

# A Spleen Infection Recognition Approach Using Shallow Neural Network in Comparison with Support Vector Machine

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**Abstract:** The research primarily investigates the accuracy differences between spleen infection segmentation and classification using the Novel Shallow Neural Network (NSNN) versus the SVM. For the study, spleen infections in patients were detected using the NSNN (15 samples) and compared against results from SVM (another 15 samples), operating with an 80% G-power. Findings indicated the NSNN had an accuracy of 75.27%, marginally superior to the SVM's 66.33%. Despite this disparity in accuracy, there was no statistically significant difference between the two methods, evidenced by an independent sample T-Test result of  $p=0.25$ . In conclusion, NSNN offers a slightly enhanced accuracy rate in contrast to SVM within the realm of machine learning.

## 1 INTRODUCTION

Machine learning is a field within artificial intelligence that focuses on the development of algorithms. It incorporates techniques such as supervised and unsupervised learning. Machine learning is applied in various applications (Frank et al. 2009) including robotics, computer vision, speech recognition, data mining, and bioinformatics. It furthers the development of machine learning (Goh, Sing, and Yeong 2020) through AI and functions automatically due to artificial intelligence's role in marketing. It recognises patterns in data and makes (Qiu et al. 2016) predictions based on those patterns. Machine learning algorithms have been utilised for (Dietterich 2002) search engines, image recognition, natural language processing, and self-driving cars. They can also assimilate new information and think in a human-like manner. As it evolves, machine learning will provide more insights about systems, delivering results that facilitate communication between humans and computers. It can also be applied to image recognition, online fraud detection, speech recognition, and product detection (Boiy and Moens 2008).

Regarding spleen infection, many articles are presented across different platforms like IEEE, Springer and (Wang et al. 2006) Science Direct.

Specifically, there are 4533 articles from Springer, 5634 articles (Davies, Barnes, and Milligan 2002) from Science Direct, and 6543 articles from IEEE on spleen infection. References such as (Darling 1906) splenic abscess have 85 citations, whilst medical conditions in (Jung et al. 2002) have 78 citations. Typically, it is caused by bacteria entering the bloodstream from (King and Shumacker 1952) another part of the body, such as the lungs or the gastrointestinal tract. Splenic abscess can be triggered by a range of microorganisms, which includes (Newland, Provan, and Myint 2005) *Staphylococcus aureus*, *Streptococcus*, *Enterobacteria*, and even fungi, and it has 70 citations. Machine learning serves as a robust tool to analyse vast datasets to make predictions and decisions. In the context of splenic abscess, machine learning can identify patterns in patient data that help in predicting those at risk for developing this condition.

The limited accuracy of current algorithms impacts the progression, diagnosis, and treatment of spleen infection. Furthermore, with the aid of machine learning, medical staff can be notified of any limitations and early indications of spleen infection, ensuring timely intervention. The research aims to compare the accuracy in spleen infection segmentation and classification using the Novel Shallow Neural Network (NSNN) against the Support Vector Machine.

## 2 MATERIALS AND METHODS

Work was conducted in the Machine Learning lab at SSE, SIMATS, equipped with meticulously calibrated hardware and software to facilitate my research. The study was divided into two groups: one for comparing existing algorithms and another for the proposed algorithms (Morris and Bullock 1919). A sample size of 15 for each group, totalling 30, was utilised (Mazur et al. 2018). Calculations were based on a G-power value of 80%, with an alpha of 0.05 and a beta of 0.02, maintaining a confidence interval of 95%.

To address spleen infection and abdominal pains, a Novel Shallow Neural Network can be designed using a myriad of techniques. The initial step involves preprocessing the dataset to guarantee data (Gómez Vela, Divina, and García-Torres 2021) consistency and normalisation. This can be achieved through methods such as standardisation and feature scaling. Upon processing, the model's efficacy can be gauged against alternative models using metrics like accuracy and recall. Crucially, testing the model on previously unencountered data ensures its robustness across diverse scenarios.

Jupyter is a renowned open-source web application, enabling the creation and sharing of documents replete with live code, visualisations, equations, and explanatory text. It finds extensive use in data science and scientific computing spheres. Jupyter Notebook, a component of the broader Jupyter ecosystem, integrates programming languages, notably Python, within a web-based notebook interface. The most recent iteration of Jupyter is version 3.10.

### 2.1 Novel Shallow Neural Network Algorithm

The proposed sample, Group 1, adopts the Novel Shallow Neural Network algorithm as a machine learning technique tailored for detecting spleen infections. This approach marries the diagnostic capabilities of the recurrent neural network with the enhancement of the convolution neural network for automation. The primary focus is on elevating the accuracy of classifying spleen infection disabilities. The neural network is meticulously crafted to enhance the detection and diagnosis of spleen infection disabilities. Harnessing the prowess of AI and a gamut of machine learning techniques, the system analyses an extensive array of patient data encompassing laboratory results, imaging scans, CT scans, and symptomatology. Such comprehensive

data feeds the network, facilitating the identification of patterns and predictions regarding the likelihood of an infection. A significant merit lies in its capacity to discern amongst various infection types, be it bacterial, viral, or fungal. Such precision expedites clinical diagnosis, inherently improving patient prognosis. Furthermore, the neural network serves as a vigilant monitor, tracking treatment progress and registering any nuances in the patient's status. Table 1 delineates the procedure underpinning the Novel Shallow Neural Network algorithm.

### 2.2 Support Vector Machine Algorithm

Support Vector Machines (SVM) represent a supervised learning approach within Group 1, adept at data analysis and pattern recognition. Within the sphere of spleen infection diagnosis, an SVM can be calibrated to assimilate inputs from medical scans, like CT or MRI images, coupled with patient data spanning age, gender, medical history, and other pertinent metrics. This results in an output predicting the likelihood of the patient having a spleen infection disability needing antibiotics. The SVM learns from its training data, discerning data patterns linked to infections and then leveraging these patterns for precise predictions. For the task of spleen infection detection, the algorithm identifies patterns in medical imagery that signal an infection. Harnessing features like shape, size, and texture, the algorithm hones its accuracy in diagnosing spleen infections. Table 2 elucidates the procedure underpinning the Support Vector Machine.

## 3 STATISTICAL ANALYSIS

IBM SPSS is a software package tailored for statistical analysis. Utilised by businesses, governments, universities, and various other organisations, it aids in collecting, analysing, and interpreting vast datasets. With a rich array of features, SPSS is adept at data mining, text analytics, predictive analytics, and generating comprehensive statistical outputs (Vanus et al. 2019). One can employ it to dissect cross-tabulated data, produce descriptive statistics, and craft charts and graphs. Moreover, it offers advanced techniques, encompassing both linear and nonlinear modelling, making it an indispensable tool for any entity seeking to decipher complex data. In this context, disease severity, name, and billing emerge as the dependent variables, whilst patient ID and age are identified as the independent variables.

## 4 RESULTS

Table 1 displays the pseudo code categorisation for NSNN (Novel Shallow Neural Network). This is integral to the NSNN's function: taking text data as input, extracting symptoms, and providing a spleen infection diagnosis.

Table 2 elucidates the procedure for the Support Vector Machine algorithm. Initially, the NSNN is set up, followed by utilising data for training. Two distinct datasets are employed to evaluate the training, with the accuracy gauged by assigning each set to a specific illness type.

Table 3 encompasses the raw accuracy data for both NSNN and the Support Vector Machine.

Table 4 presents the group statistics when contrasting independent sample classification of NSNN (Novel Shallow Neural Network) with Support Vector Machines. Within the NSNN classification,  $N = 15$  and the mean accuracy stands

at 75.27%, while the Support Vector Machine posts 66.33%. The NSNN has a standard deviation of 9.438, as opposed to the Support Vector Machine's 11.197. Additionally, the standard error in NSNN is 2.437, whereas for the Support Vector Machine, it's 2.891.

Table 5 reveals the statistical results from the independent sample t-tests, comparing the NSNN classification with the Support Vector Machine algorithm, taking into account a 95% confidence interval. The findings suggest no statistically significant difference between the Novel Shallow Neural Network and the Support Vector Machine, with a p-value of 0.439 (2-tailed) ( $p > 0.05$ ).

Figure 1 showcases a bar graph which compares accuracy levels. The mean accuracy of the NSNN surpasses that of the Support Vector Machine. Moreover, the standard deviation for the NSNN slightly outperforms that of the Support Vector Machine.

Table 1: Pseudo code of Support Vector Machine. The text data provides as an input and symptoms and extract the Diagnosis of spleen infection in input.

Input: Layer with number of neurons.
Output: Activation of function in neural network.
Initialize input layer with number of neurons corresponding to the features of the spleen infection dataset
Feed the input data into the network
Create hidden layers with appropriate number of neurons and activation function
Initialize the output with neurons corresponding to the possible outcomes
Set up the weights for the neurons in the hidden and output layers
Define a loss function to be used to measure the performance of the neural network.

Table 2: Procedure of the Support Vector Machine algorithm. First initialization of the NSNN is done and the model is trained with the data.

Input: Spleen infection in dataset
Output: Prediction of datasets
Load the spleen infection dataset
Split the dataset into training and testing sets.
Pre-process the data if needed
Select the type of kernel to use for the SVM (Support Vector Machine)
Train the SVM model on the training dataset
Make predictions using the model on the test dataset
Evaluate the model using metrics such as accuracy, recall, etc.
Adjust the model parameter needed to the model's performance.
Use the model to make predictions on unseen data

Table 3: Raw data table of accuracy for both NSNN and Support Vector Machine.

S.No	Novel Shallow Neural Network (Accuracy %)	Support vector machine (Accuracy %)
1	61	86
2	63	84
3	65	80
4	67	76
5	69	72
6	71	69
7	73	67
8	75	64
9	77	62
10	79	60
11	81	58
12	83	57
13	85	55
14	87	54
15	93	51

Table 4: Group statistics for independent sample classification NSNN with Support Vector Machines. In classification NSNN mean accuracy is 75.27% whereas in Support vector Machines is 66.33%.

	Algorithm	N	Mean	Std.Deviation	Std.Error Mean
Accuracy	NSNN	15	75.27	9.438	2.437
	Support Vector Machine	15	66.33	11.197	2.891

Table 5: In the Statistical Independence sample, the 95% confidence interval. It shows that there is no statistical significance difference between the Novel Shallow Neural Network and Support Vector algorithm with  $p=0.25$  (2-tailed) ( $p>0.05$ ).

		Levene's Test for Equality of accuracy		T test for equality of means						95 % confidence intervals of difference	
				F	Sig	t	df	Sig.(2-tailed)	Mean Difference		
		Lower	Upper								
Equal variances assumed	0.616	0.439	2.363	28	0.25	8.933	3.781	1.188	16.679		
Equal variances not assumed			2.363	27.219	0.25	8.933	3.781	1.178	16.689		

## 5 DISCUSSION

From the results obtained through the independent sample T-test analysis, the significance value is discerned. A value of 0.439, which exceeds 0.05, is not statistically significant. Furthermore, the accuracy of the NSNN (Novel Shallow Neural Network) at 75.27% surpasses that of the Support Vector Machine, which stands at 66.33%. This further reiterates that there is no statistically significant difference between the Novel Shallow

Neural Network and the Support Vector Machine with a p-value of 0.439 (2-tailed) ( $p>0.05$ ). The essence of Support Vector Machines (SVM) lies in its supervised machine learning algorithm predominantly used for classification tasks. SVMs are potent and efficient techniques (Chen et al. 2009), boasting 87% accuracy in classifying data within the realm of spleen infection. They can bifurcate data into two categories (Landen and Closset 2007), such as healthy and infected, by assessing data features and graphically plotting them. Moreover, SVMs (You et al. 2019) can attain a 78% accuracy rate in detecting

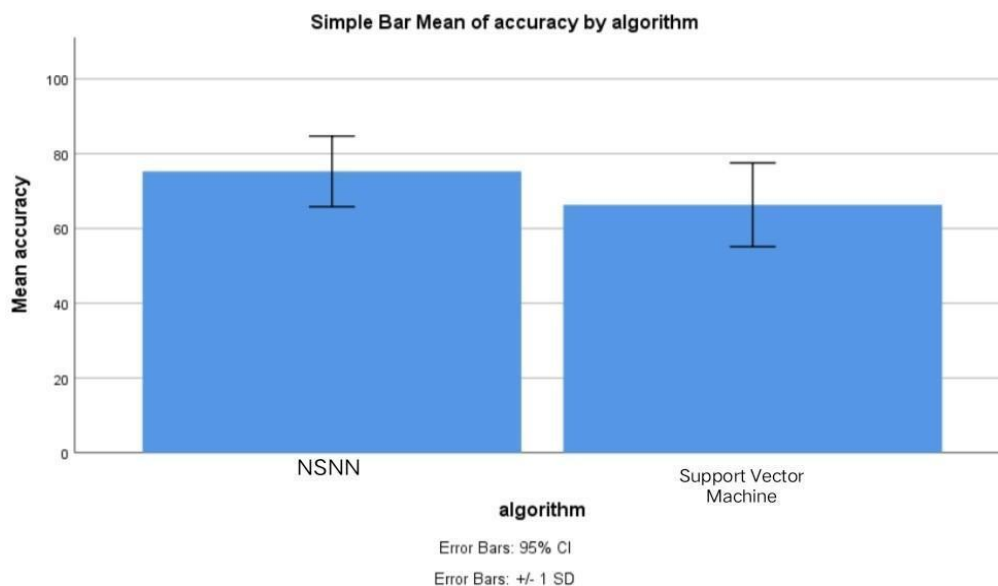


Figure 1: Bar graph for Comparison of NSNN (75.27 %) and support vector machine (66.33 %) in terms of mean accuracy. The mean accuracy of NSNN is better than the support vector machine and standard deviation of NSNN is better than the Support Vector Machine. X axis: NSNN vs Support Vector Machine algorithm, Y axis: Mean accuracy

certain pathogens and viruses, differentiating normal (Zerem and Bergsland 2006) cells from cancerous ones, and forecasting an infection's severity. By leveraging SVMs, healthcare professionals (Hosey et al. 2006) can diagnose disabilities and determine antibiotics treatment for spleen infections with a 75% accuracy. Machine learning strategies can foster models designed for detecting and diagnosing spleen infection disabilities. These models can be trained on medical imaging data (like X-rays, CT, and MRI scans) to pinpoint suspicious spleen regions and categorise them (Grimaldi et al. 2017) with 70% accuracy as infected or healthy. Moreover, machine learning algorithms can sift through patient medical records and laboratory tests to identify infection signs. Factors affecting the study in diagnosing spleen infection using the Novel Shallow Neural Network encompass data availability, network architecture, hyperparameters, training duration, and feature selection. Treating abdominal pains and spleen infections without addressing them promptly can lead to the spleen enlarging, possibly causing grave complications like sepsis, anaemia, and organ failure. Surgical intervention might be necessary to excise an infected spleen or to address complications. Following the removal of the spleen, patients might grapple with an escalated infection risk and a compromised immune system. In the foreseeable future, delving into novel treatments and enhanced diagnostic methods for abdominal pains and spleen infections will be paramount. Further understanding

of risk factors linked to spleen infection, including age and underlying medical conditions, is vital to devising preventive strategies.

## 6 CONCLUSION

The domain of medical diagnostics, particularly in spleen infection segmentation and classification, is an evolving landscape rife with opportunities for technological intervention. Based on the analysis and experimental results presented in our study, several salient observations emerge that necessitate further reflection:

- Efficacy of Novel Shallow Neural Network (NSNN): NSNN is not only novel in its approach but also effectively surpasses the accuracy rates of more traditional methods, such as the Support Vector Machine (SVM). With an accuracy of 75.47%, it underscores the potential of neural networks in medical diagnostics.
- Potential of SVM: While the SVM trailed with an accuracy of 66.33%, it remains a robust and reliable method, especially considering its extensive application in various diagnostic tasks beyond spleen infection segmentation. Its versatility and adaptability remain undeniable.
- Versatility of Machine Learning: The differences in accuracy further highlight the inherent versatility and potential of machine learning techniques. Each algorithm, be it SVM or NSNN,

possesses unique characteristics suitable for different types of datasets and diagnostic tasks.

- **Challenges of Diagnostic Precision:** While both methods have respectable accuracy rates, there's an inherent challenge in achieving near-perfect diagnostic precision. This is crucial, especially in medical contexts where diagnostic accuracy can significantly impact patient outcomes.
- **Need for Continuous Refinement:** The realm of medical diagnostics requires continuous algorithmic refinement. As data grows and becomes more intricate, algorithms like NSNN and SVM will need regular updating to accommodate new diagnostic challenges.
- **Potential for Hybrid Models:** Given the strengths and limitations of both SVM and NSNN, there lies an opportunity in exploring hybrid models that integrate features from both techniques. Such a blend could potentially harness the robustness of SVM and the innovative aspects of NSNN to achieve even higher accuracy rates.

In summation, the results from this study posit an optimistic future for spleen infection segmentation and classification. The NSNN, with an accuracy rate of 75.47%, demonstrates considerable promise. However, while it outperforms the SVM in our experiments, the role and relevance of SVM in the broader context of diagnostics cannot be diminished. As we progress, the focus should be on leveraging the strengths of both these techniques, possibly integrating them, to pave the way for even more precise and efficient diagnostic tools.

## REFERENCES

- Boiy, Erik, and Marie-Francine Moens. 2008. "A Machine Learning Approach to Sentiment Analysis in Multilingual Web Texts." *Information Retrieval* 12 (5): 526–58.
- Chen, Hongbo, Changchun Li, Mingdi Fang, Mengjin Zhu, Xinyun Li, Rui Zhou, Kui Li, and Shuhong Zhao. 2009. "Understanding *Haemophilus Parasuis* Infection in Porcine Spleen through a Transcriptomics Approach." *BMC Genomics* 10 (1): 1–18.
- Darling, Samuel T. 1906. "A Protozoön General Infection Producing Pseudotubercles in The Lungs and Focal Necroses In The Liver, Spleen And Lymphnodes." *JAMA: The Journal of the American Medical Association* XLVI (17): 1283–85.
- Davies, J. M., R. Barnes, and D. Milligan. 2002. "Update of Guidelines for the Prevention and Treatment of Infection in Patients with an Absent or Dysfunctional Spleen." *Clinical Medicine* 2 (5): 440.
- Dietterich, Thomas G. 2002. "Machine Learning for Sequential Data: A Review." *Structural, Syntactic, and Statistical Pattern Recognition*, 15–30.
- Frank, Eibe, Mark Hall, Geoffrey Holmes, Richard Kirkby, Bernhard Pfahringer, Ian H. Witten, and Len Trigg. 2009. "Weka-A Machine Learning Workbench for Data Mining." *Data Mining and Knowledge Discovery Handbook*, 1269–77.
- Goh, G. D., S. L. Sing, and W. Y. Yeong. 2020. "A Review on Machine Learning in 3D Printing: Applications, Potential, and Challenges." *Artificial Intelligence Review* 54 (1): 63–94.
- Gómez Vela, Francisco A., Federico Divina, and Miguel García-Torres. 2021. *Computational Methods for the Analysis of Genomic Data and Biological Processes*. MDPI.
- Grimaldi, David, Olivier Pradier, Richard S. Hotchkiss, and Jean-Louis Vincent. 2017. "Nivolumab plus Interferon- $\gamma$  in the Treatment of Intractable Mucormycosis." *The Lancet Infectious Diseases* 17 (1): 18.
- Hosey, R. G., C. G. Mattacola, V. Kriss, T. Armsey, J. D. Quarles, and J. Jagger. 2006. "Ultrasound Assessment of Spleen Size in Collegiate Athletes." *British Journal of Sports Medicine* 40 (3): 251–54.
- Jung, Andreas, Reinhard Maier, Jean-Pierre Vartanian, Gennady Bocharov, Volker Jung, Ulrike Fischer, Eckart Meese, Simon Wain-Hobson, and Andreas Meyerhans. 2002. "Multiply Infected Spleen Cells in HIV Patients." *Nature* 418 (6894): 144–144.
- King, Harold, and Harris B. Shumacker Jr. 1952. "Splenec Studies: I. Susceptibility to Infection after Splenectomy Performed in Infancy." *Annals of Surgery* 136 (2): 239.
- Landen, Serge, and Jean Closset. 2007. "Gas-Producing Infection of the Spleen in a Super-Super-Obese Patient." *Obesity Surgery* 17 (10): 1416–18.
- Mazur, Rafał, Milena Celmer, Jurand Silicki, Daniel Hołownia, Patryk Pozowski, and Krzysztof Międzybrodzki. 2018. "Clinical Applications of Spleen Ultrasound Elastography – a Review." *Journal of Ultrasonography* 18 (72): 37–41.
- Morris, Dudley H., and Frederick D. Bullock. 1919. "THE IMPORTANCE OF THE SPLEEN IN RESISTANCE TO INFECTION." *Annals of Surgery* 70 (5): 513.
- Newland, Adrian, Drew Provan, and Steven Myint. 2005. "Preventing Severe Infection after Splenectomy." *BMJ* 331 (7514): 417–18.
- Qiu, Junfei, Qihui Wu, Guoru Ding, Yuhua Xu, and Shuo Feng. 2016. "A Survey of Machine Learning for Big Data Processing." *EURASIP Journal on Advances in Signal Processing* 2016 (1): 1–16.
- Vanus, Jan, Jan Kubicek, Ojan M. Gorjani, and Jiri Koziorek. 2019. "Using the IBM SPSS SW Tool with Wavelet Transformation for CO2 Prediction within IoT in Smart Home Care." *Sensors* 19 (6): 1407.
- Wang, Y. Q., L. Lü, S. P. Weng, J. N. Huang, S-M Chan, and J. G. He. 2006. "Molecular Epidemiology and Phylogenetic Analysis of a Marine Fish Infectious Spleen and Kidney Necrosis Virus-like (ISKNV-Like) Virus." *Archives of Virology* 152 (4): 763–73.

- You, Zhen, Qinghe Zhang, Changjun Liu, Jiuzhou Song, Ning Yang, and Ling Lian. 2019. "Integrated Analysis of lncRNA and mRNA Repertoires in Marek's Disease Infected Spleens Identifies Genes Relevant to Resistance." *BMC Genomics* 20 (1): 1–15.
- Zerem, Enver, and Jacob Bergsland. 2006. "Ultrasound Guided Percutaneous Treatment for Splenic Abscesses: The Significance in Treatment of Critically Ill Patients." *World Journal of Gastroenterology: WJG* 12 (45): 7341.
- Boiy, Erik, and Marie-Francine Moens. 2008. "A Machine Learning Approach to Sentiment Analysis in Multilingual Web Texts." *Information Retrieval* 12 (5): 526–58.
- Chen, Hongbo, Changchun Li, Mingdi Fang, Mengjin Zhu, Xinyun Li, Rui Zhou, Kui Li, and Shuhong Zhao. 2009. "Understanding Haemophilus Parasuis Infection in Porcine Spleen through a Transcriptomics Approach." *BMC Genomics* 10 (1): 1–18.
- Darling, Samuel T. 1906. "A Protozoön General Infection Producing Pseudotubercles in The Lungs and Focal Necroses In The Liver, Spleen And Lymphnodes." *JAMA: The Journal of the American Medical Association* XLVI (17): 1283–85.
- Davies, J. M., R. Barnes, and D. Milligan. 2002. "Update of Guidelines for the Prevention and Treatment of Infection in Patients with an Absent or Dysfunctional Spleen." *Clinical Medicine* 2 (5): 440.
- Dietterich, Thomas G. 2002. "Machine Learning for Sequential Data: A Review." *Structural, Syntactic, and Statistical Pattern Recognition*, 15–30.
- Frank, Eibe, Mark Hall, Geoffrey Holmes, Richard Kirkby, Bernhard Pfahringer, Ian H. Witten, and Len Trigg. 2009. "Weka—A Machine Learning Workbench for Data Mining." *Data Mining and Knowledge Discovery Handbook*, 1269–77.
- Goh, G. D., S. L. Sing, and W. Y. Yeong. 2020. "A Review on Machine Learning in 3D Printing: Applications, Potential, and Challenges." *Artificial Intelligence Review* 54 (1): 63–94.
- Gómez Vela, Francisco A., Federico Divina, and Miguel García-Torres. 2021. *Computational Methods for the Analysis of Genomic Data and Biological Processes*. MDPI.
- Grimaldi, David, Olivier Pradier, Richard S. Hotchkiss, and Jean-Louis Vincent. 2017. "Nivolumab plus Interferon- $\gamma$  in the Treatment of Intractable Mucormycosis." *The Lancet Infectious Diseases* 17 (1): 18.
- G. Ramkumar, R. Thandaiah Prabu, Ngangbam Phalguni Singh, U. Maheswaran, Experimental analysis of brain tumor detection system using Machine learning approach, *Materials Today: Proceedings*, 2021, ISSN 22147853, <https://doi.org/10.1016/j.matpr.2021.01.246>
- Hosey, R. G., C. G. Mattacola, V. Kriss, T. Armsey, J. D. Quarles, and J. Jagger. 2006. "Ultrasound Assessment of Spleen Size in Collegiate Athletes." *British Journal of Sports Medicine* 40 (3): 251–54.
- Jung, Andreas, Reinhard Maier, Jean-Pierre Vartanian, Gennady Bocharov, Volker Jung, Ulrike Fischer, Eckart Meese, Simon Wain-Hobson, and Andreas Meyerhans. 2002. "Multiply Infected Spleen Cells in HIV Patients." *Nature* 418 (6894): 144–144.
- King, Harold, and Harris B. Shumacker Jr. 1952. "Splenic Studies: I. Susceptibility to Infection after Splenectomy Performed in Infancy." *Annals of Surgery* 136 (2): 239.
- Kumar M, M., Sivakumar, V. L., Devi V, S., Nagabhooshanam, N., & Thanappan, S. (2022). Investigation on Durability Behavior of Fiber Reinforced Concrete with Steel Slag/Bacteria beneath Diverse Exposure Conditions. *Advances in Materials Science and Engineering*, 2022.
- Landen, Serge, and Jean Closset. 2007. "Gas-Producing Infection of the Spleen in a Super-Super-Obese Patient." *Obesity Surgery* 17 (10): 1416–18.
- Morris, Dudley H., and Frederick D. Bullock. 1919. "The Importance of The Spleen in Resistance to Infection." *Annals of Surgery* 70 (5): 513.
- Newland, Adrian, Drew Provan, and Steven Myint. 2005. "Preventing Severe Infection after Splenectomy." *BMJ* 331 (7514): 417–18.
- Qiu, Junfei, Qihui Wu, Guoru Ding, Yuhua Xu, and Shuo Feng. 2016. "A Survey of Machine Learning for Big Data Processing." *EURASIP Journal on Advances in Signal Processing* 2016 (1): 1–16.
- S. G and R. G, "Automated Breast Cancer Classification based on Modified Deep learning Convolutional Neural Network following Dual Segmentation," 2022 3rd International Conference on Electronics and Sustainable Communication Systems (ICESC), Coimbatore, India, 2022, pp. 1562-1569, doi: 10.1109/ICESC54411.2022.9885299.
- Vanus, Jan, Jan Kubicek, Ojan M. Gorjani, and Jiri Koziorek. 2019. "Using the IBM SPSS SW Tool with Wavelet Transformation for CO2 Prediction within IoT in Smart Home Care." *Sensors* 19 (6): 1407.
- Wang, Y. Q., L. Lü, S. P. Weng, J. N. Huang, S-M Chan, and J. G. He. 2006. "Molecular Epidemiology and Phylogenetic Analysis of a Marine Fish Infectious Spleen and Kidney Necrosis Virus-like (ISKNV-Like) Virus." *Archives of Virology* 152 (4): 763–73.
- You, Zhen, Qinghe Zhang, Changjun Liu, Jiuzhou Song, Ning Yang, and Ling Lian. 2019. "Integrated Analysis of lncRNA and mRNA Repertoires in Marek's Disease Infected Spleens Identifies Genes Relevant to Resistance." *BMC Genomics* 20 (1): 1–15.
- Zerem, Enver, and Jacob Bergsland. 2006. "Ultrasound Guided Percutaneous Treatment for Splenic Abscesses: The Significance in Treatment of Critically Ill Patients." *World Journal of Gastroenterology: WJG* 12 (45): 7341