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Blood Content Prediction using Deep Learning Techniques

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Abstract: ***Cells in the human circulatory system and identifying the types and its functionalities cannot be done through naked eye. This asks for greater accurate methods of visualizing it and hence is vital in understanding blood disease causes, symptoms and the solution for them. But this field lacked clearance for the imaging system. Image Recognition was innovated using Deep Learning Technique.Human body cells assume an astounding job in the human resistant framework. To know more about blood-related infections and its effects, pathologists need to think about the attributes of cells. To diagnose a blood related disease, we need to identify and characterize blood samples of patients. In the medical field, automation for detecting and classifying blood cells and its subtypes have gained more importance nowadays. Recognition of an object is a basic piece for the vision of a computer that distinguishes an article in the given picture regardless of foundations, impediment, lighting or the edge of the view. Problems that are too difficult to solve can be handled using architectures that run deep using algorithms that dive deeper into the features extracted from the input and this can be possible using Deep Learning.***

Keywords: Blood samples, Deep Learning, Image recognition, medical applications.

I. INTRODUCTION

Treatment of various blood cell related diseases such as myelodysplastic syndrome, neutropenia, leukemia, lymphoma, myeloma and so on requires faster and accurate identification of the type of the affected cell. An affected cell can be identified as a result of various causes due to infection, rupture, shape mutilation or multiplication of the nucleus of the cell. Understanding the cause of deformity and non functionality reasons of a cell therefore is the prime step to be taken for further treatment of the blood cell related disease.

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Imaging systems using intravital methods can be used to visualise the different cells in the blood of a human being. The images obtained from these visualizing methods can be used for identifying the underlying macro level features such as the shape, object definition and the colour. The other features on a micro level scale that cannot be spotted by the human eye like the linearity of the edges, the intensity of the image and so on are however extracted using Deep learning techniques.

This technique is vastly used in the research area as it helps us to obtain more defined deeper features by going further into lower layers of architecture of the image obtained using imagery.The four significant constituents that make up the different unique parts of blood like Platelets, Red Blood Cells and White Blood Cells are in excess of 4,000 types. Recognizing and checking them physically by human perception is a very jading undertaking. A fairly high performing accurate algorithm that takes very less time to give its outcomes should be used for the detection of the blood cell types. For handling the picture processing and scrutinizing of images we do segmentation of the input images for obtaining better results. This method helps us in identifying the blood cells and produce cell gaps among them for efficient processing of mages. Disease detection can be done faster and accurately by proper processing of the images using appropriate methods.

II. LITERATURE SURVEY

Not many of the numerous works committed to examination of images of human blood cells do a thorough inspection or deeper evaluation of the cell images. Performing solitary breaking down and evaluation of certain types of cells seems to be the main objective of a large portion of the work done before[1]. Using images that are physically trimmed a significant number of works center around classification, arrangement, segmentation and division of the cell image[2]. The defect cells can be distinctively differentiated from a normal healthy cell as well as classification can be done using this order. Separate sorts of leukocytes using k-means grouping, entire or core leukocyte segmentation utilizing threshold method in particular the procedure of classification focused on pixels of images with basic yet robust approaches[3]. However, for the process of segmentation of the cell images and further deep feature extraction, they have adopted sophisticated but less efficient algorithms for the identification of the cell type of a human being. The erythrocyte sectioning involves methods of thresholding, traditionally implemented algorithms where there are various sorts of operations on immersion segments for the shading space of the image or algorithm implementation that involves pretreating processes of the image that are on the grey spectrum[4], [5].

For images gained from advanced magnifying instruments, in any case, traditional methodologies for division are not the most fitting implementation methods for segmentation of the cell images[6], [7]. The influence of lopsided lighting brought about by the focal point and irregular lighting should also be taken into consideration as it creates a focal and concealing regions over the edges of the cell images.

The deviations and the accuracy or low involvement of noise has been taken care of pretty well using pre-processing techniques that provides better performance on image segmentation utilizing a small bandwidth passage for taking away noises from the cell images.

III. DESIGN METHODOLOGY

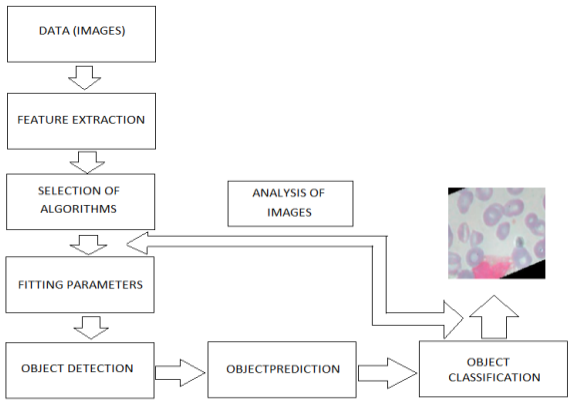

Fig. 1. Design methodology

Fig. 1 demonstrates the input (images) is tried upon and features are extracted from it based on the architecture and Convolutional Neural Network based implementation algorithm is applied on it after fitting the parameters on it. The approach that we are aiming for solving the taken problem is using Neural Networks where features exist connected in the form of layers and training of models can be done by going deeper into the underlying layer for feature extraction using deep learning techniques. The model can be trained using various architectures that come up with different parameters for the training process like Inception and Visual Geometry Group based networks which have varied salient features including the kernel and base filter specifications for general building of the solution model. After that detection of the said object in question, prediction and the type of object is robustly classified by the given set of labels that they are named as. The result is then analysed and we come to a conclusion of what the cell type is and if there is or there is not a deformity in the cell nucleus .

IV. DATASET AND PREPROCESSING

A. Dataset

The dataset consists of twelve thousand five hundred numbers of various images consisting of intravital imagery of blood cells which accompanies labeled names or names of type of cells in a comma separated value consisting file. There are approximately three thousand images for White Blood Cells which has four types in it and four various directories are used to cluster them (according to their type). The different cell types in White Blood Cells are Eosinophil, Lymphocyte, Monocyte, and Neutrophil. It also contains two other folders dedicated to mononuclear and polynuclear cell images.

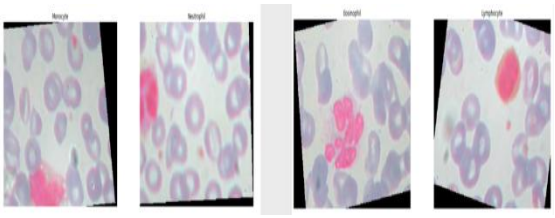

Fig. 2. Different cell types in WBC

Fig. 2 demonstrates cell types such as Eosinophil, Lymphocyte, Monocyte, and Neutrophil for which they have dedicated files for each type.

B. Preprocessing

Preprocessing the data that is needed to work with involves setting input and sample mean to 0 over the dataset, dividing each inputs by standard value of the dataset by feature wise and sample wise, applying ZCA whitening, randomly rotate images in the range 0 to 180 degrees, randomly shift images vertically and horizontally (fraction of total height and width), randomly flip images vertically and horizontally.

V. ALGORITHM USED

A. Convolutional Neural Networks

A model needs to understand from an experience and learn how to perform actions such as prediction of outcomes or type classification from the various formats of inputs given to it and this process can be most efficiently implemented using Deep Learning techniques. It consists of various types of architectures each comprising multiple deep layers of features or nodes or neurons. The current layer of the architecture that shares connection with the previous layer, takes its output as the learning input for further action to be done. Convolutional Neural Networks has a network with an extensive architecture comprising layers of neurons which is heavily used for various purposes in the field of computer vision .

CNN consists of various hidden layers whose functionalities differ from each other. A CNN model is a combination of a couple of processes, one being extracting the features of the input and the other one is classifying the input based on the trained experience . Classification of an input is done after the features are extracted from it by the layer where all the neurons are connected with each other. Extraction of very defined features leads to better accurate outcomes.

Here in this methodology, two different architecture models of it are considered and focused on their performance which are **Inception version 3** and **VGG 16** for identifying the best architecture to be implemented for better efficiency and accuracy for robustness in outcome obtainment. The former architecture is considered because of its advantages such as varied filter dimensions or size as well as randomness factor of training the models before testing and is a widely used recent technology.

The latter architecture is selected as a performance comparison method in identifying how efficiently our database can be perceived by the model running with a base of fixed dimension sized filter or kernel.

B. Inception V3

It is one of the various most recently progressed sort of architecture types of the earlier generic model building of a given solution using methods that involved networks and neurons or nodes that are connected. The model widely built for processing of input images when applied on a broadly used dataset surprisingly showed a good accuracy which was greater than seventy eight percent. The model evolved as a combined solution to numerous implementation concepts provided by developers or researchers that had contributed as a whole for the progression of the building of the architecture all over the world. The variation architecture model of CNN is built on the main focus of recognition of images by extracting defined features using one layer and classifying the input using a layer with all neurons connected along with an extra layer called SoftMax layer used for retainability of core features without losing it.

C. Visual Geometry Group 16

It is an enhanced model overAlexNet that rapidly replaced large kernels and the base filters which were bigger in dimensions and largely consisted of convolutional layers whose size was greater than five and implementing many filters that were small three by three sized. The deeper the network or the more the number of layers, the more accurate the output of one layer will be which is further taken as the input for another layer as there will be faster and more extraction of sophisticated and defined features on a minute scale with less number of performing operations to be done.

VI. FITTING PARAMETERS

A. Inception V3

Layer (type)	Output Shape	Param #
inception_v3 (Model)	(None, 6, 8, 2048)	21802784
global_average_pooling2d_1 (	(None, 2048)	0
dense_1 (Dense)	(None, 512)	1049088
dropout_1 (Dropout)	(None, 512)	0
dense_2 (Dense)	(None, 128)	65664
dropout_2 (Dropout)	(None, 128)	0
dense_3 (Dense)	(None, 32)	4128
dropout_3 (Dropout)	(None, 32)	0
dense_4 (Dense)	(None, 5)	165

Total params: 22,921,829
Trainable params: 22,887,397
Non-trainable params: 34,432

Fig. 3. Inception V3 parameters

Fig. 3 shows that the Inception V3 model has approximately 23 million parameters where 22.8 million of it are trainable and only the few of the rest are parameters that can be deemed as non trainable.

B. VGG 16

Layer (type)	Output Shape	Param #
vgg16 (Model)	(None, 7, 10, 512)	14714688
flatten_1 (Flatten)	(None, 35840)	0
batch_normalization_1 (Batch	(None, 35840)	143360
dense_1 (Dense)	(None, 32)	1146912
dropout_1 (Dropout)	(None, 32)	0
batch_normalization_2 (Batch	(None, 32)	128
dense_2 (Dense)	(None, 16)	528
dropout_2 (Dropout)	(None, 16)	0
batch_normalization_3 (Batch	(None, 16)	64
dense_3 (Dense)	(None, 8)	136
dropout_3 (Dropout)	(None, 8)	0
batch_normalization_4 (Batch	(None, 8)	32
dense_4 (Dense)	(None, 4)	36

Total params: 16,005,884
Trainable params: 8,298,828
Non-trainable params: 7,707,056

Fig.4. VGG 16 parameters

Fig. 4 shows that the VGG 16 based model built on the CNN algorithm has approximately 16 million fitting parameters and what makes it more different than Inception V3 is that it has almost 8 million non trainable parameters due to its fixed kernel size that means that less optimization and updation of values rather than varied filter sizes in Inception V3 architecture where the value of matrices are optimized rapidly .

VII. AREA AND TOOLS USED

1. DEEP LEARNING

Deep learning is a methodology which extends it's area from the machine learning process for learning about multiple layers and extraction and interpreting the inner layers from the raw input. Here using deep learning methodology ,the white blood cell count has been classified and predicted using various CNN architectures like Inception V3 and VGG 16 models.

2. GOOGLE COLAB

Using Google Colab over Jupyter Notebooks as the platform and tool for our implementation gives a great advantage as it provides inbuilt Git version controlling which eases our process of note creating, documenting, tables or figures inclusion using its markdown functionality. Further, as it runs on virtual machines of Google servers, there is no need of package installation and is quite platform-friendly.

VIII. PERFORMANCE ANALYSIS

A. CNN implementation

	precision	recall	f1-score	support
NEUTROPHIL	0.25	1.00	0.40	624
EOSINOPHIL	0.00	0.00	0.00	623
MONOCYTE	0.00	0.00	0.00	620
LYMPHOCYTE	0.00	0.00	0.00	620
accuracy			0.25	2487
macro avg	0.06	0.25	0.10	2487
weighted avg	0.06	0.25	0.10	2487

Fig. 5. CNN f1 score

Fig. 5 shows the f1 score of the CNN implemented algorithm and the accuracy of the model is found to be 25% with a support count of 2487.

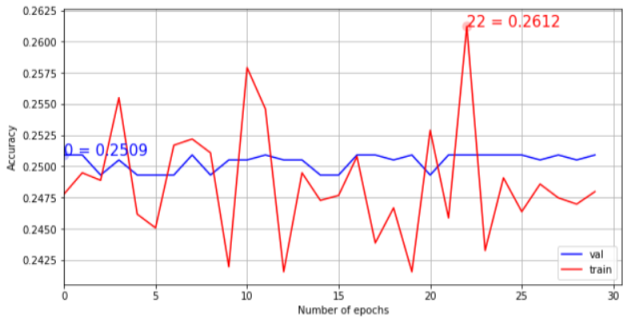

Fig. 6. Accuracy vs number of epochs

Fig. 6 depicts the validation and training accuracy graph over 30 epochs involved in training and testing the entire model with approximately 310 images in each batch.

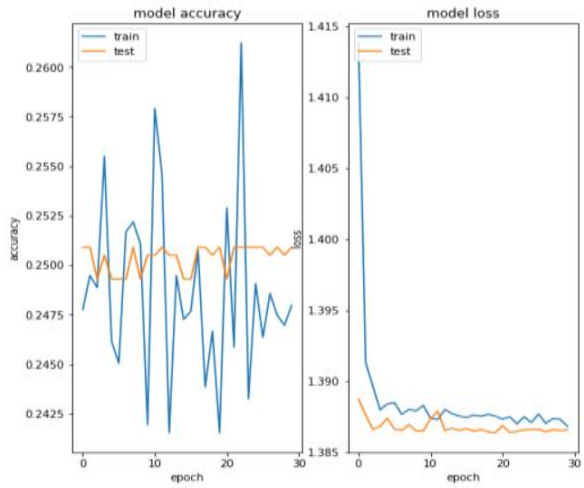

Fig. 7. CNN accuracy and loss

Fig. 7 shows the training and testing accuracy as well as training and testing of model loss of the model with loss being 13.8%.

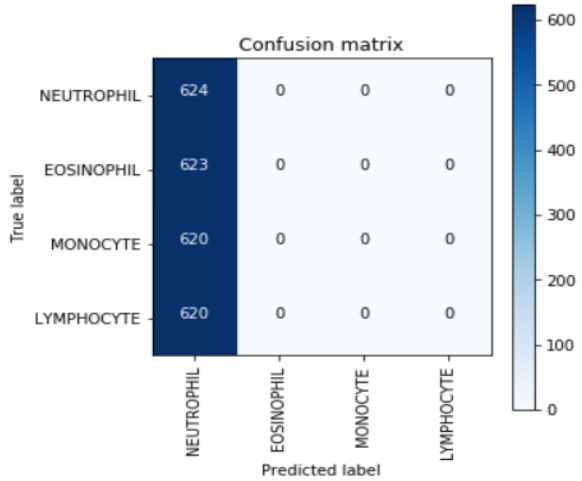

Fig. 8. Cell type confusion matrix

Fig. 8 shows the confusion matrix of the labelled cell type after grouping and classifying the images given as input. The cell scan image is grouped and classified based on the already inputted names or labels of the certain images that are put together under one common file with its original label.

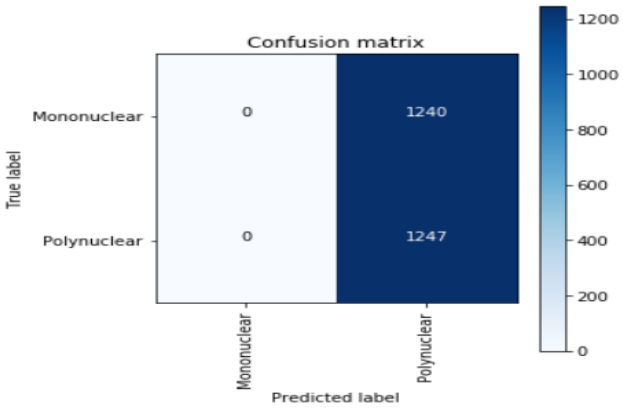

Fig. 9. Nuclear type confusion matrix

Figure 9 shows the confusion matrix of its type of the nucleus that is mononuclear or polynuclear. If the object is found to be a single-bodied then we come to a conclusion that the input image is of a red blood cell and if the result leans towards a body with one or more nuclei involved, then it is a type of white blood cell. This may be due to the various dimensions of filters used for the matrix convolution operations over floating points such as multiplication of the values present in the matrices during reduction of effective cost and optimising the intermediate values.

This low precision performance cannot be perceived as a reliable method for a risk depended predicting and grouping or classifying of the scanned images in the medical field. So we consider taking an architecture that uses a certain dimension of filters that doesn't involve randomness of base kernels for operations.

A. Inception V3 implementation

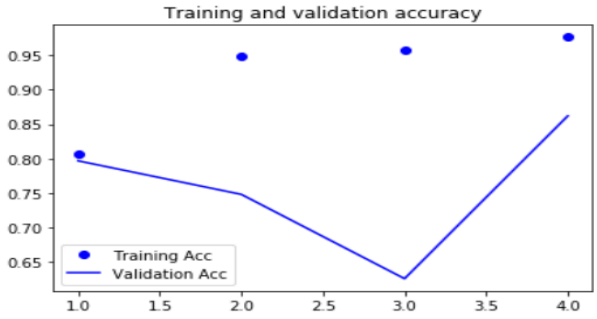

Fig. 10. Inception V3 accuracy

Figure 10 shows the training and validation accuracy of the Inception V3 model with the accuracy being 74.8% and the result is obtained after training the model in 30 epochs with approximately 310 images in one batch.

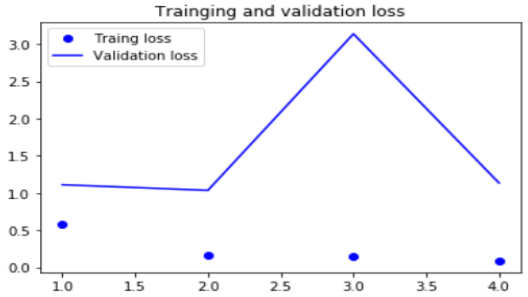

Fig. 11. Inception V3 loss

Figure 11 shows the training and validation loss of the Inception V3 model with loss being 10.4%.

This is again a result and accuracy value that is not satisfactory for the high menace involved in predicting a robust outcome cannot be used in real time applications of same or similar problem solving.

B. VGG 16 implementation

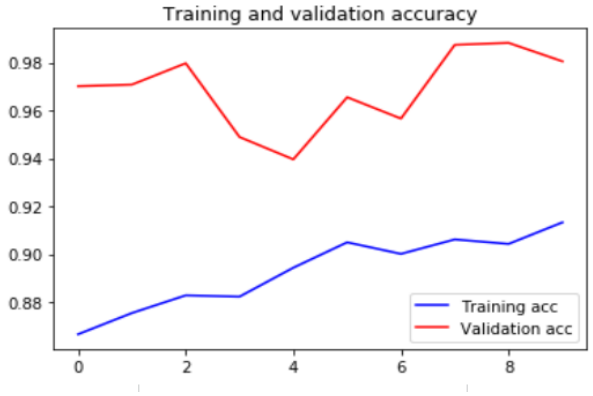

Fig. 12. VGG 16 accuracy

Fig. 12 shows the training and validation accuracy of VGG 16 model being 91.3% and 98.8% respectively by training in 30 epochs with approximately 310 images in one batch as well.

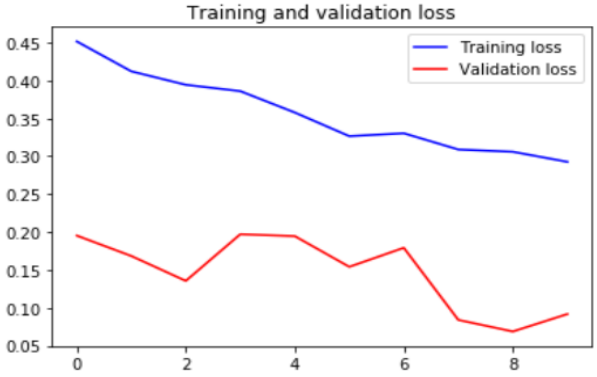

Fig. 13. VGG 16 loss

Fig. 13 shows the loss of training and validation loss of VGG 16 model.

This shows that selecting an architecture of an algorithm that uses a certain dimension of filters that doesn't involve randomness of base kernels for operations is proven to be more effective in giving more accurate outcomes that aligns with actual expected output with more robustness and efficiency as a whole over experimental advanced architectures for our taken cell images in the dataset.

IX. RESULT AND DISCUSSIONS

Among the network architectures that we used VGG 16 gave us the highest accuracy and fixed size kernels and filters proved to be way more efficient in training our model by producing the appropriate required outcome. Inception V3 architecture which has wider parallel kernels and filters as a base for the working had more fitting parameters of approximately 23 million over the VGG model which had 16 million parameters approximately. Though Inception V3 architecture had more parameters, it did not yield better accuracy of at least 80% while VGG 16 gave us very good results and accurate outcome with about 91.3% performance validation output as shown in Table-I.

Table- I: Summary of results

Network	Salient Feature	Accuracy	Parameters
Inception V3	Wider-parallel kernels	74.8%	22,921,829
VGG 16	Fixed size kernels.	91.3%	16,005,884

This shows that less the process of updating and optimizing the values occurs at the time of training the built model, less the accuracy obtainment of the required output for our dataset of blood sample scan images. Advanced extracting of deeper features turns out to be futile as there is over optimization of the matrix values during floating point operations that is not needed for input images with less underlying features and biases for input feeding of training the model which in turn results in adverse results.

X. CONCLUSION

Selecting the right kind of architecture for a certain problem solving and building an algorithm or a model for it is of immense importance as some datasets may have too many underlying deep features that needs complex methods for extracting its parameters while some datasets does not require such sophisticated process of tedious task undertaking to create a model or algorithm as it does not consist parameters that needs to be pruned deeper. A complex structured solution building for such relatively simpler feature extraction required datas often leads to over improvements of the intermediate values thereby tampering the originality or key parameters of the input taken into consideration. The prediction of specialized blood cells related diseases will involve identification and characterization of the acquired patient's blood samples and automated methods can be run on it using its microscopic scan of its images as input to artificially thinking models such as Deep Learning. Self learning models from its own experience for detecting and classifying the blood cell along with its subtypes based on its nuclear object recognition are said to have great impact in medical applications. Deciding the line of treatment to be followed can be further enhanced by extracting knowledge from such suitable results of models using the most efficient, less time consuming and accurate architecture .

REFERENCES

1. Al-jaboriy, S. S., Sjarif, N. N. A., Chuprat, S., &Abduallah, W. M. (2019). Acute lymphoblastic leukemia segmentation using local pixel information. *Pattern Recognition Letters*, *125*, 85-90.
2. Madhloom, H. T., Kareem, S. A., Ariffin, H., Zaidan, A. A., Alanazi, H. O., &Zaidan, B. B. (2010). An automated white blood cell nucleus localization and segmentation using image arithmetic and automatic threshold. *Journal of Applied Sciences*, *10*(11), 959-966.
3. Scotti, F. (2006, April). Robust segmentation and measurements techniques of white cells in blood microscope images. In *2006 IEEE Instrumentation and Measurement Technology Conference Proceedings* (pp. 43-48). IEEE.

4. Khan, S., Khan, A., Khattak, F. S., & Naseem, A. (2012). An accurate and cost effective approach to blood cell count. *International Journal of Computer Applications*, *50*(1).
5. Mahmood, N. H., Lim, P. C., Mazalan, S. M., & Razak, M. A. A. (2013). Blood cells extraction using color based segmentation technique. *International journal of life sciences biotechnology and pharma research*, *2*(2), 233-240.
6. Bhavnani, L. A., Jaliya, U. K., & Joshi, M. J. (2016). Segmentation and Counting of WBCs and RBCs from Microscopic Blood Sample Images. *International Journal of Image, Graphics & Signal Processing*, *8*(11).
7. Roos, I., & Gustafsson, A. (2011). The influence of active and passive customer behavior on switching in customer relationships. *Managing Service Quality: An International Journal*.

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