M.S. Thesis

CNN's microbiome feature extraction and utilization for host prediction

– Using small datasets to CNN models–

Host prediction을 위한 CNN의 microbiome feature 추출 및 활용방법

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– Using small datasets to CNN models –

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이 논문을 이학석사 학위논문으로 제출함

2022 년 8월

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2022 년 8월

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Abstract

This study aimed to compare the performance, strengths, and weaknesses of machine learning models based on convolutional neural networks and models not based on it; and analyzed the performance of various machine learning models according to the type and purpose of the given data. As a large number of data can be used with the continuous development of hardware, the possibility of machine learning using large datasets has already been sufficiently verified. Therefore, this study confirmed that using a relatively small gut microbiome dataset, machine learning models that predict a host could be designed with significant accuracy with appropriate tuning and loss function setting.

In this study, the operations of machine learning models were compared using a fecal microbiome dataset(4108 samples, 672 species). The training and validation dataset is a small subset of entire microbiome data(871 samples, 34 species). And it was shown that there was a difference in performance depending on the problem situation settings like the complexity of the data and the prediction purpose of ML models.

As a result of the study, the convolutional neural network-based models had the disadvantages of using more resources and taking a long time to learn. However, they maintained high accuracy compared to other discriminative models that were lumpy-labeled or more complex. Conversely, the models that did not use the convolutional neural network showed similar performance to the neural network-based model in discriminating simple data and accurately labeled data, with simple construction and learning. In addition, it was confirmed that the machine learning model could be used sufficiently even on a small dataset through appropriate design adjustments and function settings.

Summarizing the results, machine learning methods can verify data labeling of large datasets using a relatively small number of accurately labeled data. This can be used to check the labeling accuracy of large datasets that have been published as open-source before use in research.

Keyword: Machine learning, Small dataset, Gut microbiome, Host prediction, Convolution network

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Chapter 1. Introduction

The basic meaning of microbiome is a group of microorganisms living in a specific body site of a host or environment. Several microorganisms constituting the microbiome community may have a symbiotic, commensal, or parasitic relationship with each other or with a host.[1]

Recently, the meaning of the microbiome has been expanded more than the conventional meaning, including interactions between microbiomes constituting a community, interactions with hosts, and relationships with the surrounding environment.[2] In other words, current studies using big microbiome data deal with high throughput omics data covering numerous classification criteria such as various environments, life stages, body sites, and diets. In addition, the sharing of open-source data has been increasing in general academic fields, and usable data is gradually accumulated, forming massive datasets.

In this situation, machine learning, which has strong

performance in finding patterns with meaningful information in data,[3] is attracting attention. To analyze massive datasets with complex structures, machine learning methods are gradually being used in research in microbiome analysis, and significant results are being published. That is to say, the performance of the ML model trained on a large dataset has been sufficiently verified from various experimental results.[4, 5]

It has been found that a CNN model using a small dataset in a multi-classification problem can also show good performance if there is a suitable loss function.[6] Suppose these results can be applied to the microbiome dataset. In that case, it is expected that CNN-based ML methods can be used to examine whether the labeling of the data constituting the large dataset is accurately performed using a small number of accurately labeled data.

Some previous studies that used machine learning methods for microbiome dataset analysis were reviewed in this study.[7, 8] The research result that a CNN model trained on a small dataset can show adequate performance was also analyzed.[6] Afterward, five

machine learning models were created to predict hosts by learning microbiome data. The created machine learning models are divided into non-CNN models and CNN-based models. Non-CNN models used include KNN(K-Nearest Neighbor), multinomial logistic regression, FFNN(Feedforward Neural Network), and 1D CNN and 2D CNN models are used as CNN-based models. The performance between CNN-based ML models and non-CNN models was compared using a small dataset in a host prediction problem. The strengths and weaknesses of the CNN-based model compared to the non-CNN model were confirmed in microbiome host prediction.

Accurate classification and labeling of data used in research using such large datasets are very important.[9] Therefore, in research using an open-source dataset, it is necessary to review whether the labeling of the data to be used is accurate. As a result of the experiment, it is expected that ML can help solve these problems.

Chapter 2. Prior Research Review

ML models, data, and analysis methods using microbiome data as training data for machine learning models in previous studies were briefly summarized to investigate how actual ML methods were used in microbiome research.

2.1. The reasons that ML methods are used to analyze complex and enormous datasets.

One of previous research[7] investigated the possibilities of ML for developing cancer therapeutics and approaching the analysis of large amounts of complex healthcare information.

It is known that specific microbial signatures are associated with cancer in several ways, including promoting cancer development and affecting the safety, tolerability, and efficacy of treatments.[10] As the microbiome dataset grows and becomes more complex, the 'omics' technologies used to identify biological molecules involved in a cell or organism's structure, function, and dynamics have several

difficulties extracting the full potential of numerous microbiome data.[11]

Regulation of the gut microbiome is known as an innovative option for improving medication reactions in cancer patients.[12] However, a primary issue needs to be addressed to identify a direct relationship between the gut microbiome and clinical practice. The gut microbiome is affected by many factors, including the patient's health status, disease progression, and the type of medications and diet used.[13] So, it is difficult to ascertain the entire interaction between the microbiome and drug metabolism.

Machine learning includes algorithmic methods to solve problems without specific computer programming. Data analysis using ML receives input data, trains a model, and makes precise predictions on new data. In the above process, ML connects between a specific class of AI that includes a learning mechanism and a large dataset. It finds complex patterns in big datasets[3] or turns input data into more valuable and interpretable information. Also, ML can be used for data integration.[14] Therefore, ML can analyze massive

datasets from various forms (demographic, laboratory, and image data)[15] and combine them into predictions about cancer, such as disease risk, prognosis, diagnosis, and appropriate treatment. Using ML in conjunction with substantial dataset approaches can help discover which microbial characteristics are consistently and reproducibly effective in predicting or treating cancer in a patient.[16]

The most crucial point to be aware of when using ML to analyze these diverse and complex large datasets. To use ML methods for hypothesis testing, it is necessary to design a model suitable for a given experimental environment, which is context-specific.[17] A good model at solving one type of problem is unlikely to perform well at solving a different kind of problem. Researchers who use ML for data analysis need to know how to use ML algorithms in various situations.

2.2. Example of an ML model for host prediction.

A prior study[8] created an ML model that predicts objective

IBS (Irritable Bowls Syndrome) based on gut microbiome analyses. The dataset and clinical data obtained by sequencing the fecal samples with 16S rRNA were used.

It is difficult to distinguish whether differences in gut microbiome from normal individuals are the cause or consequence of IBS. This is difficult to address as the gut microbiome profile and IBS pathophysiology are influenced by shared environmental factors like diet style, various stresses, and hormones.[18] However, it is known that gut microbes exert effects on the host immune system and gut barrier function by the brain-gut axis.[19] Also, IBS patients have dysbiosis in the gut microbiome, showing lower microbial diversity than healthy controls.[20, 21]

Bacteria constituting the microbiome were analyzed at the genus level. The microbiome data consisted of 689 taxa, and feature-taxa was extracted using LASSO(L1 regularized logistic regression; Least Absolute Shrinkage and Selection Operator).[22] IBS were identified using the random forest technique included in python scikit-learn.[23] After that, the accuracy was measured

through cross-validation(10-fold, 100 repeats). The inverse parameter of regularization strength for logistic regression was optimized by internal 5-fold cross-validation. This model could distinguish IBS patients with more than 80% sensitivity and more than 90% specificity.

There are some limitations to the ML method used in this paper. The first limitation is that there was no functional investigation into the microbial community, and the number of subjects used as a control group was small(26 individuals). For example, it was thought that better results could be obtained if an approach using various meta-omics was added to the dataset[24], such as metagenomics, metatranscriptomics, metaproteomic, and metabolomics. The second limitation was that there was no dietary-related information in the dataset. Therefore, the prediction model may have missed the diet's possibility of affecting the gut microbiota profile dataset.

However, the ML method using gut microbiome data to classify IBS patients showed promising results despite limitations.

Further analysis suggested that it is possible to classify IBS patients into more diverse subtypes.

2.3. Performance of CNN model trained on small datasets.

Previous studies have confirmed that the ML models used microbiome analysis using extensive datasets.[7, 8] However, one study[6] indicates that CNN models can show high accuracy even in small dataset training by setting an appropriate loss function.

Six datasets(CUB, NAB, Cars, Flowers-102, MIT Indoor, CIFAR-100)[25, 26, 27, 28, 29, 30] were used in this paper. Although the number of classes and the number of samples are different for each dataset, the number of samples per class is 4 to 80 except for one dataset, CIFAR-100. (CIFAR-100 has 500 samples per class) When using datasets with up to 100 samples per class, the cosine loss shows better performance than cross-entropy. For example, when the ML model is trained with the smallest test set of only 10 and 25 samples per class, the cosine loss performs 17% and 26% better than cross-entropy, respectively.

Figure. 1 shows the models' validation accuracy using AG news datasets[31]. This accuracy test's purpose is to show the change in performance difference according to subsample sizes in text classification. CNN models trained on small datasets showed that the cosine loss function outperformed the cross-entropy loss after SoftMax activation in the multi-classification tasks. This result means cosine loss helps train CNN classifiers from scratch on small, limited data. On the other hand, if the size of the training dataset is large enough or if the network weight parameters trained on the extensive dataset are used, the model's performance is not significantly affected regardless of which of the two loss functions was used. BERT(fine-tuned)[32] is the pre-trained model with huge text corpora.

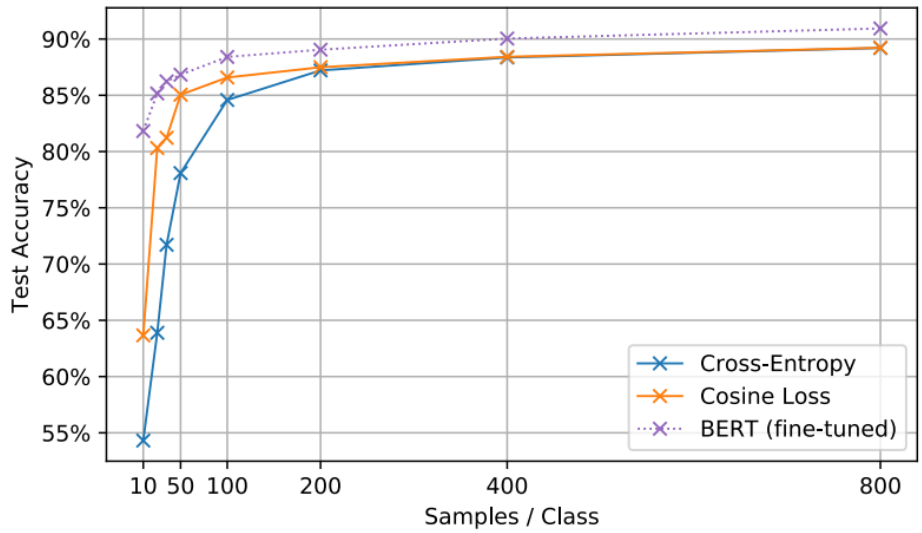


Figure. 1 Validation accuracy achieved using the cross-entropy and the cosine loss on sub-sampled versions of the AG News dataset, averaged over 10 runs.[6]

Chapter 3. Host Prediction Using ML Models

3.1. Host Prediction Pipeline

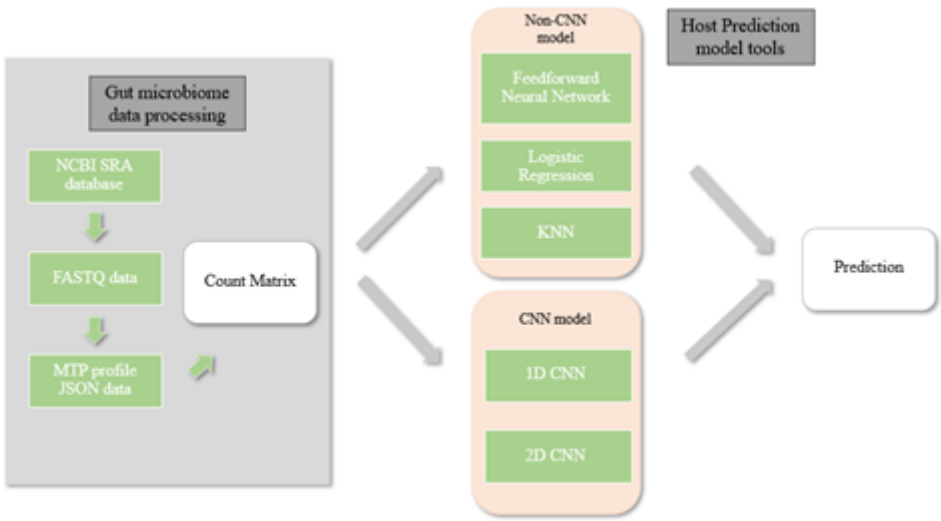


Figure. 2 Pipeline of gut microbiome data processing and host prediction

Gut microbiome data stored from the NCBI SRA database used as training, validation, and test dataset. The entire microbiome dataset used in this experiment consisted of 4108 samples, 672 species(Supplementary Table 1). The SRA study numbers of the fecal samples used are shown in Supplementary Material 1. Microbiome FASTQ files were processed into JSON format by

Microbiome Taxonomic Profiling(MTP) with QIIME using the EzBioCloud 16s database.[33] Using MTP products, the composition ratio of each individual constituting the microbiome was calculated to form a count-matrix CSV file. The CSV file parsing data of one JSON file was entered in each row. The percentage of microbiome composition according to parsing level was displayed in each column. The count-matrix files were generated per one fecal sample data by analyzing the microbiome composition at the genus and species level, respectively. Count-matrix CSV files were used as input data of ML models, and trained models predicted the host species(or genus) of fecal samples data.

3.2. ML Tools

The three models were classified into the non-CNN models' group. Multinomial logistic regression model, K-nearest neighbor model, and Feedforward neural network model were constructed using the Python Scikit-learn library.[27]

Python Keras library constructed CNN models, 1D CNN and

2D CNN.[34] The CNN model structures can be seen in Figure 3. Two CNN models with cosine loss and cross-entropy as loss functions were created in the experiment using CNN. Accuracy measurements of all ML models were repeated ten times, and the average of the highest observed values was obtained.

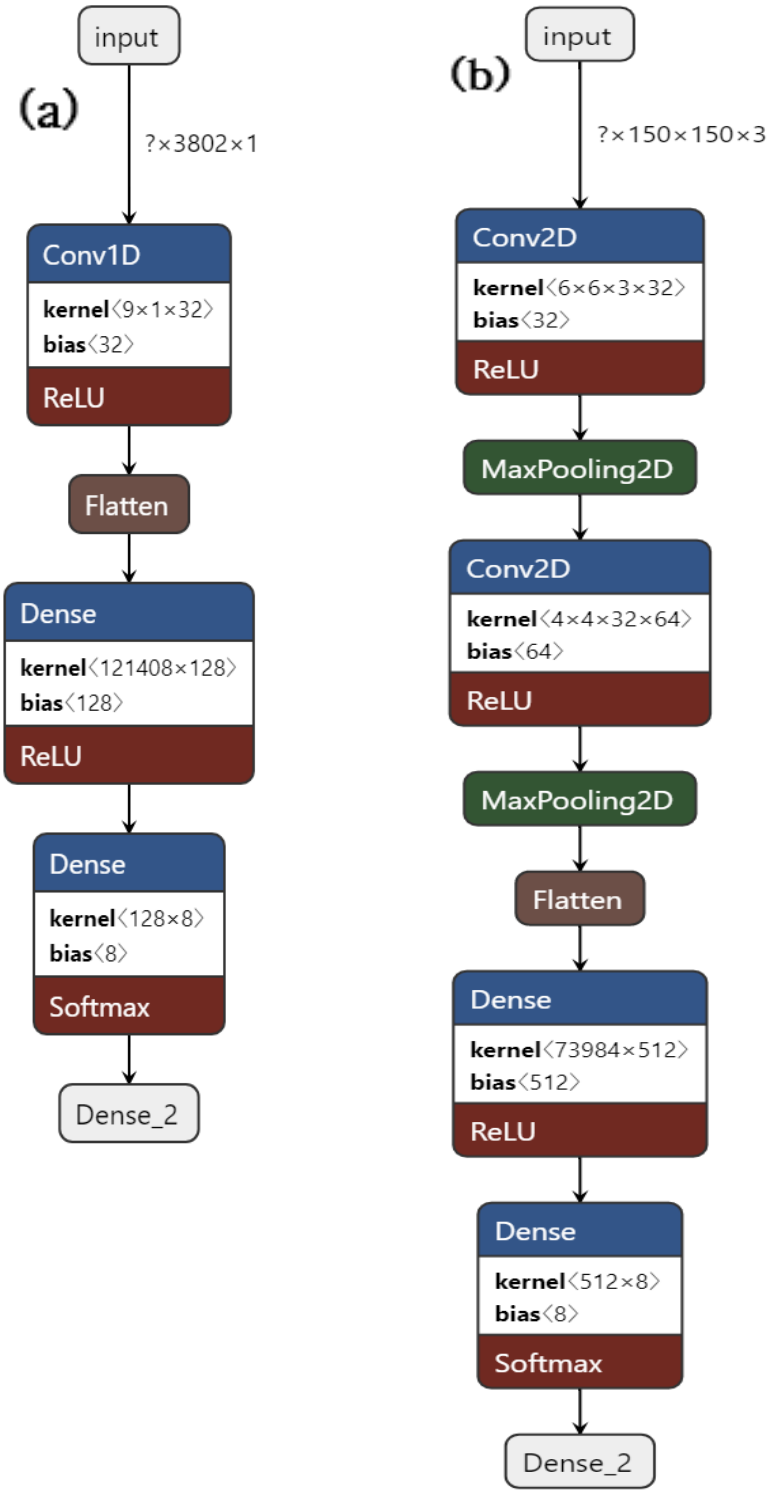


Figure. 3 (a) Basic 1D CNN model structure. (b) Basic 2D CNN model structure. Netron[35] was used to draw images.

3.3. Situation Settings

There were some unique terminologies used in this experiment's problem situation settings. 'Genus/Species-level data' means that when parsing JSON mtp profile data to make Count Matrix, the microbiome data was collected at the genus/species level. 'Labeled Species' (648 samples, 7 species: *Acinonyx jubatus, Ailuropoda melanoleuca, Bos taurus, Canis lupus familiaris, Canis mesomelas, Mus musculus, Sus scrofa domesticus*) means labeled data that the model trained on. 'Lumpy-labeled Species' means the species not named as their scientific names. 223 data of 37 species were grouped into 'etc_group. The models used this data group of various species as one 'etc_group' dataset. Figure 4 shows a brief representation of each case.

'Labeled Species Prediction' situation means that the purpose of the model is to classify the labeled species used for training. In the 'Lumpy-labeled Species Prediction' case, the purpose of the model was to classify the data of the species not used as labeled data into etc_group. Examples of each situation can be

found in Figure 5. The experiment was conducted in four situations: 1) Genus-level Labeled species prediction, 2) Species-level Labeled species prediction, 3) Genus-level Lumpy-labeled species prediction, 4) Species-level Lumpy-labeled species prediction. The model used what level of data and what the models wanted to predict became the standard for setting the situation.

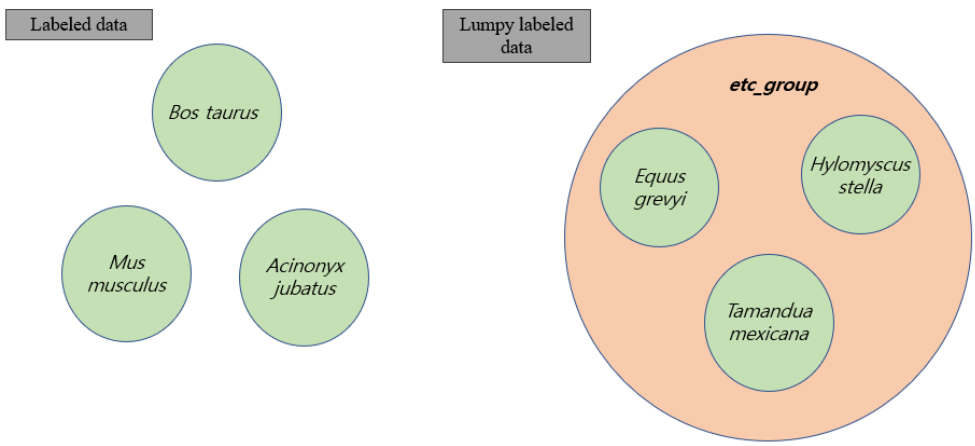


Figure. 4 Simple examples of 'Labeled data' and 'Lumpy-labeled data.' For simplicity, only three species are shown in each case. In this case, *Bos taurus, Mus musculus, and Acinonyx jubatus* were labeled as their own scientific name while *Equus grevyi, Hylomyscus stella, and Tamandua mexicana* were labeled as 'etc_group' equally.

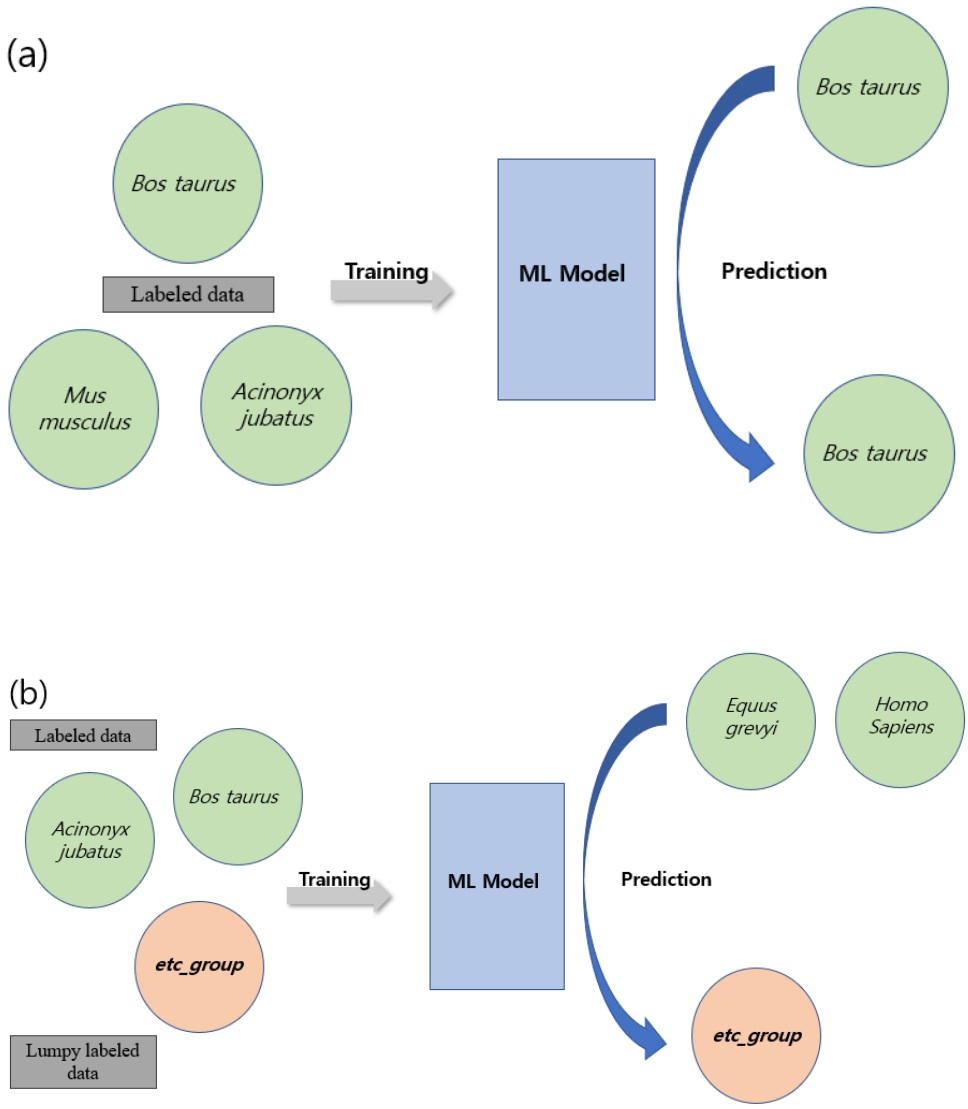


Figure. 5 (a) Labeled species prediction situation. (b) Lumpy-labeled species prediction situation. In (a), the labeled data was used for training, and the model determines the data of the species used for training, for example, *Bos taurus*. In (b), both labeled data and lumpy labeled data were used for model training. In this case, the model determines which species have been trained with etc_group (like *Equus grevyi*) or have not been trained at all, like *Homo sapiens*.

Chapter 4. Results

4.1. Accuracy Comparison

The average accuracy value was obtained by repeating ten times for each model. A random state value was assigned to none when training and validation split in an 8:2 ratio. A multi-layer perceptron(NLP) classifier was used in the NN models. While testing CNN ML models, cosine proximity and categorical cross-entropy were used as loss functions. The one showing the better accuracy of the two results was selected in each test result.

Figures 6, 7, 8 show one random example of each model among the validation tests repeated in the process of finding the average accuracy. The accuracies of the models used in all situations are summarized in Table 1. Figure 9 shows the model accuracies in lumpy-labeled prediction situation using the test dataset(3237 samples, 628 species). The test dataset was made by removing the data used for training from the entire microbiome dataset.

(a)

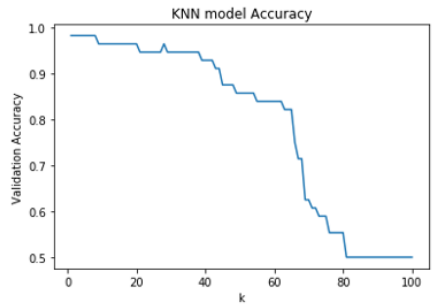
Feedforward Neural Network

Average Accuracy : 0.981928

Logistic regression

Training accuracy : 0.9333333333333333

Validation accuracy : 0.9156626506024096



(b)

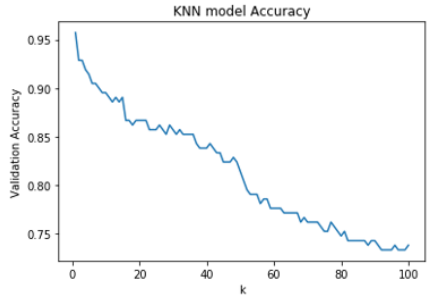
Feedforward Neural Network

Average Accuracy : 0.912243

Logistic regression

Training accuracy : 0.8724672228843862

Validation accuracy : 0.8523809523809524



(c)

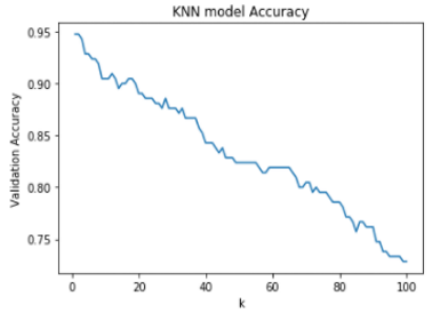
Feedforward Neural Network

Average Accuracy : 0.910124

Logistic regression

Training accuracy : 0.8688915375446961

Validation accuracy : 0.8857142857142857



(d)

Feedforward Neural Network

Average Accuracy : 0.876848

Logistic regression

Training accuracy : 0.8736591179976162

Validation accuracy : 0.8238095238095238

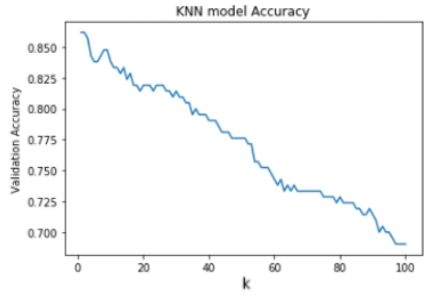


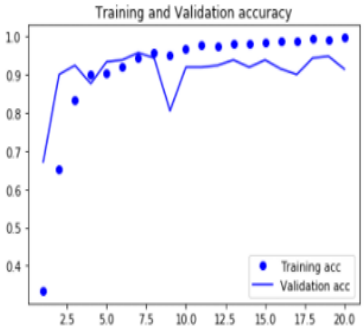
Figure. 6 (a), (b), (c), (d) show the validation accuracies of non-CNN models in four situations. Genus-level labeled species prediction, Genus-level

lumpy-labeled species prediction, Species-level labeled species prediction, and Species-level lumpy-labeled species prediction are indicated in the order.

(a) 1D CNN

(b) 2D CNN

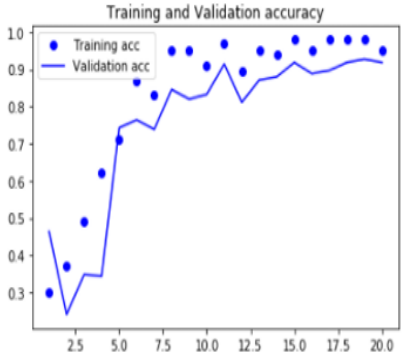
(c) 1D CNN



(d) 2D CNN

(e) 1D CNN

(f) 2D CNN



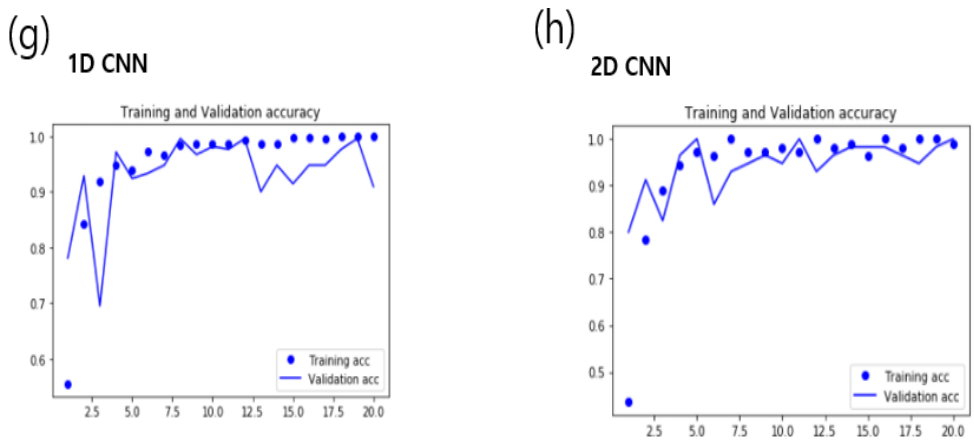


Figure. 7 (a), (c), (e), (g) show the training and validation accuracies of 1D CNN in Genus-level labeled species prediction, Genus-level lumpy-labeled species prediction, Species-level labeled species prediction, and Species-level lumpy-labeled species prediction, respectively. (b), (d), (f), (h) show the training and validation accuracies of 2D CNN in Genus-level labeled species prediction, Genus-level lumpy-labeled species prediction, Species-level labeled species prediction, and Species-level lumpy-labeled species prediction, respectively.

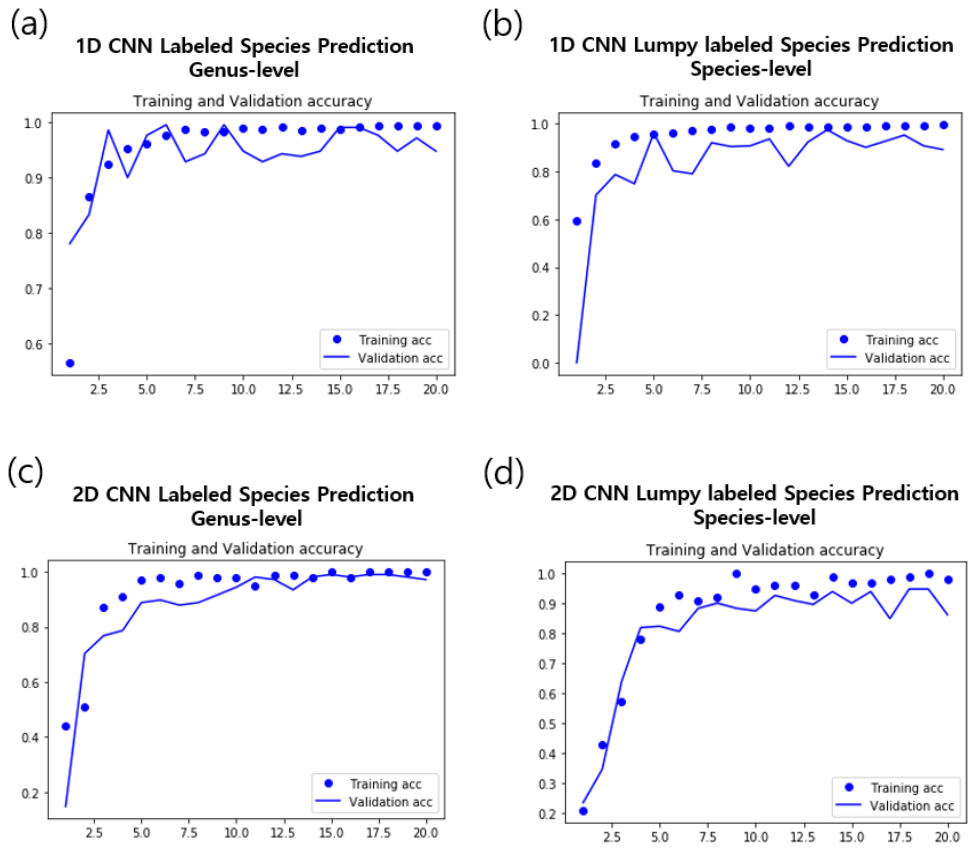


Figure. 8 Training and validation loss of CNN models using cosine-loss as loss function.

	Genus-level Labeled species prediction	Genus-level Lumpy labeled species prediction	Species-level Labeled species prediction	Species-level Lumpy labeled species prediction
KNN	0.9734	0.9047	0.9238	0.8619
LR	0.9156	0.8523	0.8857	0.8238
FFNN	**0.9819**	0.9122	0.9101	0.8768
1D CNN	0.9810	0.9524	**0.9510**	0.9374
2D CNN	0.9814	**0.9824**	0.9373	**0.9825**

Table. 1 Validation accuracy of ML models for each situation.

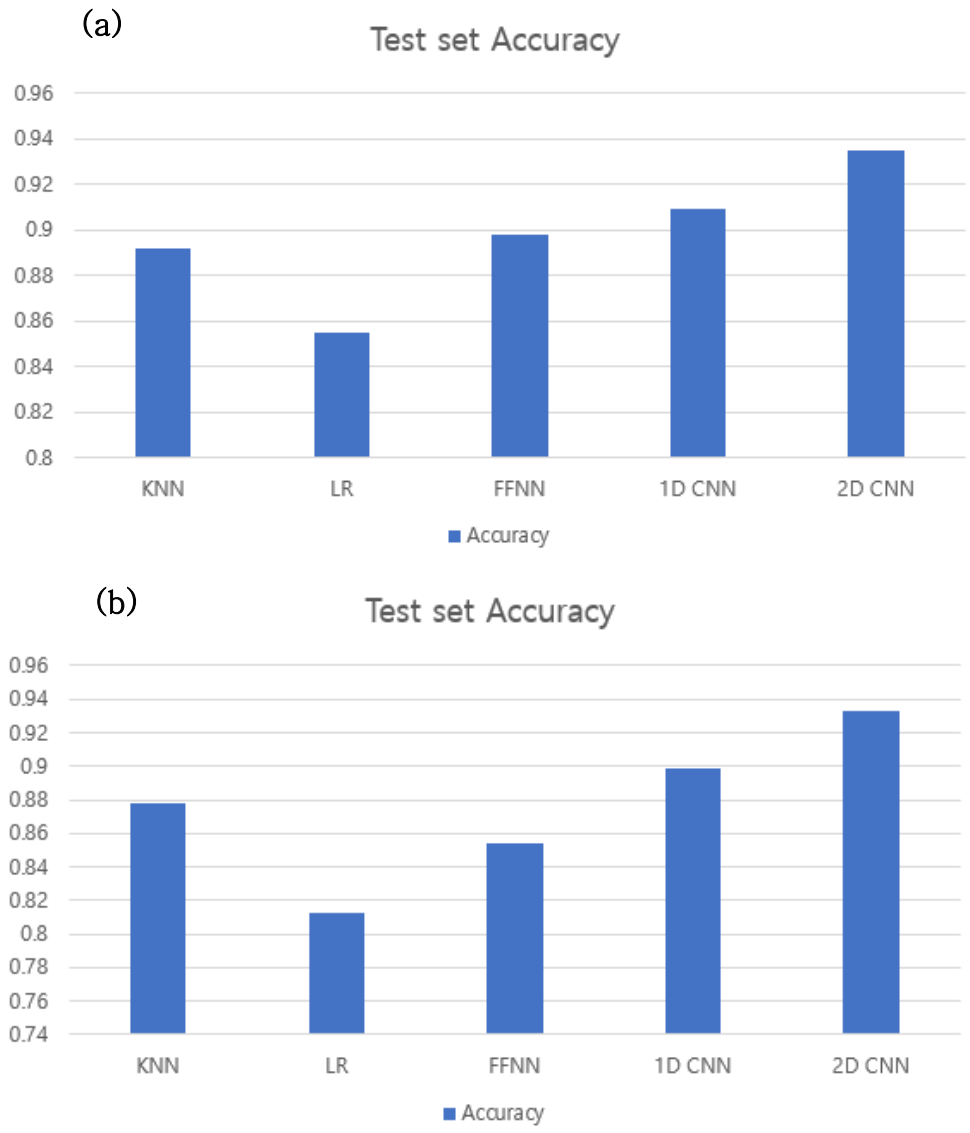


Figure. 9 ML models' accuracies using the test dataset in lumpy-labeled species prediction situation. Prediction results using a genus-level dataset were presented in (a). (b) shows the results of models using a species-level dataset.

4.2. Discussion

When using genus-level microbiome data and predicting labeled species, there was not much difference in accuracy between the two types of models (non-CNN and CNN). Therefore, simple non-CNN models were more competitive than CNN models, consuming many resources when analyzing genus-level data and predicting labeled species.

While predicting lumpy-labeled species, the accuracies of the models using CNN were relatively higher than that of other models. It was worthwhile to use the CNN models to discriminate and judge the data of rare species among the data of already labeled species.

Genus-level data had about 3800 vectors, and Species-level data had more than 14000 vectors. While using non-CNN models, the accuracy decreased as the data structure became more complex. However, CNN models were relatively unaffected by the complexity of the data.

Many factors influence the microbiome.[13, 36] Therefore, even samples collected from the same body site of the same species show significant differences in microbiome composition due to variables such as diet, health status, and life stage. For example, the C57BL/6 mouse, often used as an experimental mouse, has a different microbiome if the vendor is different.[37] Therefore, necessary data are often mixed with unnecessary data in large open-source datasets. In this situation, when labeling inspection is performed using ML methods, it is essential to classify numerous types of data that are not subject to analysis in the study. Lumpy-labeled species prediction is suitable for this situation and will classify data not needed in 'etc_group.' On the other hand, suppose the open-source datasets to be verified are predicted to consist only of samples with the same labeling as the dataset to be used in the study. This case corresponds to the labeled species prediction situation. In this situation, non-CNN ML models with a simpler structure can examine the dataset at a lower cost than the CNN models. However, there is a possibility that data with inaccurate labeling that may be mixed in the dataset to be inspected cannot be identified. This occurs because the result of labeled species

prediction is necessarily concluded as one of the learned species. It is expected to be solved to some extent by introducing an appropriate cut-off according to decode-prediction in the lowest classifier of the ML model.

The reason for the phenomenon that non-CNN models such as KNN cannot make precise predictions as the number of dimensions of data increases is expected that the generated count-matrix is a sparse matrix. When using datasets with a high sparsity level, KNNs have difficulty forming reliable neighborhoods.[38] The data used in this study are high-dimensional, and if the model tries to classify more than seven species, the data structure becomes more complex. The generated count-matrix is highly likely to become a sparse matrix. The random forest model used in previous studies is also expected to show similar results. The random forest has the advantages of simple model structure, less overfitting, and good generalization to new data. However, the structure of the model - due to the use of multiple decision trees, memory usage is high, and there are problems that it does not work well for high-dimensional data or sparse data.[39]

Chapter 5. Conclusion

As a large number of data can be used with the continuous development of hardware, the possibility of machine learning using large datasets has already been sufficiently verified in the microbiome field. To properly utilize the large open-source datasets, it is necessary to check the correct labeling of the data. Therefore, this study examined that host predicting machine learning models could be designed with sufficiently significant accuracy with appropriate tuning and loss function setting when using a small gut microbiome dataset as a training dataset.

As a result of the study, the convolutional neural network-based models had the disadvantages of using more resources and taking a long time to learn. However, they maintained high accuracy compared to other discriminative models that were lumpy-labeled or more complex. Conversely, with simple construction and learning, the non-CNN ML models showed similar performance to the CNN-based models in discriminating genus-level data and accurately labeled data. In addition, it was confirmed that the machine learning

model could be used sufficiently even on a small dataset through appropriate design adjustments and function settings. Therefore, researchers can check whether the data is appropriately labeled by using ML models that have been trained on a small number of data that have been reliably investigated before using a large public dataset.

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초 록

본 연구는 합성곱 신경망에 기반한 기계학습 모델들과 기반하지 않은 모델들의 성능과 장단점 비교를 목적으로 하며, 주어진 데이터의 종류와 목적에 따라 다양한 기계학습 모델들의 성능을 분석했다. 계속되는 하드웨어의 발달로 다수의 데이터를 활용할 수 있게 되면서 미생물 군집 분석에 매우 큰 데이터세트를 활용한 기계학습의 가능성은 이미 충분히 검증되고 있다. 분석결과에 의도치 않은 노이즈가 포함되지 않기 위해서는, 오픈소스 거대 데이터세트를 사용하기 전에 사용할 데이터세트가 정확히 라벨링이 되어있는지 확인하여야 한다. 본 연구는 상대적으로 작은 장내 미생물 군집 데이터 세트를 사용하여 호스트를 예측하는 기계 학습 모델이 적절한 조정 및 손실 기능 설정으로 상당한 정확도로 설계될 수 있음을 확인했다.

본 연구에서는 분변 미생물 군집 데이터세트(샘플 4108개, 672종)를 이용하여 머신 러닝 모델의 성능을 비교하였다. 훈련 및 검증 데이터 세트(871개 샘플, 34종)는 전체 미생물 군집 데이터세트의 작은 하위 집합으로 구성되었다. 그리고 데이터의 복잡도와 ML 모델의 예측 목적 등 문제 상황 설정에 따라 성능에 차이가 있는 것으로 나타났다. 연구 결과, 합성곱 신경망 기반 모델들은 사용하는 리소스가 많고 학습에 필요한 시간이 더 오래 걸린다는 단점들이 있었다. 그러나

데이터의 복잡도가 증가하고 레이블이 정확하게 지정되지 않은 데이터들을 판별함에 있어 다른 모델들에 비해 높은 정확도를 유지하였다. 반대로 합성곱 신경망을 사용하지 않은 모델들은 구성과 학습이 간단하고, 단순한 데이터들과 정확하게 레이블이 지정된 데이터들을 판별함에 있어 신경망 기반 모델과 비슷한 성능을 보였다. 또한 적절한 구조설계와 함수 설정을 통해 기계학습 모델이 작은 데이터셋을 기반으로도 충분히 사용될 수 있음을 확인하였다.

간단한 기계 학습 방법으로 적은 수의 정확하게 레이블이 지정된 데이터를 사용하여 대규모 데이터 세트의 데이터 레이블을 검증할 수 있다. 이는 연구에 사용하기 전에 오픈 소스로 게시된 대규모 데이터 세트의 레이블 지정 정확도를 확인하는 데 사용할 수 있다.

주요어 : 기계학습, 작은 데이터셋, 장내 미생물 군집, 숙주 예측, 합성곱 신경망

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Orycteropı	ERR328049
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Orycteropı	ERR328057
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Hystrix ind	SRR5190026
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Trachypith	ERR2860682
Cyprinus c	ERR2860683
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Sus scrofa	ERR2860688
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Carassius	ERR2860690
Strix uralen	ERR2860691
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Nycticebus	ERR2860694
Phocoena	ERR2860695
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Cervus ela	ERR2860698
Lepus tola	ERR2860701
Ovis aries	ERR2860702
Homo sap	ERR2860703
Cervus ela	ERR2860704
Balaenopte	ERR2860705
Lynx lynx	ERR2860706

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Meleagris	ERR2860737
Homo sap	ERR2860738
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Procyon lo	ERR2860743
Asio otus	ERR2860744
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Canis lupu	ERR2860746
Nomascus	ERR2860747
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Anas platy	ERR2860749
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Felis catus	ERR2860751

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Natrix natr	ERR2860754
Esox lucius	ERR2860755
Bradypus \	ERR2860756
Testudo he	ERR2860757
Rupicapra	ERR2860758
Lepus eurc	ERR2860759
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Dama dam	ERR2860773
Loxodonta	ERR2860774
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Phalacrocc	ERR2860779
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Vulpes vul	ERR2860785
Manis tem	ERR2860786
Capra ibex	ERR2860788
Lepus eurc	ERR2860789
Salvelinus	ERR2860790
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Phascolarc	ERR2860794
Corvus fru	ERR2860795
Martes ma	ERR2860796
Cricetus cr	ERR2860797
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Sander luc	ERR2860804
Panthera p	ERR2860805
Cervus uni	ERR2860806
Spermoph	ERR2860807
Castor fibe	ERR2860808
Bos taurus	ERR2860809
Oryctolagu	ERR2860810
Giraffa can	ERR2860811
Crocodylus	ERR2860812
Bufo viridi	ERR2860813
Odocoileus	ERR2860814
Hemidacty	ERR2860815
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Chinchilla	ERR3672791
Uromastyx	ERR3672792
Scopus um	ERR3672793
Tyto alba a	ERR3672794
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Suricata su	ERR3672797

Stigmoche ERR3672798
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Phoenicop ERR3672801
Podargus s ERR3672802
Phacochoe ERR3672803
Torgos tra ERR3672804
Chinchilla ERR3672806
Dacelo no ERR3672809
Coendou p ERR3672810
Lemur catt ERR3672812
Varecia va ERR3672813
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Bucorvus l ERR3672817
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Cynomys l ERR3672819
Psittacus e ERR3672820
Colobus a ERR3672821
Cercopithe ERR3672822
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Cercopithe ERR3672825
Pongo abe ERR3672826
Colobus a ERR3672827
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Gorilla gor ERR3672829
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Atelopus v ERR3672838
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Trachycepl	ERR3672850
Lepidobatr	ERR3672851
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Choloepus	ERR3672853
Anolis allis	ERR3672854
Incilius sig	ERR3672855
Basiliscus ı	ERR3672856
Ceratobatr	ERR3672857
Saguinus ç	ERR3672859
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Anolis barl	ERR3672875
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Loxodonta	ERR3672993
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Giraffa can	ERR3672998
Bos taurus	ERR3673001
Cervus nip	ERR3673003
Lama guar	ERR3673004
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Tragelaphı	ERR3673007
Tragulus ja	ERR3673008
Tragulus ja	ERR3673009

Orycteropu	ERR3673012
Orycteropu	ERR3673013
Caracal ca	ERR3673014
Canis lupu	ERR3673015
Panthera l	ERR3673016
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Callithrix g	ERR3673043
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Equus zeb	ERR3673049
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Connocha	ERR3673054
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Equus asin	ERR3673061
Saimiri bol	ERR3673062
Equus gre	ERR3673063
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Equus bur	ERR3673066
Panthera l	ERR3673067
Saimiri bol	ERR3673068

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Equus hem	ERR3673074
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Cercopithe	ERR3673089
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Notamacr	ERR3673093
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Antilope c	ERR3673107
Equus asin	ERR3673108
Pongo pyg	ERR3673110
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Antilope c	ERR3673113
Axis axis	ERR3673114
Equus asin	ERR3673115
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Ara chloro	ERR3673178
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Eurycea lo	ERR3673182
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Aneides ae	ERR3673187
Fukomys c	ERR3673188
Heterocep	ERR3673189
Callosciuru	ERR3673190
Heterocep	ERR3673191
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Platalea aj	ERR3673196

Aix sponsa	ERR3673197
Dendrobat	ERR3673198
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Dendrocyg	ERR3673205
Echinops t	ERR3673206
Aneides ae	ERR3673207
Eurypyga h	ERR3673208
Plethodon	ERR3673209
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Dendrobat	ERR3673211
Todiramph	ERR3673212
Psarocoliu	ERR3673215
Mergellus	ERR3673216
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Dendrocyg	ERR3673232
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Anas acuta	ERR3673246
Paroaria c	ERR3673248
Anas disco	ERR3673250
Platalea aj	ERR3673253
Tangara ep	ERR3673256
Guira guir	ERR3673257
Anas platy	ERR3673258
Zenaida gr	ERR3673259
Zenaida gr	ERR3673260
Athene cu	ERR3673261
Ramphoce	ERR3673262
Bubulcus i	ERR3673263

Grus amer	ERR3673264
Mergellus	ERR3673266
Macrosceli	ERR3673270
Dendrocyg	ERR3673272
Macrosceli	ERR3673273
Apteryx au	ERR3673274
Mantella a	ERR3673279
Athene cu	ERR3673280
Dendrobat	ERR3673281
Pheucticus	ERR3673282
Pheucticus	ERR3673283
Corvus cor	ERR3673284
Aix galeric	ERR3673285
Octodon d	ERR3673286
Echinops t	ERR3673287
Macrosceli	ERR3673288
Fukomys c	ERR3673289
Tockus de	ERR3673290
Callosciuru	ERR3673292
Macrosceli	ERR3673293
Octodon d	ERR3673295
Athene cu	ERR3673296
Chinchilla	ERR3673297
Kerodon ru	ERR3673299
Macrosceli	ERR3673300
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Equus feru	ERR3673303
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Vulpes zer	ERR3673305
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Tolypeutes	ERR3673308
Alouatta p	ERR3673309
Procavia ca	ERR3673310
Tamandua	ERR3673311
Astrochely	ERR3673313
Pithecia pi	ERR3673314
Melursus u	ERR3673315
Equus feru	ERR3673316
Dracaena c	ERR3673317
Tamandua	ERR3673318
Hypogeom	ERR3673319

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Felis marg	ERR3673321
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Suricata su	ERR3673324
Hypogeom	ERR3673325
Octodon d	ERR3673326
Apteryx au	ERR3673327
Plecturoce	ERR3673328
Leontopith	ERR3673329
Mungos m	ERR3673332
Cariama cr	ERR3673333
Sarcoramp	ERR3673334
Grus amer	ERR3673335
Choloepus	ERR3673336
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Mustela ni	ERR3673338
Suricata su	ERR3673339
Aceros cor	ERR3673340
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Platalea aj	ERR3673342
Coendou p	ERR3673345
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Leontopith	ERR3673347
Suricata su	ERR3673348
Bettongia	ERR3673350
Leontopith	ERR3673352
Callithrix g	ERR3673354
Mephitis m	ERR3673355
Grus amer	ERR3673357
Plecturoce	ERR3673358
Leontopith	ERR3673359
Melursus u	ERR3673360
Equus feru	ERR3673361
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Caracal ca	ERR3673367
Erethizon d	ERR3673368
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Panthera t	ERR3673370
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Eublephari	ERR3673378
Melursus u	ERR3673380
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Coendou p	ERR3673386
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Pavo crista	ERR3673388
Callithrix g	ERR3673389
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Mungos m	ERR3673393
Leontopith	ERR3673394
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Tragulus n	ERR3673396
Pithecia pi	ERR3673398
Varecia rul	ERR3673399
Pavo crista	ERR3673401
Vulpes zer	ERR3673403
Tamandua	ERR3673404
Dasyprocta	ERR3673405
Callosciuru	ERR3673406
Cariama cr	ERR3673408
Procavia ca	ERR3673409
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Tragulus n	ERR3673411
Ardeotis ku	ERR3673412
Grus amer	ERR3673414
Grus amer	ERR3673415
Python mo	ERR3673417
Rhea amer	ERR3673418
Platalea aj	ERR3673419
Rhea amer	ERR3673420
Drymarcho	ERR3673421
Varecia rul	ERR3673422
Leontopith	ERR3673423
Melursus u	ERR3673424
Phoenicop	ERR3673425
Rhea amer	ERR3673427
Alouatta p	ERR3673428

Uroplatus	ERR3673429
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Gonocephi	ERR3673432
Shinisauru	ERR3673436
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Shinisauru	ERR3673439
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Eunectes n	ERR3673447
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Aldabrache	ERR3673451
Corucia ze	ERR3673452
Alligator m	ERR3673453
Apteryx au	ERR3673454
Cariama cr	ERR3673455
Cariama cr	ERR3673456
Ardeotis ki	ERR3673457
Bettongia	ERR3673459
Pithecia pi	ERR3673460
Apteryx au	ERR3673462
Choloepus	ERR3673464
Rhea amer	ERR3673465
Pavo crista	ERR3673467
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Ardeotis ki	ERR3673477
Manouria i	ERR3673478
Equus feru	ERR3673479
Uroplatus	ERR3673480
Helogale p	ERR3673483
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Tremarctos	ERR3673494
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Nestor not	ERR3673513
Anas auckl	ERR3673515
Nestor not	ERR3673517
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Anas auckl	ERR3673525
Apteryx au	ERR3673527
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Nestor me	ERR3673543
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Apteryx au	ERR3673553
Strigops h	ERR3673557
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Anas rhyn	ERR3673563
Anas auckl	ERR3673567
Anas auckl	ERR3673569
Himantopu	ERR3673571
Nestor not	ERR3673573
Ninox nov	ERR3673575
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Apteryx au	ERR3673579
Apteryx au	ERR3673583
Nestor not	ERR3673585
Hymenolai	ERR3673587
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Ninox nov	ERR3673613

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Nestor me	ERR3673639
Nestor me	ERR3673641
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Nestor me	ERR3673649
Nestor me	ERR3673651
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Prosthema	ERR3673655
Nestor me	ERR3673659
Nestor me	ERR3673661
Anas rhyn	ERR3673665
Psittacus e	ERR3673667
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Diceros bi	ERR3673781
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Pongo abe	ERR3673786
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Elephas m	ERR3673801
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Varecia rul	ERR3673807
Equus feru	ERR3673811
Pongo abe	ERR3673812
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Notamacr	ERR3673908

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Struthio ca	ERR3673911
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Euplectes	ERR3674036
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Cisticola e	ERR3674039
Caprimulg	ERR3674040
Dryoscopu	ERR3674041
Cisticola e	ERR3674042
Anthus no	ERR3674043
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Dryoscopu	ERR3674048
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Kaupifalco	ERR3674052
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Anthus no	ERR3674062
Anthreptes	ERR3674063
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Cervus nip	ERR3680762
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