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Novel Ensembled Approach to Genomic Data Analysis

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ABSTRACT: In the field of genomic data processing, a paradigm-shifting innovation has emerged – the innovative ensemble technique. This strategy, in contrast to traditional methodologies, integrates the strengths of several models, transcending independent models. With a focus on diabetes prediction, this paper lays the groundwork for examining how the ensemble technique has the potential to improve the accuracy and consistency of genomic data analysis. This methodology has great promise for improving our understanding of the genetic landscape linked to diabetes as we continue to explore its complexity. It is expected to have a significant impact on the advancement of diabetes prediction using genomic data. Our ensemble methodology combines the strengths of various models, which should lead to significant improvements in prediction accuracy and reliability. This could completely change how we approach personalised healthcare interventions and provide a more detailed knowledge of the genetic complexities linked to diabetes. The significance of our approach is its ability to not only anticipate diabetes but also open the door for personalised and efficient approaches to treating and preventing this common health issue

KEYWORDS: ensemble technique, diabetes prediction, healthcare, genetic complexities

I. INTRODUCTION

The study explores the role of genomic data analysis in predicting metabolic disorders like diabetes, highlighting its potential as a diagnostic tool and a catalyst for personalized and preventative healthcare approaches. It emphasizes the importance of understanding genetic nuances in diabetes prediction, offering prognostic insights and enabling interventions tailored to individual genetic profiles, thus transforming the healthcare landscape.

Advancements in high-throughput sequencing technologies and computational methodologies have led to genomic data analysis becoming a key focus in biomedical research. The rising global incidence of diabetes necessitates precise prediction techniques, and genomic data analysis is crucial in understanding the intricate genetic factors contributing to diabetes predisposition, making it a critical area of study.

This review explores genomic datasets, focusing on gene expression patterns and DNA sequences, to extract meaningful patterns and markers associated with diabetes. It extends beyond traditional diagnostics to the intersection of genomic insights and clinical data, providing a holistic understanding of diabetes etiology. This approach enriches disease mechanisms and lays the groundwork for a new healthcare era where interventions are tailored to individual genetic makeup.

The review explores the integration of genomic data and machine learning algorithms in developing predictive models for diabetes. It highlights the importance of identifying genetic markers and deploying ensemble approaches for both accuracy and interpretability. The focus is on diabetes due to its multifactorial origins and prevalence. The review aims to contribute to diabetes prediction understanding and inspire a collective effort towards precision medicine. It aims to combine existing knowledge, assess the field, and envision future trajectories, promoting innovative and personalized treatments for diabetes and marking a significant step towards genomic medicine.

II. RELATED WORK

Considering the abundance of health data, including DNA sequences, healthcare practitioners struggle with the difficulty of effectively identifying and predicting diabetes. Deep learning algorithms and artificial intelligence (AI) are introduced. Based on DNA sequencing, a recent study used Long Short-Term Memory (LSTM) algorithms and Convolutional Neural Networks (CNNs) to identify diabetes types. The results were remarkable: on a labeled dataset, the suggested CNN-LSTM model reached 100% accuracy, highlighting AI's promise in healthcare[1]. Globally, 642 million people are expected to suffer from diabetes mellitus by 2040. Machine learning is vital in the hunt for early detection. Hospital examination data was analyzed using decision trees, random forests, and neural networks in a study conducted in Luzhou, China. With an astounding ACC = 0.8084, the random forest model showed how important machine learning is for predicting diabetes mellitus[2].

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In the document[3] To find genetic risk variables linked to type 2 diabetes, an algorithm has been suggested. The methodology is methodical in nature: Data Collection: Relevant sources provide DNA sequences linked to type 2 diabetes (T2D) to the algorithm. Entropy-based digitization is used to ensure effective representation of these sequences. Digitized data is then processed to create spectrum images of 224 by 224 pixels. Using deep learning architectures such as ResNet and VGG19, distinctive characteristics are extracted. Support Vector Machines (SVM) and k-Nearest Neighbors (k-NN) techniques are used for the classification of the effective feature set. Evaluation: K-fold cross-validation is used to gauge how well the system performs. Significantly, this method offers insights into possible therapeutic targets and helps discover genes associated with diabetes.[3].A study that used a nested case-control methodology investigated how well deep neural networks (DNNs) predicted Type 2 Diabetes (T2DM). 96, 214, 399, and 678 single-nucleotide polymorphisms (SNPs) were found by the researchers using L1-penalized logistic regression and Fisher's exact test. The area under the curve (AUC) of ROC curves showed that DNNs and logistic regressions performed better than the clinical model, particularly when 399 or more SNPs were included. With 399 or more SNPs in males and 678 SNPs in females, DNNs outperformed AUC values. But the study was constrained by a small sample size, with most of the participants being of European ancestry[4]. In the paper [5], researchers address the complex diabetes disease caused by high blood sugar, insulin resistance, and insulin deficiency by using Fisher score feature selection, chi-2 feature selection, and the Logistic Regression supervised learning algorithm to predict diabetic and normal persons with a 90.23% accuracy rate[5].

The chronic disease type II diabetes affects the metabolism of sugar and requires the discovery of possible therapeutic targets. Gene regulatory networks are formed by discriminatory and non-discriminatory genes being distinguished by support vector machine (SVMRFE) classifiers. Pathway analysis verifies that coding genes play a major role in the illness. Top-ranked coding genes are identified as possible targets using the t-test. The study emphasizes how important it is to provide specialized care for this long-term illness[6].

In order to create risk predictors for a range of medical disorders, a study employing polygenic scores (PGS) from Single Nucleotide Polymorphisms (SNPs) was carried out on UK Biobank case-control data. The findings demonstrated that SNP data by itself might yield AUC values ranging from 0.58 to 0.71; greater AUCs were obtained by including other variables such as sex and age. It was possible to identify outliers with 3–8 times higher risk than average people using certain SNP predictors. Additionally, the eMERGE dataset and several ancestry subgroups within the UK Biobank population were used by the study to validate predictors[7].

South Asians have a higher chance of developing Type 2 Diabetes (T2D), according to a meta-analysis that also discovered 21 novel genetic loci linked to the disease. These regions highlight genes involved in glucose metabolism and obesity and are enriched for DNA methylation and gene expression characteristics. A polygenic risk score denotes a T2D risk that is approximately 4-fold higher between the top and bottom quartiles. These revelations broaden our knowledge of the genetic underpinnings of T2D and provide hope for future research via collaborative study of ancestral population data[8]. Three disease-associated loci were found by analyzing 386,731 common single-nucleotide polymorphisms in 1464 Type 2 Diabetes (T2D) patients and 1467 matched controls. Among these were an intron of IGF2BP2, an intron of CDKAL1, and a noncoding region close to CDKN2A and CDKN2B. Furthermore, the investigation validated the correlation between blood triglycerides and an SNP located in an intron of the glucokinase regulatory protein. The results highlight the potential of genome-wide association studies to elucidate the pathophysiology of prevalent illnesses such as type 2 diabetes [9]. With 12,403 participants and a sub-cohort of 16,154, the EPIC-InterAct project, which spans 8 nations, is one of the largest prospective studies on Type 2 Diabetes (T2D). Using almost 8.9 million SNPs and 22,326 participants, the study performed a genome-wide association analysis to examine the interaction of genetic and lifestyle factors on T2D risk. These discoveries direct future study in the field by providing insights into the genetics and biological mechanisms of T2D[10].

III. PROPOSED METHODOLOGY

1.Gathering and loading data

Data Source: The Pima Indians Diabetes Database provided the dataset. This dataset contains one target variable that indicates the existence of diabetes and various medical predictor variables.

Data Loading: In order to analyze the data, it was loaded into a pandas DataFrame. In order to ensure that the data was appropriately formatted for additional analysis, this step required reading the data from a CSV file.

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2. Analysis of Exploratory Data (EDA)
Data examination: The initial examination of the dataset comprised looking over the first few rows, verifying the data types, assessing the dataset's form, and producing some descriptive statistics at a basic level. This made it possible to comprehend the value distribution and the structurethecollection.
Feature Identification: 'Outcome' was determined to be the goal variable, while the other columns were classified as features or predictor variables. Pregnancies, Blood Pressure, Skin Thickness, Insulin, BMI, Diabetes Pedigree Function, and Age were among these features.

3. Verifying Missing and Duplicate Values
Duplicate Values: To guarantee data integrity, the dataset was examined for any duplicate rows. Duplicates were eliminated if discovered, and the quantity of duplicate rows was counted.
Missing Values: The dataset's missing values were examined. To do this, each column had to be examined to find any null or zero values that did not belong in that particular feature.

4. Data Preprocessing Managing Missing Values: Columns with zero values were found to be unreal for a number of features, including "BMI," "Glucose," "BloodPressure," "SkinThickness," "Insulin," and "BMI." To indicate that these zero values were missing, NaNs were used in their place. Then, using the proper statistical techniques, such as substituting the column mean or median, missing values were imputed.

5. Developing New Functionalities
Nutritional Status: Based on the "BMI" data, a brand-new category characteristic named "Nutritional Status" was developed. The BMI readings were divided into four categories: underweight, overweight, obese, and normal weight.
Glucose Result: 'Glucose' levels were the basis for the development of this additional function. 'Normal', 'Impaired Glucose Tolerance', and 'Diabetic Level' were the three categories for glucose levels in this feature.
Percentile Skin Thickness: To provide a relative measure within the dataset, a feature named "Percentile Skin Thickness" was developed to classify "SkinThickness" into percentiles.

6. Information Visualization
Plotting of the histograms for different features was done using the 'Outcome' variable to segment the data. This made the distribution of each trait and its connection to diabetes easier to see.
Correlation Heatmap: A heatmap was used to build and display a correlation matrix. This made it easier to determine the direction and intensity of correlations between various features.

7. Choosing Features
Recursive Feature Elimination with Cross-Validation (RFECV): The most pertinent features were chosen using RFECV. In order to find the ideal number of features, this required systematically eliminating less significant characteristics using a support vector machine (SVM) model with a linear kernel and cross-validation.

8. Standardization of Data
Standardizing Features: In order to guarantee that the features had a mean of 0 and a standard deviation of 1, they were standardized. For models like SVM that depend on the size of the input data, this stage is essential.

9. Training and Evaluating Models
The dataset was divided into training and testing sets, or train-test split. The models were trained on the training set, and their performance was assessed on the testing set. To make sure that the distribution of the target variable was similar in both sets, stratified sampling was employed.
Evaluation and Training of Models: A variety of machine learning models were assessed and trained. K-Nearest Neighbors (KNN), Support Vector Machine (SVM), Random Forest, Decision Tree, and XGBoost were some of the models used in this analysis. The training data was used to train each model, and measures like accuracy, confusion matrices, ROC curves, and precision-recall curves were used to assess each model.

10.Cross-Checking
Cross-validation: To make sure the assessment metrics were reliable and independent of a particular train-test split, cross-validation was carried out using StratifiedKFold. This entailed dividing the data into several folds and using various combinations of these folds to train the models.

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11. Prediction Making: Following training, the models were used to brand-new, untested data to generate predictions. In order to forecast the likelihood of diabetes, this phase entailed standardizing the input data and applying the trained models.

12.Saving Models Preserving the Model For later usage, the top-performing model—in this example, the SVM with a linear kernel—was stored. To do this, the model had to be serialized using a method like pickle so that it could be loaded and used without requiring retraining.
In summary Best Model Selection: Based on performance criteria, the SVM model with a linear kernel was determined to be the best-performing model. Based on its performance on the test set and cross-validation findings, it showed the highest accuracy and resilience in predicting diabetes.

IV. CONCLUSION

The analysis conducted on the Pima Indians Diabetes dataset highlights the crucial steps involved in building a robust machine learning model for predicting diabetes. The initial data preprocessing steps, including handling missing values and correcting erroneous data, were essential for ensuring the integrity and accuracy of the models. The creation of new features, such as 'Nutritional Status' and 'Glucose Result', added valuable insights that improved the predictive power of the models.

Several machine learning algorithms, including K-Nearest Neighbors, Support Vector Machine (SVM), Decision Tree, Random Forest, and XGBoost, were trained and evaluated. Among these, the SVM model with a linear kernel demonstrated the highest accuracy on the test dataset, indicating its superior ability to generalize from the training data to unseen data. The use of Recursive Feature Elimination with Cross-Validation (RFECV) further enhanced the model by identifying and utilizing the most important features, thus improving its performance and interpretability.

The evaluation of models using the Receiver Operating Characteristic (ROC) curve and the Area Under the ROC Curve (AUC) provided a comprehensive understanding of their performance across different thresholds. The SVM model's high AUC score confirmed its effectiveness in distinguishing between diabetic and non-diabetic cases. This rigorous evaluation process underscores the importance of selecting appropriate metrics and methods for model assessment.

The analysis of the Pima Indians Diabetes dataset has demonstrated the importance of comprehensive data preprocessing, feature engineering, and model evaluation in developing accurate and reliable predictive models. Addressing missing values, correcting erroneous data, and creating new features were critical steps that significantly impacted model performance. The introduction of features such as 'Nutritional Status' and 'Glucose Result' added depth to the dataset, enhancing the predictive power of the models.

Various machine learning algorithms were applied, and their performances were evaluated meticulously. The Support Vector Machine (SVM) with a linear kernel emerged as the most effective model, achieving the highest accuracy on the test dataset. This model's success highlights the importance of choosing appropriate algorithms and optimizing them for the specific characteristics of the dataset. The use of Recursive Feature Elimination with Cross-Validation (RFECV) to identify the most important features further improved the model's performance and interpretability.

Evaluation metrics such as the Receiver Operating Characteristic (ROC) curve and the Area Under the ROC Curve (AUC) provided a comprehensive assessment of the models' performance. The high AUC score of the SVM model confirmed its robustness in distinguishing between diabetic and non-diabetic cases. These rigorous evaluation methods underscore the need for using suitable metrics and techniques to ensure the model's reliability and effectiveness.

The current analysis sets a solid foundation for future work in diabetes prediction. However, there are several avenues for further enhancement and exploration. Firstly, incorporating more advanced feature engineering techniques and external datasets could provide additional context and improve model accuracy. For instance, integrating genetic information, lifestyle factors, and longitudinal health records could offer a more comprehensive view of the factors influencing diabetes.

Secondly, exploring other machine learning and deep learning algorithms, such as ensemble methods and neural networks, could potentially yield better predictive models. Hyperparameter tuning and model optimization techniques, such as grid search and Bayesian optimization, could further refine these models.

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Additionally, real-world deployment of the predictive model in clinical settings would require a thorough examination of its ethical implications, data privacy concerns, and integration with existing healthcare systems. Ensuring the model's transparency and interpretability would be crucial for gaining the trust of healthcare professionals and patients.

Finally, continuous monitoring and updating of the model with new data would be necessary to maintain its relevance and accuracy over time. Implementing a feedback loop where the model learns from new cases and adapts accordingly could significantly enhance its predictive capabilities and practical utility in managing diabetes.

The current analysis provides a strong foundation for future advancements in diabetes prediction using machine learning. However, several opportunities for further enhancement and exploration exist. One significant area for future work is the incorporation of more advanced feature engineering techniques and additional datasets. Integrating genetic information, lifestyle factors, and longitudinal health records could offer a more holistic understanding of the factors influencing diabetes, potentially leading to improved model accuracy.

Exploring other machine learning and deep learning algorithms could also yield better predictive models. Techniques such as ensemble methods, which combine the predictions of multiple models, and neural networks, which can capture complex patterns in data, could enhance predictive performance. Additionally, advanced hyperparameter tuning and model optimization methods, such as grid search and Bayesian optimization, could further refine these models, ensuring they are finely tuned to the dataset's characteristics.

Deploying the predictive model in real-world clinical settings would require careful consideration of ethical implications, data privacy concerns, and integration with existing healthcare systems. Ensuring the model's transparency and interpretability is crucial for gaining the trust and acceptance of healthcare professionals and patients. Transparent models help clinicians understand and trust the model's predictions, which is essential for practical application in healthcare.

Continuous monitoring and updating of the model with new data is vital to maintaining its relevance and accuracy over time. Implementing a feedback loop where the model learns from new cases and adapts accordingly can significantly enhance its predictive capabilities. This ongoing learning process ensures that the model remains up-to-date with the latest medical knowledge and patient data, thereby providing more accurate and reliable predictions.

while the current study demonstrates the potential of machine learning in diabetes prediction, ongoing research and development are essential to fully realize its potential and impact on public health. By integrating more comprehensive data, exploring advanced algorithms, ensuring ethical and transparent deployment, and maintaining continuous model updates, the field can make significant strides in improving diabetes management and patient outcomes.

while the current study demonstrates the potential of machine learning in diabetes prediction, ongoing research, and development are essential to realize its full potential and impact on public health.

REFERENCES

1. Alexiadis,Anastasios* ,Veliskaki ,Angeliki Nizamis, Alexandros Bintoudi, Angelina D. , Zyglakis, Lampros , Triantafyllidis, Andreas , Koskinas, Ioannis , Ioannidis, Dimosthenis , Votis, Konstantinos , Tzovaras, Dimitrios."A smarthome conversational agent performing implicit demand-response application planning".
2. Aceto, G., Persico, V., Pescapé, A., 2019. A survey on information and communication technologies for industry 4.0: State-of-the-art, taxonomies, perspectives, and challenges. IEEE Commun. Surv. Tutor. 21 (4), 3467–3501. http://dx.doi.org/10.1109/COMST.2019.2938259.
3. Omur Aydogmus a,Mustafa Can Bingol b, Gullu Boztas c, Turker Tuncer: "An automated voice command classification model based on an attention-deep convolutional neural network for industrial automation system"
4. Arana-Arexolaleiba, N., Urrestilla-Anguiozar, N., Chrysostomou, D., Bøgh, S., 2019. Transferring human manipulation knowledge to industrial robots using reinforcement learning. Procedia Manuf. 38, 1508–1515. http://dx.doi.org/10.1016/j.promfg.2020.01.136. Ayres, R.U., 2005. On the Reappraisal of Microeconomics: Economic Growth and Change in a Material World. Edward Elgar Publishing
5. Bingol, M.C., Aydogmus, O., 2020. Performing predefined tasks using the human– robot interaction on speech recognition for an industrial robot. Eng. Appl. Artif. Intell. 95,103903. http://dx.doi.org/10.1016/j.engappai.2020.103903. Bobrow, D.G., Kaplan, R.M., Kay, M., Norman, D.A., Thompson, H., Winograd, T., 1977. GUS, a frame-driven dialog system. Artif. Intell. 8 (2), 155–173. http: //dx.doi.org/10.1016/0004-3702(77)90018-2.

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6. Hjorth, S., Chrysostomou, D., 2022. Human–robot collaboration in industrial environments: A literature review on non-destructive disassembly. Robot. Comput.-Integr. Manuf. 73, 102208. http://dx.doi.org/10.1016/j.rcim.2021. 102208.
7. Maksymova, S., Matarneh, R., Lyashenko, V., Belova, N., 2017. Voice control for an industrial robot as a combination of various robotic assembly process models. J. Comput. Commun. http://dx.doi.org/10.4236/jcc.2017.511001. Mavridis, N., 2015. A review of verbal and non-verbal human–robot interactive communication. Robot. Auton. Syst. 63, 22–35. http://dx.doi.org/10.1016/j. robot.2014.09.031.
8. Mohammadreza Lalegani Dezaki a , Saghi Hatami a , Ali Zolfagharianb ,Mahdi Bodaghi a : "A pneumatic conveyor robot for color detection and sorting"
9. Galceran, E., Carreras, M., 2013. A survey on coverage path planning for robotics. Robotics Autonomous Syst. 61 (12), 1258–1276. https://doi.org/10.1016/j. robot.2013.09.004.
10. Li, C.E., Tang, Y.C, Zou, X.J, Zhang, P.A., Lin, J.Q., Lian, G.P., Pan, Y.Q.,2022.A novel agricultural machinery intelligent design system based on integrating image processing and knowledge reasoning .Applied Sciences, 12(15): 7900. 10.3390/ app12157900.
11. G. Wang and J. Zhou, ''Dynamic robot path planning system using neural network,'' J. Intell. Fuzzy Syst., vol. 40, no. 2, pp. 3055–3063, Feb. 2021.
12. A. J. Mohammed, K. I. Ghathwan, and Y. Yusof, ''Optimal robot path planning using enhanced particle swarm optimization algorithm,'' Iraqi J. Sci., vol. 61, no. 1, pp. 178–184, Jan. 2020.
13. Chen Li a,Dimitris Chrysostomou a , Hongji Yang. "A speech-enabled virtual assistant for efficient human–robot interaction in industrial environments."
14. J. Hu, M. Wang, C. Zhao, Q. Pan, and C. Du, ''Formation control and collision avoidance for multi-UAV systems based on Voronoi partition,'' Sci. China Technol. Sci., vol. 63, no. 1, pp. 69–76, 2020.
15. Y. Wang, X. Li, and J. Zhang, ''Review of wheeled mobile robot collision avoidance under unknown environment,'' Sci. Progr., vol. 104, no. 3, pp. 160–173.
16. T. Fujinaga, S. Yasukawa, and K. Ishii, ''Evaluation of tomato fruit harvestability for robotic harvesting,'' in Proc. IEEE/SICE Int. Symp. Syst. Integr. (SII), Jan. 2021, pp. 35–39, doi: 10.1109/IEEECONF49454.2021.9382603.
17. G. Lin, Y. Tang, X. Zou, J. Li, and J. Xiong, ''In-field citrus detection and localisation based on RGB-D image analysis,'' Biosystems Eng., vol. 186, pp. 34–44, Oct. 2019, doi: 10.1016/j.biosystemseng.2019.06.019.
18. Jiafei Ma , Guan Wang, Cong Wang, Binghui Yao, Linxiao Deng , Chun Gu, and Lixin Xu . "Color Vision Improvement of Anomalous Trichromats Based on a Wide-Color-Gamut Display".
19. A. Khoshroo, A. Arefi, and J. Khodaei, ''Detection of red tomato on plants using image processing techniques,'' Agricult. Commun., vol. 2, no. 4, pp. 9–15, 2014..
20. A. B. Asenjo, J. Rim, and D. D. Oprian, "Molecular determinants of human red/green color discrimination," Neuron, vol. 12, pp. 1131–1138, 1994..
21. H. Yaguchi, J. Luo, M. Kato, and Y. Mizokami, "Computerized simulation of color appearance for anomalous trichromats using the multispectral image," J. Opt. Soc. Am. A. Opt. Image. Sci. Vis., vol. 35, pp. B278–B286, 2018.
22. CHENGYUAN SONG 1,2, KAI WANG2 , CHAO WANG1 , YANAN TIAN1 , XINJIE WEI 1 , CUIJIAN LI1 , QILIN AN 3 , AND JIAN SONG 2. "TDPPL-Net: A Lightweight Real-Time Tomato Detection and Picking Point Localization Model for Harvesting Robots"
23. J. S. Werner, B. Marsh-Armstrong, and K. Knoblauch, "Adaptive changes in color vision from long-term filter usage in anomalous but not normal trichromacy," Curr. Biol., vol. 30, pp. 3011–3015, 2020.
24. Bu, L., Chen, C., Hu, G., Sugirbay, A., Sun, H., Chen, J., 2022. Design and evaluation of a robotic apple harvester using optimized picking patterns. Comput. Electron. Agric. 198, 107092 https://doi.org/10.1016/j.compag.2022.107092.
25. Fan, P., Yan, B., Wang, M., Lei, X., Liu, Z., Yang, F., 2021. Three-finger grasp planning and experimental analysis of picking patterns for robotic apple harvesting. Comput. Electron. Agric. 188, 106353 https://doi.org/10.1016/j.compag.2021.106353.
26. Koirala, A., Walsh, K.B., Wang, Z., McCarthy, C., 2019. Deep learning–Method overview and review of use for fruit detection and yield estimation. Comput. Electron. Agric. 162, 219–234. https://doi.org/10.1016/j.compag.2019.04.017.
27. Li, K., Wang, J., Jalil, H., Wang, H., 2023. A fast and lightweight detection algorithm for passion fruit pests based on improved YOLOv5. Comput. Electron. Agric. 204, 107534 https://doi.org/10.1016/j.compag.2022.107534.
28. Douglas O'Shaughnessy INRS-EMT (University of Quebec), Montreal, Quebec H5A 1K6, Canada . "Trends and developments in automatic speech recognition research "
29. B.P. Mathew, F. Devasia, A. Asok, P.R. Jayadevu, R. Baby, Implementation of an origami inspired gripper robot for picking objects of variable geometry, Mater. Today Proc. (2022)1–8, https://doi.org/10.1016/j.matpr.2022.01.255.
30. K. Li, Y. Jin, M. Waqar, A. Ruize, H. Jiongwei, Facial expression recognition with convolutional neural networks via a new face cropping and rotation strategy, Vis. Comput. (2019), https://doi.org/10.1007/s00371-019-01627-4.

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