.94	0.97	17
1	0.91	1.00	0.95	10
avg / total	0.97	0.96	0.96	27

SVM RBF
0.7777777777777778

	precision	recall	f1-score	support
0	1.00	0.65	0.79	17
1	0.62	1.00	0.77	10
avg / total	0.86	0.78	0.78	27

DNA classification

Random Forest
0.5925925925925926

	precision	recall	f1-score	support
0	0.88	0.41	0.56	17
1	0.47	0.90	0.62	10
avg / total	0.73	0.59	0.58	27

Neural Net
0.9259259259259259

	precision	recall	f1-score	support
0	1.00	0.88	0.94	17
1	0.83	1.00	0.91	10
avg / total	0.94	0.93	0.93	27

AdaBoost
0.8518518518518519

	precision	recall	f1-score	support
0	1.00	0.76	0.87	17
1	0.71	1.00	0.83	10
avg / total	0.89	0.85	0.85	27

SVM Sigmoid
0.4444444444444444

	precision	recall	f1-score	support
0	1.00	0.12	0.21	17
1	0.40	1.00	0.57	10
avg / total	0.78	0.44	0.34	27

4. CONCLUSIONS

Healthcare delivery has over years become complex and challenging. an outsized a part of the complexity in delivering healthcare is due to the voluminous data that's generated within the process of healthcare, which has got to be interpreted in an intelligent fashion. AI systems with their problem solving approach can address this need. Their intelligent architecture, which includes learning and reasoning and skill to act autonomously without requiring constant human attention, is alluring. Thus the medical domain has provided a fertile ground for A researchers to

check their techniques and in many instances; AI applications have successfully solved problems with outcomes like that of human clinicians. As health care delivery becomes costlier, stakeholders will increasingly look to solutions which will replace the expensive elements in patient care and AI solutions are going to be wanted in these situations. However cold technology cannot totally replace the human elements in patient care and a model that comes with both technological innovations and human care has got to be investigated.

REFERENCES

- [1] Amit David and Boaz Lerner, "PATTERN CLASSIFICATION USING A SUPPORT VECTOR MACHINE FOR GENETIC DISEASE DIAGNOSIS" Proceedings. 2004 23rd IEEE Convention of Electrical and Electronics Engineers in Israel, pp 289~292.
- [2] Yan Zhang, Fugui Liu, Zhigang Zhao, Dandan Li, Xiaoyan Zhou, Jingyuan Wang, "Studies on application of Support Vector Machine in diagnose of coronary heart disease" Sixth International Conference on Electromagnetic Field Problems and Applications (ICEF), 2012, pp 1~4.
- [3] Saeed Shariati, Mahdi Motavalli Haghighi, "Comparison of ANFIS Neural Network with Several Other ANNs and Support Vector Machine for Diagnosing Hepatitis and Thyroid Diseases", International Conference on Computer Information Systems and Industrial Management Applications (CISIM), 2010, pp 596~599.
- [4] Hanaa Ismail Elshazly, Abeer Mohamed Elkorany, Aboul Ella Hassanien, "Lymph diseases diagnosis approach based on support vector machines with different kernel functions", 9th International Conference on Computer Engineering & Systems (ICCES), 2014, pp 198~203.
- [5] D. Tomar; B. R. Prasad; S. Agarwal, "An efficient Parkinson disease diagnosis system based on Least Squares Twin Support Vector Machine and Particle Swarm Optimization" 9th International Conference on Industrial and Information Systems (ICIIS), 2014, pp 1~6.
- [6] Tomar, Divya, and Sonali Agarwal. "Feature Selection based Least Square Twin Support Vector Machine for Diagnosis of Heart Disease." International Journal of Bio-Science & Bio-Technology 6(2), (2014).
- [7] S. Ghosh; S. Mondal; B. Ghosh, "A Comparative Study of Breast Cancer Detection based on SVM and MLP BPN Classifier", First International Conference on Automation, Control, Energy and Systems (ACES), 2014, pp 1~4.
- [8] Avik Basu, Sanjiban Sekhar Roy, Ajith Abraham, "A Novel Diagnostic Approach Based on Support Vector Machine with Linear Kernel for classifying the erythematosquamous disease", International Conference on Computing Communication Control and Automation (ICCUBEA), 2015, pp 343 - 347.
- [9] Seyede Zahra Paylakhi, Sadjad Ozgoli, Seyed Hassan Paylakhi, "A novel gene selection method using GA/SVM and Fisher criteria in Alzheimer's disease", IEEE 23rd Iranian Conference on Electrical Engineering (ICEE) 2015.
- [10] Mohammed El Amine LAZOUNI, Nesma SETTOUTI, Mostafa El HABIB DAHO, Mostafa El HABIB DAHO, "An SVM Intelligent System for Pre-anesthetic Examination", IEEE Second World Conference on Complex Systems (WCCS), 2014, pp 73 - 78.
- [11] Tipawan Silwattananusarn, Wanida Kanarkard, Kulthida Tuamsuk, "Enhanced Classification Accuracy for Cardiotocogram Data with Ensemble Feature Selection and Classifier Ensemble", Journal of Computer and Communications, 2016, 4, 20-35.
- [12] Austeclino Magalhaes Barros Junior, Angelo Amancio Duarte, Manoel Barral Netto/Bruno Bezerril Andrade, "ARTIFICIAL NEURAL NETWORKS AND BAYESIAN NETWORKS AS SUPPORTING TOOLS FOR DIAGNOSIS OF ASYMPTOMATIC MALARIA" 12th IEEE International Conference on e-Health Networking Applications and Services (Healthcom), 2010, pp 106 - 111.
- [13] Carlos Arizmendi, Daniel A. Sierra, Alfredo Vellido, Enrique Romero, "Brain Tumour Classification Using Gaussian Decomposition and Neural Networks", 33rd Annual International Conference of the IEEE EMBS Boston, Massachusetts USA, August 30 - September 3, 2011, pp 5645-5648.
- [14] Luis Javier Herrera, Ignacio Rojas, H. Pomares, A. Guillén, O. Valenzuela, O. Baños, "Classification of MRI images for Alzheimer's disease detection", SocialCom/PASSAT/BigData/EconCom/BioMedCom 2013, pp 846-851.
- [15] Mrudula Gudadhe, Kapil Wankhade, Snehlata Dongre, "Decision Support System for Heart Disease based on Support Vector Machine and Artificial Neural Network", IEEE International Conference on Computer & Communication Technology (ICCC'10), pp 741-745.
- [16] Suchita Saha, Santanu Ghorai, "Effect of Feature Fusion for Discrimination of Cardiac Pathology", Third International Conference on Computer, Communication, Control and Information Technology (C3IT), 2015, pp 1-6.
- [17] R. Suganya, S. Rajaram, "Feature Extraction and Classification of Ultrasound Liver Images using Haralick Texture-Primitive Features: Application of SVM Classifier", 2013 International Conference on Recent Trends in Information Technology (ICRTIT), pp 596 - 602.
- [18] Muhammad Fathurachman, Umi Kalsum, Noviyanti Safitri, Chandra Prasetyo Utomo, "Heart Disease Diagnosis using Extreme Learning Based Neural Networks", 2014 International Conference of Advanced Informatics: Concept, Theory and Application (ICAICTA), pp 23-27.
- [19] Paweł Marciniak, Rafał Kotas, Marek Kamiski, Zygmunt Ciota, "Implementation of Artificial Intelligence Methods on Example of Cardiovascular Diseases Risk Stratification", MIXDES 2014, 21st
- [20] International Conference "Mixed Design of Integrated Circuits and Systems", June 19- 21, 2014, Lublin, Poland, pp 503-507. Kornack and P. Rakic, "Cell Proliferation without Neurogenesis in Adult Primate Neocortex," Science, vol. 294, Dec. 2001, pp. 2127-2130, doi:10.1126/science.1065467. M. Young, The Technical Writer's Handbook. Mill Valley, CA: University Science, 1989. R. Nicole, "Title of paper with only first word capitalized," J. Name Stand. Abbrev., in press. K. Elissa, "Title of paper if known," unpublished.

BIOGRAPHIES



Hemkar Goswami

I want to utilize essential elements of my learning in developing, evolving, and implementing the best of software programming.



Darsh Sharma

I have been interested in Artificial Intelligence and strive to work towards gaining more knowledge in many different algorithms .