ABSTRACT 1 - PMID:15374860
1. A serious limitation in microarray analysis is the unreliability of the data generated from low signal intensities.
2. Such data may produce erroneous gene expression ratios and cause unnecessary validation or post-analysis follow-up tasks.
3. Therefore, the elimination of unreliable signal intensities will enhance reproducibility and reliability of gene expression ratios produced from microarray data.
4. In this study, we applied fuzzy c-means (FCM) and normal mixture modeling (NMM) based classification methods to separate microarray data into reliable and unreliable signal intensity populations.
5. We compared the results of FCM classification with those of classification based on NMM.
6. Both approaches were validated against reference sets of biological data consisting of only true positives and true negatives.
7. We observed that both methods performed equally well in terms of sensitivity and specificity.
8. Although a comparison of the computation times indicated that the fuzzy approach is computationally more efficient, other considerations support the use of NMM for the reliability analysis of microarray data.
9. The programs can be run/tested on many different computer platforms where Matlab is available.

METHODS: ['fuzzy c-means,normal mixture modeling']

SUMMARY A
4. In this study, we applied fuzzy c-means (FCM) and normal mixture modeling (NMM) based classification methods to separate microarray data into reliable and unreliable signal intensity populations.
7. We observed that both methods performed equally well in terms of sensitivity and specificity.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
4. In this study, we applied fuzzy c-means (FCM) and normal mixture modeling (NMM) based classification methods to separate microarray data into reliable and unreliable signal intensity populations.
5. We compared the results of FCM classification with those of classification based on NMM.
7. We observed that both methods performed equally well in terms of sensitivity and specificity.
8. Although a comparison of the computation times indicated that the fuzzy approach is computationally more efficient, other considerations support the use of NMM for the reliability analysis of microarray data.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY C
4. In this study, we applied fuzzy c-means (FCM) and normal mixture
modeling (NMM) based classification methods to separate microarray data
into reliable and unreliable signal intensity populations.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 2 - PMID:15374866
1. The adhesion of microbial pathogens to host cells is mediated by adhesins.
2. Experimental methods used for characterizing adhesins are time-consuming and demand large resources.
3. The availability of specialized software can rapidly aid experimenters in simplifying this problem.
4. We have employed 105 compositional properties and artificial neural networks to develop SPAAN, which predicts the probability of a protein being an adhesin (Pad).
5. SPAAN had optimal sensitivity of 89% and specificity of 100% on a defined test set and could identify 97.4% of known adhesins at high Pad value from a wide range of bacteria.
6. Furthermore, SPAAN facilitated improved annotation of several proteins as adhesins.
7. Novel adhesins were identified in 17 pathogenic organisms causing diseases in humans and plants.
8. In the severe acute respiratory syndrome (SARS) associated human corona virus, the spike glycoprotein and nsps (nsp2, nsp5, nsp6 and nsp7) were identified as having adhesin-like characteristics.
9. These results offer new lead for rapid experimental testing.

METHODS: ['artificial neural networks']

SUMMARY A
4. We have employed 105 compositional properties and artificial neural networks to develop SPAAN, which predicts the probability of a protein being an adhesin (Pad).
9. These results offer new lead for rapid experimental testing.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
4. We have employed 105 compositional properties and artificial neural networks to develop SPAAN, which predicts the probability of a protein being an adhesin (Pad).
5. SPAAN had optimal sensitivity of 89% and specificity of 100% on a defined test set and could identify 97.4% of known adhesins at high Pad value from a wide range of bacteria.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY C
4. We have employed 105 compositional properties and artificial neural networks to develop SPAAN, which predicts the probability of a protein being an adhesin (Pad).
5. SPAAN had optimal sensitivity of 89% and specificity of 100% on a defined test set and could identify 97.4% of known adhesins at high Pad value from a wide range of bacteria.
8. In the severe acute respiratory syndrome (SARS) associated human corona virus, the spike glycoprotein and nsps (nsp2, nsp5, nsp6 and nsp7) were identified as having adhesin-like characteristics.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY D
4. We have employed 105 compositional properties and artificial neural networks to develop SPAAN, which predicts the probability of a protein being an adhesin (Pad).
5. SPAAN had optimal sensitivity of 89% and specificity of 100% on a defined test set and could identify 97.4% of known adhesins at high Pad value from a wide range of bacteria.
6. Furthermore, SPAAN facilitated improved annotation of several proteins as adhesins.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 3 - PMID:15539447
1. Structural genomics projects aim to solve a large number of protein structures with the ultimate objective of representing the entire protein space.
2. The computational challenge is to identify and prioritize a small set of proteins with new, currently unknown, superfamilies or folds.
3. We develop a method that assigns each protein a likelihood of it belonging to a new, yet undetermined, structural superfamily.
4. The method relies on a variant of ProtoNet, an automatic hierarchical classification scheme of all protein sequences from SwissProt.
5. Our results show that proteins that are remote from solved structures in the ProtoNet hierarchy are more likely to belong to new superfamilies.
6. The results are validated against SCOP releases from recent years that account for about half of the solved structures known to date.
7. We show that our new method and the representation of ProtoNet are superior in detecting new targets, compared to our previous method using ProtoMap classification.
8. Furthermore, our method outperforms PSI-BLAST search in detecting potential new superfamilies.

METHODS: ['classification']

SUMMARY A
2. The computational challenge is to identify and prioritize a small set of proteins with new, currently unknown, superfamilies or folds.
4. The method relies on a variant of ProtoNet, an automatic hierarchical classification scheme of all protein sequences from SwissProt.
5. Our results show that proteins that are remote from solved structures in the ProtoNet hierarchy are more likely to belong to new superfamilies.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
3. We develop a method that assigns each protein a likelihood of it belonging to a new, yet undetermined, structural superfamily.
4. The method relies on a variant of ProtoNet, an automatic hierarchical classification scheme of all protein sequences from SwissProt.
7. We show that our new method and the representation of ProtoNet are superior in detecting new targets, compared to our previous method using ProtoMap classification.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY C
3. We develop a method that assigns each protein a likelihood of it
belonging to a new, yet undetermined, structural superfamily.
4. The method relies on a variant of ProtoNet, an automatic hierarchical
classification scheme of all protein sequences from SwissProt.
5. Our results show that proteins that are remote from solved structures in
the ProtoNet hierarchy are more likely to belong to new superfamilies.
7. We show that our new method and the representation of ProtoNet are
superior in detecting new targets, compared to our previous method using
ProtoMap classification.

SUMMARY D
4. The method relies on a variant of ProtoNet, an automatic hierarchical
classification scheme of all protein sequences from SwissProt.
5. Our results show that proteins that are remote from solved structures in
the ProtoNet hierarchy are more likely to belong to new superfamilies.
7. We show that our new method and the representation of ProtoNet are
superior in detecting new targets, compared to our previous method using
ProtoMap classification.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 4 - PMID:15558746
1. PhosphaBase is an ontology-driven database resource containing information on the protein phosphatase family.
2. It is the first public resource dedicated to protein phosphatases, which are enzymes that perform dephosphorylation reactions.
3. In conjunction with the phosphorylation action of protein kinases, phosphatases are involved in important control and communication mechanisms in the cell.
4. They have also been implicated in many human diseases, including diabetes and obesity, cancers, and neurodegenerative conditions.
5. PhosphaBase aims to centralize the growing base of knowledge in the phosphatase research domain.
6. The resource is built around a formal, domain-specific DAML+OIL ontology, and the data are collected from heterogeneous biological sources using Gene Ontology terms as a means of data extraction.
7. The overall ontology-driven architecture provides a robust structure with distinct advantages for sustainability and provides the potential for the development of diagnostic tools, as well as a data repository.

METHODS: ['data extraction', 'knowledge base']

SUMMARY A
5. PhosphaBase aims to centralize the growing base of knowledge in the phosphatase research domain.
6. The resource is built around a formal, domain-specific DAML+OIL ontology, and the data are collected from heterogeneous biological sources using Gene Ontology terms as a means of data extraction.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
5. PhosphaBase aims to centralize the growing base of knowledge in the phosphatase research domain.
6. The resource is built around a formal, domain-specific DAML+OIL ontology, and the data are collected from heterogeneous biological sources using Gene Ontology terms as a means of data extraction.
7. The overall ontology-driven architecture provides a robust structure with distinct advantages for sustainability and provides the potential for the development of diagnostic tools, as well as a data repository.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY C
1. PhosphaBase is an ontology-driven database resource containing information on the protein phosphatase family.
6. The resource is built around a formal, domain-specific DAML+OIL ontology, and the data are collected from heterogeneous biological sources using Gene Ontology terms as a means of data extraction.
7. The overall ontology-driven architecture provides a robust structure with distinct advantages for sustainability and provides the potential for the development of diagnostic tools, as well as a data repository.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY D
7. The overall ontology-driven architecture provides a robust structure with distinct advantages for sustainability and provides the potential for the development of diagnostic tools, as well as a data repository.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 5 - PMID:15567182
1. Doppler ultrasound is known as a reliable technique, which demonstrates the flow characteristics and resistance of ophthalmic arteries.
2. In this study, ophthalmic arterial Doppler signals were obtained from 106 subjects, 54 of whom suffered from ocular Behcet disease while the rest were healthy subjects.
3. Multilayer perceptron neural network (MLPNN) employing delta-bar-delta training algorithm was used to detect the presence of ocular Behcet disease.
4. Spectral analysis of the ophthalmic arterial Doppler signals was performed by least squares (LS) autoregressive (AR) method for determining the MLPNN inputs.
5. The MLPNN was trained with training set, cross validated with cross validation set and tested with testing set.
6. All these data sets were obtained from ophthalmic arteries of healthy subjects and subjects suffering from ocular Behcet disease.
7. Performance indicators and statistical measures were used for evaluating the MLPNN.
8. The correct classification rate was 96.43% for healthy subjects and 93.75% for unhealthy subjects suffering from ocular Behcet disease.
9. The classification results showed that the MLPNN employing delta-bar-delta training algorithm was effective to detect the ophthalmic arterial Doppler signals with Behcet disease.

METHODS: ['multilayer perceptron neural network', 'least squares autoregression']

SUMMARY A
3. Multilayer perceptron neural network (MLPNN) employing delta-bar-delta training algorithm was used to detect the presence of ocular Behcet disease.
4. Spectral analysis of the ophthalmic arterial Doppler signals was performed by least squares (LS) autoregressive (AR) method for determining the Multilayer perceptron neural network (MLPNN) inputs.
9. The classification results showed that the MLPNN employing delta-bar-delta training algorithm was effective to detect the ophthalmic arterial Doppler signals with Behcet disease.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
3. Multilayer perceptron neural network (MLPNN) employing delta-bar-delta training algorithm was used to detect the presence of ocular Behcet disease.
8. The correct classification rate was 96.43% for healthy subjects and 93.75% for unhealthy subjects suffering from ocular Behcet disease.
9. The classification results showed that the Multilayer perceptron neural network (MLPNN) employing delta-bar-delta training algorithm was effective to detect the ophthalmic arterial Doppler signals with Behcet disease.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY C
3. Multilayer perceptron neural network (MLPNN) employing delta-bar-delta
training algorithm was used to detect the presence of ocular Behcet
disease.
9. The classification results showed that the Multilayer perceptron neural
network (MLPNN) employing delta-bar-delta training algorithm was effective
to detect the ophthalmic arterial Doppler signals with Behcet disease.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 6 - PMID:15640173

1. Cryptosporidium parvum and Giardia lamblia are protozoa capable of causing gastrointestinal diseases.
2. Currently, these organisms are identified using immunofluorescent antibody (IFA)-based microscopy, and identification requires trained individuals for final confirmation.
3. Since artificial neural networks (ANN) can provide an automated means of identification, thereby reducing human errors related to misidentification, ANN were developed to identify Cryptosporidium oocyst and Giardia cyst images.
4. Digitized images of C. parvum oocysts and G. lamblia cysts stained with various commercial IFA reagents were used as positive controls.
5. The images were captured using a color digital camera at 400 x (total magnification), processed, and converted into a binary numerical array.
6. A variety of "negative" images were also captured and processed.
7. The ANN were developed using these images and a rigorous training and testing protocol.
8. The Cryptosporidium oocyst ANN were trained with 1,586 images, while Giardia cyst ANN were trained with 2,431 images.
9. After training, the best-performing ANN were selected based on an initial testing performance against 100 images (50 positive and 50 negative images).
10. The networks were validated against previously "unseen" images of 500 Cryptosporidium oocysts (250 positive, 250 negative) and 282 Giardia cysts (232 positive, 50 negative).
11. The selected ANNs correctly identified 91.8 and 99.6% of the Cryptosporidium oocyst and Giardia cyst images, respectively.
12. These results indicate that ANN technology can be an alternate to having trained personnel for detecting these pathogens and can be a boon to underdeveloped regions of the world where there is a chronic shortage of adequately skilled individuals to detect these pathogens.

METHODS: ['image analysis', 'classification', 'artificial neural networks']

SUMMARY A
3. Since artificial neural networks (ANN) can provide an automated means of identification, thereby reducing human errors related to misidentification, ANN were developed to identify Cryptosporidium oocyst and Giardia cyst images.
12. These results indicate that ANN technology can be an alternate to having trained personnel for detecting these pathogens and can be a boon to underdeveloped regions of the world where there is a chronic shortage of adequately skilled individuals to detect these pathogens.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
3. Since artificial neural networks (ANN) can provide an automated means of identification, thereby reducing human errors related to misidentification, ANN were developed to identify Cryptosporidium oocyst and Giardia cyst images.
11. The selected ANNs correctly identified 91.8 and 99.6% of the Cryptosporidium oocyst and Giardia cyst images, respectively.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY C
3. Since artificial neural networks (ANN) can provide an automated means of identification, thereby reducing human errors related to misidentification, ANN were developed to identify Cryptosporidium oocyst and Giardia cyst images.
9. After training, the best-performing ANN were selected based on an initial testing performance against 100 images (50 positive and 50 negative images).
11. The selected ANNs correctly identified 91.8 and 99.6% of the Cryptosporidium oocyst and Giardia cyst images, respectively.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY D
3. Since artificial neural networks (ANN) can provide an automated means of identification, thereby reducing human errors related to misidentification, ANN were developed to identify Cryptosporidium oocyst and Giardia cyst images.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 7 - PMID:15786933
1. To present a virtual model, the venous return simulator (VRS), designed
to compute venous hemodynamic variations when compression is applied to the
leg.
2. The VRS defines a numerical network of the lower extremity and computes
the dynamic variables (flow rate, venous diameter and internal pressure)
for a defined external pressure.
3. The VRS was based on physiological data from the literature and clinical
studies on healthy subjects.
4. Clinical correlations were required to confirm its validity; for this
purpose, we carried out experiments simulating the conditions of a clinical
trial, in which the diameter of superficial and deep veins was measured
while increasing pressures (20, 40 and 60 mmHg.)
5. were applied to the thighs of patients enduring deep valvular
insufficiency and venous ulcers.
6. The diameters and flow rates calculated using our VRS model were
compared with the experimental data obtained at the same thigh compression
levels.
7. The numerical results of VRS are in good agreement with the clinical
data obtained by Duplex, (R2 = 0.96).
8. In accordance with the in vivo measurement the computed results show
that only a pressure greater than 40 mmHg is able to reduce the venous
diameter at thigh-level, both in the great saphenous vein and in the
femoral vein.
9. The venous return simulator computes lower limb hemodynamic parameters
under static conditions.
10. The good correlation existing between the VRS and the data obtained in
a previous clinical study shows that this numerical approach could provide
a useful means of predicting the hemodynamic consequences of compression
therapy.

METHODS: ['venous return simulator', 'simulation']

SUMMARY A
1. To present a virtual model, the venous return simulator (VRS), designed
to compute venous hemodynamic variations when compression is applied to the
leg.
2. The VRS defines a numerical network of the lower extremity and computes
the dynamic variables (flow rate, venous diameter and internal pressure)
for a defined external pressure.
10. The good correlation existing between the VRS and the data obtained in
a previous clinical study shows that this numerical approach could provide
a useful means of predicting the hemodynamic consequences of compression
therapy.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
1. To present a virtual model, the venous return simulator (VRS), designed to compute venous hemodynamic variations when compression is applied to the leg.
10. The good correlation existing between the VRS and the data obtained in a previous clinical study shows that this numerical approach could provide a useful means of predicting the hemodynamic consequences of compression therapy.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY C
1. To present a virtual model, the venous return simulator (VRS), designed to compute venous hemodynamic variations when compression is applied to the leg.
4. Clinical correlations were required to confirm its validity; for this purpose, we carried out experiments simulating the conditions of a clinical trial, in which the diameter of superficial and deep veins was measured while increasing pressures (20, 40 and 60 mmHg.)
10. The good correlation existing between the VRS and the data obtained in a previous clinical study shows that this numerical approach could provide a useful means of predicting the hemodynamic consequences of compression therapy.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY D
1. To present a virtual model, the venous return simulator (VRS), designed to compute venous hemodynamic variations when compression is applied to the leg.
8. In accordance with the in vivo measurement the computed results show that only a pressure greater than 40 mmHg is able to reduce the venous diameter at thigh-level, both in the great saphenous vein and in the femoral vein.
9. The venous return simulator computes lower limb hemodynamic parameters under static conditions.
10. The good correlation existing between the VRS and the data obtained in a previous clinical study shows that this numerical approach could provide a useful means of predicting the hemodynamic consequences of compression therapy.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 8 - PMID:32441663
1. Electrocardiography (ECG) signals and the information obtained through
the analysis of these signals constitute the main source of diagnosis for
many cardiovascular system diseases.
2. Therefore, accurate analyses of ECG signals are very important for
correct diagnosis.
3. In this study, an ECG analysis toolbox together with a user-friendly
graphical user interface, which contains the all ECG analysis steps between
the recording unit and the statistical investigation, is developed.
4. Furthermore, a new feature calculation methodology is proposed for ECG
analysis, which carries distinct information than amplitudes and durations
of ECG main waves and can be used in artificial intelligence studies.
5. Developed toolbox is tested using both Massachusetts Institute of
Technology-Beth Israel Hospital (MIT-BIH) Arrhythmia ECG Database and an
experimentally collected dataset for performance evaluation.
6. The results show that ECG analysis toolbox presented in this study
increases the accuracy and reliability of the ECG main wave detection
analysis, highly fasten the process duration compared to manual ones and
the new feature set can be used as a new parameter for decision support
systems about ECG based on artificial intelligence.

METHODS: ['decision support systems', 'feature extraction']

SUMMARY A
3. In this study, an ECG analysis toolbox together with a user-friendly
graphical user interface, which contains the all ECG analysis steps between
the recording unit and the statistical investigation, is developed.
4. Furthermore, a new feature calculation methodology is proposed for ECG
analysis, which carries distinct information than amplitudes and durations
of ECG main waves and can be used in artificial intelligence studies.
6. The results show that ECG analysis toolbox presented in this study
increases the accuracy and reliability of the ECG main wave detection
analysis, highly fasten the process duration compared to manual ones and
the new feature set can be used as a new parameter for decision support
systems about ECG based on artificial intelligence.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
3. In this study, an ECG analysis toolbox together with a user-friendly
graphical user interface, which contains the all ECG analysis steps between
the recording unit and the statistical investigation, is developed.
6. The results show that ECG analysis toolbox presented in this study
increases the accuracy and reliability of the ECG main wave detection
analysis, highly fasten the process duration compared to manual ones and
the new feature set can be used as a new parameter for decision support
systems about ECG based on artificial intelligence.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 9 - PMID:32435646
1. Recent studies have shown that deep learning is capable of classifying
dermatoscopic images at least as well as dermatologists.
2. However, many studies in skin cancer classification utilize non-biopsy-
verified training images.
3. This imperfect ground truth introduces a systematic error, but the
effects on classifier performance are currently unknown.
4. Here, we systematically examine the effects of label noise by training
and evaluating convolutional neural networks (CNN) with 804 images of
melanoma and nevi labeled either by dermatologists or by biopsy.
5. The CNNs are evaluated on a test set of 384 images by means of 4-fold
cross validation comparing the outputs with either the corresponding
dermatological or the biopsy-verified diagnosis.
6. With identical ground truths of training and test labels, high
accuracies with 75.03% (95% CI: 74.39-75.66%) for dermatological and 73.80%
(95% CI: 73.10-74.51%) for biopsy-verified labels can be achieved.
7. However, if the CNN is trained and tested with different ground truths,
accuracy drops significantly to 64.53% (95% CI: 63.12-65.94%, p < 0.01) on
a non-biopsy-verified and to 64.24% (95% CI: 62.66-65.83%, p < 0.01) on a
biopsy-verified test set.
8. In conclusion, deep learning methods for skin cancer classification are
highly sensitive to label noise and future work should use biopsy-verified
training images to mitigate this problem.

METHODS: ['classification', 'convolutional neural network', 'deep
learning']

SUMMARY A
4. Here, we systematically examine the effects of label noise by training
and evaluating convolutional neural networks (CNN) with 804 images of
melanoma and nevi labeled either by dermatologists or by biopsy.
8. In conclusion, deep learning methods for skin cancer classification are
highly sensitive to label noise and future work should use biopsy-verified
training images to mitigate this problem.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
4. Here, we systematically examine the effects of label noise by training
and evaluating convolutional neural networks (CNN) with 804 images of
melanoma and nevi labeled either by dermatologists or by biopsy.
6. With identical ground truths of training and test labels, high
accuracies with 75.03% (95% CI: 74.39-75.66%) for dermatological and 73.80%
(95% CI: 73.10-74.51%) for biopsy-verified labels can be achieved.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY C
4. Here, we systematically examine the effects of label noise by training
and evaluating convolutional neural networks (CNN) with 804 images of
melanoma and nevi labeled either by dermatologists or by biopsy.
7. However, if the CNN is trained and tested with different ground truths,
accuracy drops significantly to 64.53% (95% CI: 63.12-65.94%, p < 0.01) on
a non-biopsy-verified and to 64.24% (95% CI: 62.66-65.83%, p < 0.01) on a
biopsy-verified test set.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY D
4. Here, we systematically examine the effects of label noise by training
and evaluating convolutional neural networks (CNN) with 804 images of
melanoma and nevi labeled either by dermatologists or by biopsy.
6. With identical ground truths of training and test labels, high
accuracies with 75.03% (95% CI: 74.39-75.66%) for dermatological and 73.80%
(95% CI: 73.10-74.51%) for biopsy-verified labels can be achieved.
8. In conclusion, deep learning methods for skin cancer classification are
highly sensitive to label noise and future work should use biopsy-verified
training images to mitigate this problem.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 10 - PMID:32433694
1. The factors that determine Serum Thyrotropin (TSH) levels have been
examined through different methods, using different covariates.
2. However, the use of machine learning methods has so far not been studied
in population databases like NHANES (National Health and Nutritional
Examination Survey) to predict TSH.
3. In this study, we performed a comparative analysis of different machine
learning methods like Linear regression, Random forest, Support vector
machine, multilayer perceptron and stacking regression to predict TSH and
classify individuals with normal, low and high TSH levels.
4. We considered Free T4, Anti-TPO antibodies, T3, Body Mass Index (BMI),
Age and Ethnicity as the predictor variables.
5. A total of 9818 subjects were included in this comparative analysis.
6. We used coefficient of determination (r2) value to compare the results
for predicting the TSH and show that the Random Forest, Gradient Boosting
and Stacking Regression perform equally well in predicting TSH and achieve
the highest r2 value = 0.13, with mean absolute error of 0.78.
7. Moreover, we found that Anti-TPO is the most important feature in
predicting TSH followed by Age, BMI, T3 and Free-T4 for the regression
analysis.
8. While classifying TSH into normal, high or low levels, our comparative
analysis also shows that Random forest performs the best in the
classification study, performed with individuals with normal, high and low
levels of TSH.
9. We found the following Areas Under Curve (AUC); for low TSH, AUC = 0.61,
normal TSH, AUC = 0.61 and elevated TSH AUC = 0.69.
10. Additionally, we found that Anti-TPO was the most important feature in
classifying TSH.
11. In this study, we suggest that artificial intelligence and machine
learning methods might offer an insight into the complex hypothalamic-
pituitary -thyroid axis and may be an invaluable tool that guides us in
making appropriate therapeutic decisions (thyroid hormone dosing) for the
individual patient.

METHODS: ['classification', 'linear regression', 'random forest',
'multilayer perceptron', 'gradient boosting', 'support vector machines']

SUMMARY A
3. In this study, we performed a comparative analysis of different machine
learning methods like Linear regression, Random forest, Support vector
machine, multilayer perceptron and stacking regression to predict TSH and
classify individuals with normal, low and high TSH levels.
6. We used coefficient of determination (r2) value to compare the results
for predicting the TSH and show that the Random Forest, Gradient Boosting
and Stacking Regression perform equally well in predicting TSH and achieve
the highest r2 value = 0.13, with mean absolute error of 0.78.
11. In this study, we suggest that artificial intelligence and machine
learning methods might offer an insight into the complex hypothalamic-
pituitary -thyroid axis and may be an invaluable tool that guides us in
making appropriate therapeutic decisions (thyroid hormone dosing) for the
individual patient.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
3. In this study, we performed a comparative analysis of different machine learning methods like Linear regression, Random forest, Support vector machine, multilayer perceptron and stacking regression to predict TSH and classify individuals with normal, low and high TSH levels.
6. We used coefficient of determination (r2) value to compare the results for predicting the TSH and show that the Random Forest, Gradient Boosting and Stacking Regression perform equally well in predicting TSH and achieve the highest r2 value = 0.13, with mean absolute error of 0.78.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY C
3. In this study, we performed a comparative analysis of different machine learning methods like Linear regression, Random forest, Support vector machine, multilayer perceptron and stacking regression to predict TSH and classify individuals with normal, low and high TSH levels.
6. We used coefficient of determination (r2) value to compare the results for predicting the TSH and show that the Random Forest, Gradient Boosting and Stacking Regression perform equally well in predicting TSH and achieve the highest r2 value = 0.13, with mean absolute error of 0.78.
8. While classifying TSH into normal, high or low levels, our comparative analysis also shows that Random forest performs the best in the classification study, performed with individuals with normal, high and low levels of TSH.
11. In this study, we suggest that artificial intelligence and machine learning methods might offer an insight into the complex hypothalamic-pituitary -thyroid axis and may be an invaluable tool that guides us in making appropriate therapeutic decisions (thyroid hormone dosing) for the individual patient.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 11 - PMID:29891981

1. In the era of precision medicine, cancer therapy can be tailored to an individual patient based on the genomic profile of a tumour.
2. Despite the ever-increasing abundance of cancer genomic data, linking mutation profiles to drug efficacy remains a challenge.
3. Herein, we report Cancer Drug Response profile scan (CDRscan) a novel deep learning model that predicts anticancer drug responsiveness based on a large-scale drug screening assay data encompassing genomic profiles of 787 human cancer cell lines and structural profiles of 244 drugs.
4. CDRscan employs a two-step convolution architecture, where the genomic mutational fingerprints of cell lines and the molecular fingerprints of drugs are processed individually, then merged by 'virtual docking', an in silico modelling of drug treatment.
5. Analysis of the goodness-of-fit between observed and predicted drug response revealed a high prediction accuracy of CDRscan (R2 > 0.84; AUROC > 0.98).
6. We applied CDRscan to 1,487 approved drugs and identified 14 oncology and 23 non-oncology drugs having new potential cancer indications.
7. This, to our knowledge, is the first-time application of a deep learning model in predicting the feasibility of drug repurposing.
8. By further clinical validation, CDRscan is expected to allow selection of the most effective anticancer drugs for the genomic profile of the individual patient.

METHODS: ['deep learning']

SUMMARY A
3. Herein, we report Cancer Drug Response profile scan (CDRscan) a novel deep learning model that predicts anticancer drug responsiveness based on a large-scale drug screening assay data encompassing genomic profiles of 787 human cancer cell lines and structural profiles of 244 drugs.
4. CDRscan employs a two-step convolution architecture, where the genomic mutational fingerprints of cell lines and the molecular fingerprints of drugs are processed individually, then merged by 'virtual docking', an in silico modelling of drug treatment.
5. Analysis of the goodness-of-fit between observed and predicted drug response revealed a high prediction accuracy of CDRscan (R2 > 0.84; AUROC > 0.98).

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 12 - PMID:29889095
1. Statistical noise may degrade the x-ray image quality of digital radiography (DR) system.
2. This corruption can be alleviated by extending exposure time of detectors and increasing the intensity of radiation.
3. However, in some instances, such as the security check and medical imaging examination, the system demands rapid and low-dose detection.
4. In this study, we propose and test a generative adversarial network (GAN) based x-ray image denoising method.
5. Images used in this study were acquired from a digital radiography (DR) imaging system.
6. Promising results have been obtained in our experiments with x-ray images for the security check application.
7. The Experiment results demonstrated that the proposed new image denoising method was able to effectively remove the statistical noise from x-ray images, while kept sharp edge and clear structure.
8. Thus, comparing with the traditional convolutional neural network (CNN) based method, the proposed new method generates more plausible-looking images, which contains more details.

METHODS: ['image analysis', 'convolutional neural network', 'generative adversarial network']

SUMMARY A
4. In this study, we propose and test a generative adversarial network (GAN) based x-ray image denoising method.
7. The Experiment results demonstrated that the proposed new image denoising method was able to effectively remove the statistical noise from x-ray images, while kept sharp edge and clear structure.
8. Thus, comparing with the traditional convolutional neural network (CNN) based method, the proposed new method generates more plausible-looking images, which contains more details.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
4. In this study, we propose and test a generative adversarial network (GAN) based x-ray image denoising method.
6. Promising results have been obtained in our experiments with x-ray images for the security check application.
7. The Experiment results demonstrated that the proposed new image denoising method was able to effectively remove the statistical noise from x-ray images, while kept sharp edge and clear structure.
8. Thus, comparing with the traditional convolutional neural network (CNN) based method, the proposed new method generates more plausible-looking images, which contains more details.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 13 - PMID:29886268

1. Targeted prostate biopsy, incorporating multi-parametric magnetic resonance imaging (mp-MRI) and its registration with ultrasound, is currently the state-of-the-art in prostate cancer diagnosis.
2. The registration process in most targeted biopsy systems today relies heavily on accurate segmentation of ultrasound images.
3. Automatic or semi-automatic segmentation is typically performed offline prior to the start of the biopsy procedure.
4. In this paper, we present a deep neural network based real-time prostate segmentation technique during the biopsy procedure, hence paving the way for dynamic registration of mp-MRI and ultrasound data.
5. In addition to using convolutional networks for extracting spatial features, the proposed approach employs recurrent networks to exploit the temporal information among a series of ultrasound images.
6. One of the key contributions in the architecture is to use residual convolution in the recurrent networks to improve optimization.
7. We also exploit recurrent connections within and across different layers of the deep networks to maximize the utilization of the temporal information.
8. Furthermore, we perform dense and sparse sampling of the input ultrasound sequence to make the network robust to ultrasound artifacts.
9. Our architecture is trained on 2,238 labeled transrectal ultrasound images, with an additional 637 and 1,017 unseen images used for validation and testing, respectively.
10. We obtain a mean Dice similarity coefficient of 93%, a mean surface distance error of 1.10 mm and a mean Hausdorff distance error of 3.0 mm.
11. A comparison of the reported results with those of a state-of-the-art technique indicates statistically significant improvement achieved by the proposed approach.

METHODS: ['recurrent neural network', 'deep neural network']

SUMMARY A
4. In this paper, we present a deep neural network based real-time prostate segmentation technique during the biopsy procedure, hence paving the way for dynamic registration of mp-MRI and ultrasound data.
5. In addition to using convolutional networks for extracting spatial features, the proposed approach employs recurrent networks to exploit the temporal information among a series of ultrasound images.
11. A comparison of the reported results with those of a state-of-the-art technique indicates statistically significant improvement achieved by the proposed approach.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B

4. In this paper, we present a deep neural network based real-time prostate segmentation technique during the biopsy procedure, hence paving the way for dynamic registration of mp-MRI and ultrasound data.
5. In addition to using convolutional networks for extracting spatial features, the proposed approach employs recurrent networks to exploit the temporal information among a series of ultrasound images.
10. We obtain a mean Dice similarity coefficient of 93%, a mean surface distance error of 1.10 mm and a mean Hausdorff distance error of 3.0 mm.
11. A comparison of the reported results with those of a state-of-the-art technique indicates statistically significant improvement achieved by the proposed approach.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 14 - PMID:29788482

1. This paper presents the development and real-time testing of an automated expert diagnostic telehealth system for the diagnosis of 2 respiratory diseases, asthma and Chronic Obstructive Pulmonary Disease (COPD).
2. The system utilizes Android, Java, MATLAB, and PHP technologies and consists of a spirometer, mobile application, and expert diagnostic system.
3. To evaluate the effectiveness of the system, a prospective study was carried out in 3 remote primary healthcare institutions, and one hospital in Bosnia and Herzegovina healthcare system.
4. During 6 months, 780 patients were assessed and diagnosed with an accuracy of 97.32%.
5. The presented approach is simple to use and offers specialized consultations for patients in remote, rural, and isolated communities, as well as old and less physically mobile patients.
6. While improving the quality of care delivered to patients, it was also found to be very beneficial in terms of healthcare.

METHODS: ['mobile computing', 'expert systems']

SUMMARY A
1. This paper presents the development and real-time testing of an automated expert diagnostic telehealth system for the diagnosis of 2 respiratory diseases, asthma and Chronic Obstructive Pulmonary Disease (COPD).
2. The system utilizes Android, Java, MATLAB, and PHP technologies and consists of a spirometer, mobile application, and expert diagnostic system.
4. During 6 months, 780 patients were assessed and diagnosed with an accuracy of 97.32%.
5. The presented approach is simple to use and offers specialized consultations for patients in remote, rural, and isolated communities, as well as old and less physically mobile patients.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
1. This paper presents the development and real-time testing of an automated expert diagnostic telehealth system for the diagnosis of 2 respiratory diseases, asthma and Chronic Obstructive Pulmonary Disease (COPD).
2. The system utilizes Android, Java, MATLAB, and PHP technologies and consists of a spirometer, mobile application, and expert diagnostic system.
5. The presented approach is simple to use and offers specialized consultations for patients in remote, rural, and isolated communities, as well as old and less physically mobile patients.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY C
1. This paper presents the development and real-time testing of an automated expert diagnostic telehealth system for the diagnosis of 2 respiratory diseases, asthma and Chronic Obstructive Pulmonary Disease (COPD).
2. The system utilizes Android, Java, MATLAB, and PHP technologies and consists of a spirometer, mobile application, and expert diagnostic system.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 15 - PMID:29768415
1. In this work, a computer-aided tool for detection was developed to
segment breast masses from clinical ultrasound (US) scans.
2. The underlying Multi U-net algorithm is based on convolutional neural
networks.
3. Under the Mayo Clinic Institutional Review Board protocol, a prospective
study of the automatic segmentation of suspicious breast masses was
performed.
4. The cohort consisted of 258 female patients who were clinically
identified with suspicious breast masses and underwent clinical US scan and
breast biopsy.
5. The computer-aided detection tool effectively segmented the breast
masses, achieving a mean Dice coefficient of 0.82, a true positive fraction
(TPF) of 0.84, and a false positive fraction (FPF) of 0.01.
6. By avoiding positioning of an initial seed, the algorithm is able to
segment images in real time (13-55 ms per image), and can have potential
clinical applications.
7. The algorithm is at par with a conventional seeded algorithm, which had
a mean Dice coefficient of 0.84 and performs significantly better (P<
0.0001) than the original U-net algorithm.

METHODS: ['image analysis', 'convolutional neural network']

SUMMARY A
1. In this work, a computer-aided tool for detection was developed to
segment breast masses from clinical ultrasound (US) scans.
2. The underlying Multi U-net algorithm is based on convolutional neural
networks.
7. The algorithm is at par with a conventional seeded algorithm, which had
a mean Dice coefficient of 0.84 and performs significantly better (P<
0.0001) than the original U-net algorithm.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
1. In this work, a computer-aided tool for detection was developed to
segment breast masses from clinical ultrasound (US) scans.
2. The underlying Multi U-net algorithm is based on convolutional neural
networks.
5. The computer-aided detection tool effectively segmented the breast
masses, achieving a mean Dice coefficient of 0.82, a true positive fraction
(TPF) of 0.84, and a false positive fraction (FPF) of 0.01.
7. The algorithm is at par with a conventional seeded algorithm, which had
a mean Dice coefficient of 0.84 and performs significantly better (P<
0.0001) than the original U-net algorithm.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 16 - PMID:29765586

1. More than 1 billion people suffer from chronic respiratory diseases worldwide, accounting for more than 4 million deaths annually.
2. Inhaled corticosteroid is a popular medication for treating chronic respiratory diseases.
3. Its side effects include decreased bone mineral density and osteoporosis.
4. The aims of this study are to investigate the association of inhaled corticosteroids and fracture and to design a clinical support system for fracture prediction.
5. The data of patients aged 20 years and older, who had visited healthcare centers and been prescribed with inhaled corticosteroids within 2002-2010, were retrieved from the National Health Insurance Research Database (NHIRD).
6. After excluding patients diagnosed with hip fracture or vertebrate fractures before using inhaled corticosteroid, a total of 11645 patients receiving inhaled corticosteroid therapy were included for this study.
7. Among them, 1134 (9.7%) were diagnosed with hip fracture or vertebrate fracture.
8. The statistical results showed that demographic information, chronic respiratory diseases and comorbidities, and corticosteroid-related variables (cumulative dose, mean exposed daily dose, follow-up duration, and exposed duration) were significantly different between fracture and nonfracture patients.
9. The clinical decision support systems (CDSSs) were designed with integrated genetic algorithm (GA) and support vector machine (SVM) by training and validating the models with balanced training sets obtained by random and cluster-based undersampling methods and testing with the imbalanced NHIRD dataset.
10. Two different objective functions were adopted for obtaining optimal models with best predictive performance.
11. The predictive performance of the CDSSs exhibits a sensitivity of 69.84-77.00% and an AUC of 0.7495-0.7590.
12. It was concluded that long-term use of inhaled corticosteroids may induce osteoporosis and exhibit higher incidence of hip or vertebrate fractures.
13. The accumulated dose of ICS and OCS therapies should be continuously monitored, especially for patients with older age and women after menopause, to prevent from exceeding the maximum dosage.

METHODS: ['decision support systems', 'support vector machines', 'genetic algorithms', 'clustering']

SUMMARY A
4. The aims of this study are to investigate the association of inhaled corticosteroids and fracture and to design a clinical support system for fracture prediction.
9. The clinical decision support systems (CDSSs) were designed with integrated genetic algorithm (GA) and support vector machine (SVM) by training and validating the models with balanced training sets obtained by random and cluster-based undersampling methods and testing with the imbalanced National Health Insurance Research Database (NHIRD) dataset.
11. The predictive performance of the CDSSs exhibits a sensitivity of 69.84-77.00% and an AUC of 0.7495-0.7590.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
4. The aims of this study are to investigate the association of inhaled corticosteroids and fracture and to design a clinical support system for fracture prediction.
9. The clinical decision support systems (CDSSs) were designed with integrated genetic algorithm (GA) and support vector machine (SVM) by training and validating the models with balanced training sets obtained by random and cluster-based undersampling methods and testing with the imbalanced National Health Insurance Research Database (NHIRD) dataset.
11. The predictive performance of the CDSSs exhibits a sensitivity of 69.84-77.00% and an AUC of 0.7495-0.7590.
12. It was concluded that long-term use of inhaled corticosteroids may induce osteoporosis and exhibit higher incidence of hip or vertebrate fractures.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 17 - PMID:31946067
1. Despite recent advances in cancer treatment, patients with brain metastasis still suffer from poor overall survival (OS) after standard treatment.
2. Predicting the treatment outcome before or early after the treatment can potentially assist the physicians in improving the therapy outcome by adjusting a standard treatment on an individual patient basis.
3. In this study, a data-driven computational framework was proposed and investigated to predict the local control/failure (LC/LF) outcome in patients with brain metastasis treated with hypo-fractionated stereotactic radiation therapy (SRT).
4. The framework extracted several geometrical and textural features from the magnetic resonance (MR) images of the tumour and edema regions acquired for 38 patients.
5. Subsequent to a multi-step feature reduction/selection, a quantitative MR biomarker consisting of two features was constructed.
6. A support vector machine classifier was used for outcome prediction using the constructed MR biomarker.
7. The bootstrap .632+ and leave-one-patient-out cross-validation methods were used to assess the model's performance.
8. The results indicated that the outcome of LF after SRT could be predicted with an area under the curve of 0.80 and a cross-validated accuracy of 82%.
9. The results obtained implied a good potential of the proposed framework for local outcome prediction in patients with brain metastasis treated with SRT and encourage further investigations on a larger cohort of patients.

METHODS: ['classification', 'support vector machines']

SUMMARY A
3. In this study, a data-driven computational framework was proposed and investigated to predict the local control/failure (LC/LF) outcome in patients with brain metastasis treated with hypo-fractionated stereotactic radiation therapy (SRT).
6. A support vector machine classifier was used for outcome prediction using the constructed magnetic resonance (MR) biomarker.
8. The results indicated that the outcome of LF after SRT could be predicted with an area under the curve of 0.80 and a cross-validated accuracy of 82%.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
3. In this study, a data-driven computational framework was proposed and investigated to predict the local control/failure (LC/LF) outcome in patients with brain metastasis treated with hypo-fractionated stereotactic radiation therapy (SRT).
5. Subsequent to a multi-step feature reduction/selection, a quantitative magnetic resonance (MR) biomarker consisting of two features was constructed.
6. A support vector machine classifier was used for outcome prediction using the constructed MR biomarker.
8. The results indicated that the outcome of LF after SRT could be predicted with an area under the curve of 0.80 and a cross-validated accuracy of 82%.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 18 - PMID:31946036
1. Training data is the key component in designing algorithms for medical image analysis and in many cases it is the main bottleneck in achieving good results.
2. Recent progress in image generation has enabled the training of neural network based solutions using synthetic data.
3. A key factor in the generation of new samples is controlling the important appearance features and potentially being able to generate a new sample of a specific class with different variants.
4. In this work we suggest the synthesis of new data by mixing the class specified and unspecified representation of different factors in the training data which are separated using a disentanglement based scheme.
5. Our experiments on liver lesion classification in CT show an average improvement of 7.4% in accuracy over the baseline training scheme.

METHODS: ['classification', 'image analysis', 'artificial neural networks']

SUMMARY A
4. In this work we suggest the synthesis of new data by mixing the class specified and unspecified representation of different factors in the training data which are separated using a disentanglement based scheme.
5. Our experiments on liver lesion classification in CT show an average improvement of 7.4% in accuracy over the baseline training scheme.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 19 - PMID:31945837
1. Angle estimation is an important step in the Doppler ultrasound clinical workflow to measure blood velocity.
2. It is widely recognized that incorrect angle estimation is a leading cause of error in Doppler-based blood velocity measurements.
3. In this paper, we propose a deep learning-based approach for automated Doppler angle estimation.
4. The approach was developed using 2100 human carotid ultrasound images including image augmentation.
5. Five pre-trained models were used to extract images features, and these features were passed to a custom shallow network for Doppler angle estimation.
6. Independently, measurements were obtained by a human observer reviewing the images for comparison.
7. The mean absolute error (MAE) between the automated and manual angle estimates ranged from 3.9° to 9.4° for the models evaluated.
8. Furthermore, the MAE for the best performing model was less than the acceptable clinical Doppler angle error threshold thus avoiding misclassification of normal velocity values as a stenosis.
9. The results demonstrate potential for applying a deep-learning based technique for automated ultrasound Doppler angle estimation.
10. Such a technique could potentially be implemented within the imaging software on commercial ultrasound scanners.

METHODS: ['classification', 'deep learning']

SUMMARY A
3. In this paper, we propose a deep learning-based approach for automated Doppler angle estimation.
5. Five pre-trained models were used to extract images features, and these features were passed to a custom shallow network for Doppler angle estimation.
7. The mean absolute error (MAE) between the automated and manual angle estimates ranged from 3.9° to 9.4° for the models evaluated.
8. Furthermore, the MAE for the best performing model was less than the acceptable clinical Doppler angle error threshold thus avoiding misclassification of normal velocity values as a stenosis.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
3. In this paper, we propose a deep learning-based approach for automated Doppler angle estimation.
5. Five pre-trained models were used to extract images features, and these features were passed to a custom shallow network for Doppler angle estimation.
7. The mean absolute error (MAE) between the automated and manual angle estimates ranged from 3.9° to 9.4° for the models evaluated.
9. The results demonstrate potential for applying a deep-learning based technique for automated ultrasound Doppler angle estimation.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY C
3. In this paper, we propose a deep learning-based approach for automated
Doppler angle estimation.
5. Five pre-trained models were used to extract images features, and these
features were passed to a custom shallow network for Doppler angle
estimation.
8. Furthermore, the mean absolute error (MAE) for the best performing model
was less than the acceptable clinical Doppler angle error threshold thus
avoiding misclassification of normal velocity values as a stenosis.
9. The results demonstrate potential for applying a deep-learning based
technique for automated ultrasound Doppler angle estimation.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY D
2. It is widely recognized that incorrect angle estimation is a leading
cause of error in Doppler-based blood velocity measurements.
3. In this paper, we propose a deep learning-based approach for automated
Doppler angle estimation.
9. The results demonstrate potential for applying a deep-learning based
technique for automated ultrasound Doppler angle estimation.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

ABSTRACT 20 - PMID:31923277
1. Several European countries have established criteria for prioritising
initiation of treatment in patients infected with the hepatitis C virus
(HCV) by grouping patients according to clinical characteristics.
2. Based on neural network techniques, our objective was to identify those
factors for HIV/HCV co-infected patients (to which clinicians have given
careful consideration before treatment uptake) that have not being included
among the prioritisation criteria.
3. An evolutionary algorithm was used to determine the architecture and
estimate the coefficients of the model.
4. This machine learning methodology found that radial basis neural
networks provided a very simple model in terms of the number of patient
characteristics to be considered by the classifier (in this case, six),
returning a good overall classification accuracy of 0.767 and a minimum
sensitivity (for the classification of the minority class, untreated
patients) of 0.550.
5. Finally, the area under the ROC curve was 0.802, which proved to be
exceptional.
6. The parsimony of the model makes it especially attractive, using just
eight connections.
7. The independent variable "recent PWID" is compulsory due to its
importance.
8. The simplicity of the model means that it is possible to analyse the
relationship between patient characteristics and the probability of
belonging to the treated group.

METHODS: ['classification', 'radial basis neural networks', 'evolutionary
algorithms', 'decision support systems']

SUMMARY A
2. Based on neural network techniques, our objective was to identify those
factors for HIV/HCV co-infected patients (to which clinicians have given
careful consideration before treatment uptake) that have not being included
among the prioritisation criteria.
3. An evolutionary algorithm was used to determine the architecture and
estimate the coefficients of the model.
4. This machine learning methodology found that radial basis neural
networks provided a very simple model in terms of the number of patient
characteristics to be considered by the classifier (in this case, six),
returning a good overall classification accuracy of 0.767 and a minimum
sensitivity (for the classification of the minority class, untreated
patients) of 0.550.
5. Finally, the area under the ROC curve was 0.802, which proved to be
exceptional.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY B
2. Based on neural network techniques, our objective was to identify those factors for HIV/HCV co-infected patients (to which clinicians have given careful consideration before treatment uptake) that have not being included among the prioritisation criteria.
4. This machine learning methodology found that radial basis neural networks provided a very simple model in terms of the number of patient characteristics to be considered by the classifier (in this case, six), returning a good overall classification accuracy of 0.767 and a minimum sensitivity (for the classification of the minority class, untreated patients) of 0.550.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate

SUMMARY C
1.   Several European countries have established criteria for prioritising initiation of treatment in patients infected with the hepatitis C virus (HCV) by grouping patients according to clinical characteristics.
2. Based on neural network techniques, our objective was to identify those factors for HIV/HCV co-infected patients (to which clinicians have given careful consideration before treatment uptake) that have not being included among the prioritisation criteria.
4. This machine learning methodology found that radial basis neural networks provided a very simple model in terms of the number of patient characteristics to be considered by the classifier (in this case, six), returning a good overall classification accuracy of 0.767 and a minimum sensitivity (for the classification of the minority class, untreated patients) of 0.550.

☐   Summary misses important information

☐   Summary includes unnecessary information

Summary Rating:

1 ☐   2 ☐   3 ☐   4 ☐   5 ☐

☐ Cannot evaluate