Generate novel and robust samples from data: accessible sharing without privacy concerns

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Abstract

Generating new samples from data sets can mitigate extra expensive operations, increased invasive procedures, and mitigate privacy issues. These novel samples that are statistically robust can be used as a temporary and intermediate replacement when privacy is a concern. This method can enable better data sharing practices without problems relating to identification issues or biases that are flaws for an adversarial attack.

Keywords: data sampling, balanced sampling, data sharing, data access, data privacy, latent samples

GitHub: https://github.com/AskExplain/sampling4sharing

1 Introduction

Mitigating the restrictions caused by privacy and safety concerns for individuals can be solved by generating computationally new samples without identifiers. This can resolve the many and various trade-offs of enforced privacy on data [1], [2], [3]. Here, generating novel samples from observed data is shown to unexpectedly improve accuracy, precision, statistical robustness and unbiasedness, due to the benefits of generating large and balanced sample sizes.

The technique known as linear encoding shares many fundamental aspects that investigate structure, balance and dimensionality. Structure relates to the concepts of graphical structures including Bayesian networks and complex or random graphs, such as with model-based sampling [4]. The idea of balanced data ensures the (known or unknown) sample classes are proportionally representative such as with Synthetic Minority Over-sampling Technique or SMOTE [5]. Dimensionality involves viewing the data by summarising into core components and extending the space like with [6].

2 Model

2.1 Linear Encoding

\[ \alpha_Y Y \beta_Y = \alpha_X X \beta_X = \alpha_Z Z \beta_Z \]

Multiple modalities of data can be projected or "encoded" into the same subspace. The datasets \( Y, X \) and \( Z \) can be of any size, from matrix to tensor.

\[ Y = \alpha_Y C_Y \beta_Y + i_Y + \epsilon_Y \]
\[ X = \alpha_X C_X \beta_X + i_X + \epsilon_X \]
\[ Z = \alpha_Z C_Z \beta_Z + i_Z + \epsilon_Z \]
The projections $\alpha$ and $\beta$ transform the datasets $Y$, $X$, and $Z$ into a latent dimensional space - where information is common across multiple datasets constructed by the latent code $C$. The latent code can be fixed at $C_Y = C_X = C_Z$, and is constrained across all datasets. An intercept $i_j$ can be added with residuals $\epsilon$ from a distribution (e.g. Gaussian, Poisson, Negative Binomial).

Notice the similarities to Singular Value Decomposition, and extensions to involve a statistical, model-based “generalisation” with the residual noises, and linear algebraic extension to channel information into a shared space via the common latent code $C$.

### 2.2 Coordinate descent updates for learning parameters

The coordinate descent update to estimate the parameters is very simple and straightforward. It iterates through multiple steps outlined by Algorithm 1 until convergence. The full step loops over multiple datasets (and runs across a complete set, full list, or tuple of datasets):

**Algorithm 1 Linear Encoding**

**Input:** $D_L$ Dataset for each modality $L$

**Output:** $\alpha_L$ sample parameters, $\beta_L$ feature parameters, $Z$ code

For each object in the list of data sets

\[
\alpha_L = D_L^T (Z\beta_L^T)^T ((Z\beta_L^T)(Z\beta_L^T)^T)^{-1}
\]

\[\triangleright \text{ Update sample parameters}\]

\[
\beta_L = ((\alpha_L^T Z (\alpha_L^T Z))^{-1}(\alpha_L^T Z)D_L
\]

\[\triangleright \text{ Update feature parameters}\]

\[
Z = (\alpha_L^T \alpha_L)^{-1} \alpha_L^T D_L \beta_L^T (\beta_L \beta_L^T)^{-1}
\]

\[\triangleright \text{ Update Code}\]

### 3 Generative Sampling

Following, the $\alpha$ model is treated as a latent sampling structure that considers how samples are related. Based on this information, a Gaussian mixture model is applied to learn the distribution of the latent space:

\[A_{i,g} \sim \pi_g \mathcal{N}((\mu_g, D_g)\]

The mixture model of $\alpha$ are used to draw from a random multivariate Gaussian based on the estimated parameters known as $A_{i,g}$. The sampling probability of each mixture can be ignored, or set to uniform to generate balanced classes (e.g. each class can be drawn for $n = 1000$ samples).

Finally, the response $Y$ and the covariates $X$ are projected from the mixture-based latent sample space $A$ and the encoding-based latent sample space $\alpha$ via the expression:

\[
\hat{X} = A_{i,g}^T (\alpha \alpha^T)^{-1} \alpha X = A_{i,g}^T \beta_X
\]

\[
\hat{Y} = A_{i,g}^T (\alpha \alpha^T)^{-1} \alpha Y = A_{i,g}^T \beta_Y
\]

### 4 Results

This involves 3 parts:

1) a regression on ten real datasets: comparing original against newly sampled points to look at statistically significant differences in Mean-Absolute Deviation (via a standard T-test);

2) a differential gene expression test via a standard T-test for tissues from different regions of the brain to show functional aspects on noisy biological data;
3) an illustration of the top 5 sampled MNIST digits to show that new samples are representative of the original image;

4.1 Regression on real and synthetic datasets

The test here is to compare the regression performance on real datasets against synthetic datasets generated using the real dataset as a foundation. In all cases, the synthetic datasets outperformed in terms of Mean-Absolute Deviation (M.A.D) on all 10 datasets in a statistically significant manner (P-value comparing M.A.D for a standard T-test). The regression technique used is glmnet [7].

| Dataset                 | P-value   |
|-------------------------|-----------|
| Wine                    | 1.32e-59  |
| Oliveoil                | 1.76e-42  |
| Glass                   | 2.53e-13  |
| Thyroid                 | 1.96e-37  |
| WDBC                    | 2.64e-64  |
| PimaIndiansDiabetes     | 3.18e-63  |
| BostonHousing           | 1.52e-44  |
| Ionosphere              | 9.74e-170 |
| Shuttle                 | 4.58e-14  |
| Satellite               | 1.59e-38  |

The ten datasets are sourced from R library packages (pdfCluster, mlbench and mclust).

4.2 Biological validation with differential gene tests on real and synthetic data

Genes are expressed to form proteins. Different parts of the body and different tissues have different functions and thus express differential levels of protein and genes. The greater the difference in function, the more likely the difference in gene expression can be detected.

The test here is to compare the similarity between synthetic and real RNA-seq on the Brain GTEX dataset (Genotype-Tissue Expression dataset). A standard differential based test on the gene expression is done, as per the literature. The closer the differential-based scores are per synthetic and real, the more similar the synthetic dataset represents real biological signals (via a correlation analysis).

Here, with a simple correlation calculation, the cerebellum and cerebellar hemisphere of the brain are compared against other regions of the brain in a differential gene test comparing tissues. Notice that there are many other parts of the brain tested in this analysis, but the top two highest correlation scores against all other brain tissues are similar - the cerebellum, which is part of the cerebellar hemisphere.

|                  | Cerebellum | Cerebellar Hemisphere |
|------------------|------------|-----------------------|
| Cortex           | 0.852      | 0.808                 |
| Putamen (basal ganglia) | 0.853 | 0.864                 |
| Hypothalamus     | 0.906      | 0.896                 |
| Hippocampus      | 0.903      | 0.899                 |
| Substantia nigra | 0.904      | 0.881                 |
| Amygdala         | 0.915      | 0.895                 |

These two brain parts are most distinct compared to the other parts of the brain, and thus present well in a differential gene based test comparing tissue function.

4.3 MNIST synthetic sampling

The standard MNIST dataset is synthetically sampled along with the class label. For each synthetic image, there is also an assigned synthetic class matrix of labels with scores between 0 and 1.

Taking the top 5 images by selecting the best 5 scores per class by taking the difference between the top [1] Class Score and the top [2] Class Score and then ranking them and selecting the top 5, gives the figure below.
Figure 1: Sampling of the ten MNIST digits for 5 images selected by taking the best scores within each digit class.

Note, these are fully synthetic samples based on linear encoding.

5 Algorithmic properties

5.1 Density Estimation and Mixture Modelling

A Gaussian mixture model can model any known density estimate. Especially with the numerous literature findings on multivariate gaussian models, mixture modelling and multivariate sampling from existing libraries makes this desirable.

The structure $A$ provided by extending the sample space via the latent sample parameter $\alpha$ is similar to K-nearest neighbour interpolation. The latent sample space $\alpha$ is treated as a data process from the Gaussian mixture model and the covariance structures based on the latent samples exhibits a graphical structure: variance-covariance matrices can be considered a graph, or in terms of networks analysis, an "adjacency" matrix.

5.2 Concepts on Generative Sampling

For example, take $\text{samples}_{n,g} \in \Omega_S$ and let the observed sampling structure be defined by $D$. A sampling structure can be exhibited by a graphical model: a complex network or random graph, a Bayesian network with prior distributions, or quite simply, a (mixture) of multivariate Gaussian models. Here, let $D$ be the variance-covariance structure of the Gaussian (mixture) model $GMM(L_g; \theta_g)$ to represent the sampling structure of $\Omega_S$.

Treating samples as structures or collective units rather than an individual set of random samples contains more information for later analysis by other statistical or machine learning models. Thus, as a whole the newly generated samples contains more sample structure than a random set. The aim of any sampling strategy is to gain insights from a structural (parametric) or statistical (probabilistic) analysis of the data (e.g. $D_g \in GMM(L_g; \theta_g(\mu_g, D_g))$) to relate to a closer representation of the data generating process (e.g. $\Omega_S$).

6 Conclusion

With the ability to generate fully synthetic samples without identifiers, data can be shared more easily. In fact, the concerns regarding data privacy can be looked at in light of fully synthetic data that surpasses the original dataset in terms of accuracy and precision. The synthetic samples have been shown to be robust to statistical biological noise and image variation.


7 References

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