



AI Based Disease Prediction Technology Research on DPT-AI

Mr. Buddh Bhagwan Sahu
Assistant Professor

Columbia Institute of Engineering and Technology, Raipur-493111

Abstract: AI Based disease prediction technology will provide the latest in preconception screening and non-invasive prenatal testing for a variety of genetic and developmental disorders. We have established a network of counseling services & other resources to help our patients understand the results and make the most informed medical decisions possible [12]. At present our research work will be executed based on manual data and dataset. In the department of computer science & engineering implementing disease predictions methods given by **Buddh Bhagwan Sahu (Asst. Professor, Dept. of CS&E at Columbia Institute of Engineering and Technology, Tekari-493111, Raipur-CG)** at initial we are building its manual version that disease prediction technology will change the human health in outstanding and it will be a futuristic personal evaluations designed to assess and address your individual risk factors for **Dementia, Including Alzheimer's, Cancer, Heart Attachés disease**[11]. We couple this testing with counseling services to help you understand the results and make the most informed decisions regarding any potential interventions. It is now possible to test an individual for risk of a number of treatable genetic conditions, and also to assess overall risk of some common conditions including animal health, emerging diseases, good practice, modeling, public health, risk factors [10].

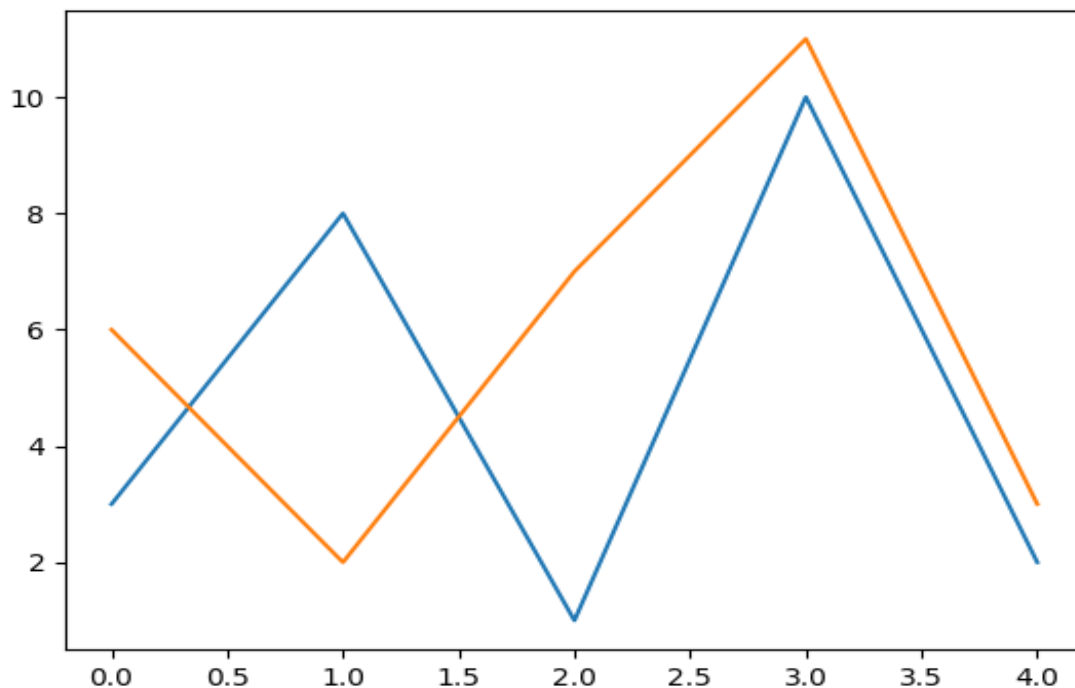
Keys: Prediction, Personalization, Participation, Database, Non-communicable chronic diseases, Proactive, Healthcare innovation and Prevention, Dataset.

React with quantitative models:

Making the kinds of predictions listed in requires some kind of 'model', even if this is only a mental model presenting here based on previous experience, expert opinion or a back-of-the-envelope calculation [15]. For some questions, this may be adequate. For other questions, these informal approaches can be highly unreliable, the reason being that **infectious diseases have nonlinear dynamics** [9]. One way to express this is that the biggest risk factor for acquiring an infection is the presence of infectious individuals, which introduces **positive feedback into epidemic processes**, in turn making the expected trajectory of an epidemic or the likely impact of control measures considerably more **difficult to predict** than is the case for non-communicable diseases such as **stroke, cancer or obesity** [14]. On occasion, these nonlinearities can make infectious disease dynamics counterintuitive.

Examples are:

Non-linearity's in infection dynamics. Force-of-infection and duration of an outbreak. Reduced force-of-infection can increase the expected duration of an outbreak, as illustrated by two numerical realizations of the **standard susceptible–latent–infectious–recovered (SLIR)** model [13]. Illustrates the simple but important observation that decreasing the transmission rate does, as might be expected, reduce the size of an outbreak but may increase rather than decrease the duration of the outbreak [16]. When some of the major consequences of an epidemic are indirect—such as common factors **closure of schools, restrictions on travel or trade or loss of tourism revenue**—and reflect only the presence of disease rather than the absolute numbers of cases, then the increased duration represents a serious problem[8].

**Technical Support:**

1. **Python:** Object Scripting
2. **Scribe:** AI-powered process documentation tool.
3. **Tabnine:** AI-powered code completion tool.
4. **Copilot:** AI-powered code completion and prediction tool.
5. **Otter.Ai:** AI-powered meeting and transcription tool[1].
6. **DeepCode AI:** Bug detection and code analysis tool.

Workflow & Implementation:

At present we are implementing manual version based huge collection of data [17]. Data will give hundred percent accurate data and result will be more accurate because in this method we are using linear, nonlinear algorithms. In this study, extensive research efforts were made to identify those studies that applied support vector machine, logistic regression and artificial neural network more than one supervised machine learning algorithm on single disease prediction comes might be ad ones[18]. Specifically - supervised learning algorithms. Models based on these algorithms use labeled training data of patients for training for the test set; patients are classified into several groups such as low risk and high

risk. Given the growing applicability and effectiveness of supervised machine learning algorithms on predictive disease modeling, the breadth of research still seems progressing [7].

```
import matplotlib.pyplot as plt
import numpy as np
d1 = np.array([3, 8, 1, 10, 2])
d2 = np.array([6, 2, 7, 11, 3])
plt.plot(d1)
plt.plot(d2)
plt.show()
```

A explainer histogram is a graph showing frequency distributions based on data [6]. It is a graph showing the number of observations within each given interval. For simplicity we use NumPy to randomly generate an array with 150 values, where the values will concentrate around 270, and the standard deviation is 10[2]. Learn more about Normal Data Distribution in our Machine Learning Techniques [19].

```
[266.69846888 260.77141614 284.72131917 270.84359957 265.19465117
256.8159584 273.27472654 254.88012427 266.54630958 285.0825665
269.52201696 281.1336315 268.75283559 283.90365555 266.68255649
270.0059768 265.17199175 258.44740357 268.32674187 280.88844796
287.41434316 276.02913608 266.86705348 278.44523973 256.03525592
276.5449366 266.5789355 259.51761077 285.62354318 263.60434115
269.02151649 265.99602115 281.49098228 274.43841164 275.80790161
266.63093663 254.91505863 273.32042075 272.07106474 280.79760056
262.6083223 276.7090443 253.23917285 262.31118221 251.74270531
285.68613877 279.06272351 281.41975209 277.75632278 276.82567571
270.61969835 254.85709501 283.92880215 264.7958871 266.87703049
271.54234396 272.08285392 260.46363622 266.63054755 276.96937613
272.02479191 276.47696227 266.35010354 293.61241702 290.29652951
277.10371199 265.79913661 262.13304393 264.80998332 282.98545907
275.49808353 283.42565083 262.35895522 266.96120387 251.66377026
263.14104651 265.93355039 273.99795007 292.70123389 281.7512179
262.0701459 266.62410392 253.22323574 272.74322591 267.20079429
284.58275851 257.97998243 272.9501147 261.74488401 269.99588371
284.58458676 269.30348581 268.07174638 280.27637077 259.57863839
266.79249515 281.58708967 267.25801945 267.81367768 280.18556265
272.16164147 273.34428137 270.46944949 265.00259331 269.75177145
282.45709189 272.54977376 263.9486766 273.29826807 266.71042637
267.81593537 280.61101985 286.87173433 255.92814935 283.104576
270.28580294 268.24320888 270.82171344 260.25890633 269.32073762
270.79767992 281.36722977 257.45724876 269.61464361 274.08496585
278.47934502 258.96958043 286.86598267 263.20774861 280.17546627
275.45442485 274.33459623 268.93795165 266.03014899 250.99912314
261.4849068 273.66948658 270.48412714 279.97216983 288.14344339
288.3025187 267.05819367 264.21485739 260.65457158 265.38784007
281.89044758 260.58028671 275.24960852 266.66313042 276.40751774]
```

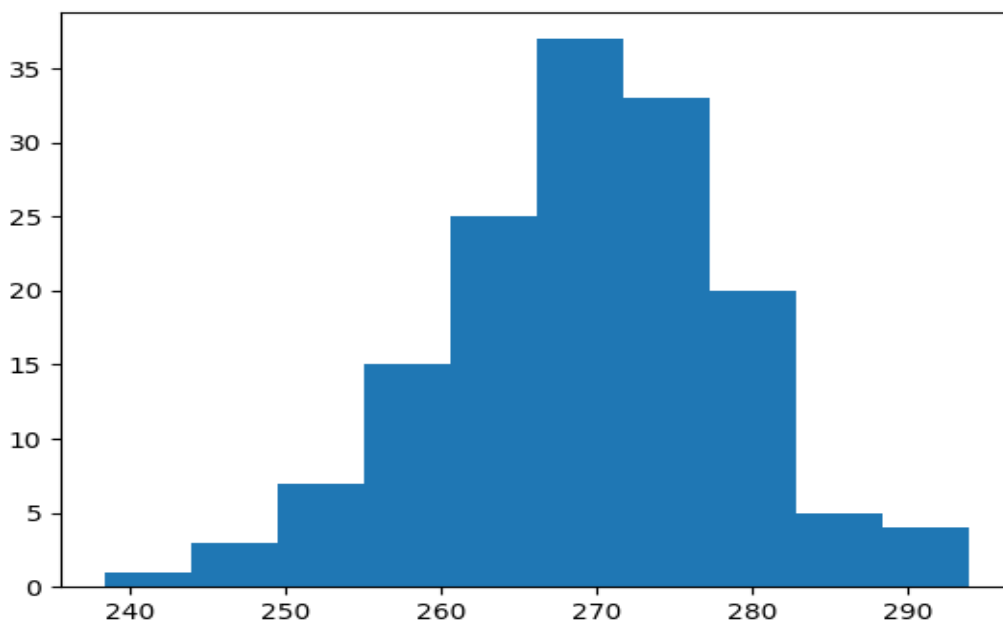
Using the simple NumPy and displayed random histogram on the screen it will be more accurate in futures [5].

```
import numpy as np
x = np.random.normal(270, 10, 150)
print(x)
```

or

The hist() function will read the array and produce a histogram in random format like[4].

```
import matplotlib.pyplot as plt
import numpy as np
d = np.random.normal(270, 10, 150)
plt.hist(d)
plt.show()
```



i.e.

Futures:

The kinds of formal, quantitative analysis described here can be valuable guides towards answering questions such as how **probable a disease outbreak is, how far and how fast it will spread, and how best to control it**[3]. But how much reliance should be placed on the outputs of these analyses. One area where quantitative analysis and prediction have been highly successful in informing policy is climate change modeling.

Reference:

1. T. M. Mitchell, "Machine learning WCB": McGraw-Hill Boston, MA:, 1997.
2. Sebastiani F. Machine learning in automated text categorization. *ACM Comput Surveys (CSUR)*. 2002;34(1):1–47.
3. Sinclair C, Pierce L, Matzner S. An application of machine learning to network intrusion detection. In: *Computer Security Applications Conference, 1999. (ACSAC'99) Proceedings. 15th Annual; 1999*. p. 371–7. IEEE.
4. Sahami M, Dumais S, Heckerman D, Horvitz E. A Bayesian approach to filtering junk e-mail. In: *Learning for Text Categorization: Papers from the 1998 workshop*, vol. 62; 1998. p. 98–105. Madison, Wisconsin.
5. Aleskerov E, Freisleben B, Rao B. Cardwatch: A neural network based database mining system for credit card fraud detection. In: *Computational Intelligence for Financial Engineering (CIFER), 1997., Proceedings of the IEEE/IAFE 1997; 1997*. p. 220–6. IEEE.
6. E, Kim W, Lee Y. Combination of multiple classifiers for the customer's purchase behavior prediction. *Decis Support Syst*. 2003;34(2):167–75.
7. Palaniappan S, Awang R. Intelligent heart disease prediction system using data mining techniques. In: *Computer Systems and Applications, 2008. AICCSA 2008. IEEE/ACS International Conference on; 2008*. p. 108–15. IEEE.
8. Joachims T. Making large-scale SVM learning practical. SFB 475: *Komplexitätsreduktion Multivariaten Datenstrukturen*, Univ. Dortmund, Dortmund, Tech. Rep. 1998. p. 28.
9. Quinlan JR. Induction of decision trees. *Mach Learn*. 1986;1(1):81–106.

10. Cruz JA, Wishart DS. Applications of machine learning in cancer prediction and prognosis. *Cancer Informat.* 2006;2:59–77.
11. Palaniappan S, Awang R. Intelligent heart disease prediction system using data mining techniques. In: *Computer Systems and Applications, 2008. AICCSA 2008. IEEE/ACS International Conference on*; 2008. p. 108–15. IEEE.
12. Joachims T. Making large-scale SVM learning practical. SFB 475: Komplexitätsreduktion Multivariaten Datenstrukturen, Univ. Dortmund, Dortmund, Tech. Rep. 1998. p. 28.
13. Cruz JA, Wishart DS. Applications of machine learning in cancer prediction and prognosis. *Cancer Informat.* 2006;2:59–77.
14. I. Rish, “An empirical study of the naive Bayes classifier,” in *IJCAI 2001 workshop on empirical methods in artificial intelligence*, 2001, vol. 3, 22, pp. 41–46: IBM New York.
15. McCulloch WS, Pitts W. A logical calculus of the ideas immanent in nervous activity. *Bull Math Biophys.* 1943;5(4):115–33.
16. Falagas ME, Pitsouni EI, Malietzis GA, Pappas G. Comparison of PubMed, Scopus, web of science, and Google scholar: strengths and weaknesses. *FASEB J.* 2008;22(2):338–42.
17. Borah MS, Bhuyan BP, Pathak MS, Bhattacharya P. Machine learning in predicting hemoglobin variants. *Int J Mach Learn Comput.* 2018;8(2):140–3.
18. Ayer T, Chhatwal J, Alagoz O, Kahn CE Jr, Woods RW, Burnside ES. Comparison of logistic regression and artificial neural network models in breast cancer risk estimation. *Radiographics.* 2010;30(1):13–22.
19. Chen M, Hao Y, Hwang K, Wang L, Wang L. Disease prediction by machine learning over big data from healthcare communities. *IEEE Access.* 2017;5:8869–79.

