# Missing Value Imputation in a Data Matrix Using the Regularized Singular Value Decomposition

**NLA 2023** 

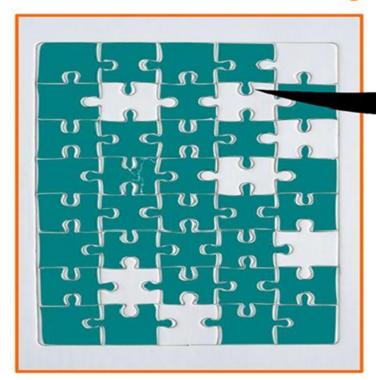
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#### **Problem Statement:**

- > Issue: Prevalence of incomplete datasets in statistical analysis.
- > Challenges: Limitations of traditional imputation techniques.
- > Consequences: Inadequate imputation affects data integrity.
- > **Demand:** Need for an advanced, reliable imputation method.

- > Solution: GabrielEigen Imputation System
- > **Method:** Combines regression with lower rank approximations
- > Innovation: Regularised Singular Value Decomposition
- > Benefits: Improves imputation quality, reduces overfitting
- > Applicability: Suitable for various multivariate data matrices

Mixture between regression and regularised lower rank approximations



Regularisation (reg)

$$X = \begin{bmatrix} x_{ij} & x_{\bullet 1}^T \\ x_{\bullet 1} & X_{11} \end{bmatrix}$$

$$x_{ij}^{(m)} = \boldsymbol{x}_{1 \bullet}^T \boldsymbol{V_{reg}} \boldsymbol{D_{reg}^+} \boldsymbol{U_{reg}^T} \boldsymbol{x_{\bullet 1}}$$

Incomplete matrices

Imputation

Completed Matrix

#### Singular Value Decomposition

Singular Value Decomposition is a mathematical method where any matrix  $A \in \mathbb{R}^{m \times n}$  can be decomposed into three matrices:

$$A = U\Sigma V^*$$

#### where:

- U is an  $n \times K$  unitary matrix.
- V is an  $m \times K$  unitary matrix, where  $K = \min(m, n)$ .
- $\Sigma$  is a diagonal matrix with non-negative elements  $\sigma_1 \geq \sigma_2 \geq \cdots \geq \sigma_K$  on the diagonal.
- If *A* has rank *r*, then  $\sigma_{r+1} = \sigma_{r+2} = \cdots = \sigma_K = 0$ .

#### GabrielEigen Method

García-Peña et al. introduced GabrielEigen, an imputation method that combines regression with lower rank approximations for matrix structured datasets, without relying on distributional or structural assumptions. It leverages Gabriel's cross-validation approach and SVD eigenvectors and eigenvalues to derive lower rank approximations.

#### **Algorithm**

Given a data matrix  $X \in \mathbb{R}^{n \times p}$  with missing elements  $x_{ij}$ , where i = 1, ..., n and j = 1, ..., p, the following algorithm is used for imputation:

Step 1: Fill each missing entry with the mean of its respective column:

$$\hat{x}_{ij} = \frac{1}{n} \sum_{i=1}^{n} x_{ij}$$
 for missing  $x_{ij}$ 

Step 2: Standardize the columns of the completed matrix:

$$z_{ij} = \frac{x_{ij} - \bar{x}_j}{s_j}$$

where  $\bar{x}_j$  is the mean and  $s_j$  is the standard deviation of the *j*-th column.

**Step 3:** For each originally missing entry  $x_{ij}$ , replace with:

$$\hat{x}_{ij} = \mathbf{U}_{(i)} \mathbf{D}^+ \mathbf{V}_{(j)}^T$$

where  $\mathbf{D}^+$  is the generalized inverse of  $\mathbf{D}$ , and  $\mathbf{U}_{(i)}$ ,  $\mathbf{V}_{(j)}$ , and  $\mathbf{D}$  are obtained from the SVD of  $X_{11}$ :

$$X_{11} = \sum_{k=1}^{m} \sigma_k \mathbf{u}_k \mathbf{v}_k^T$$

with  $m \le \min\{n - 1, p - 1\}$ .

**Step 4:** Choose *m* to be the smallest value satisfying:

$$\frac{\sum_{k=1}^{m} \sigma_k^2}{\sum_{k=1}^{\min\{n-1,p-1\}} \sigma_k^2} \ge 0.75$$

**Step 5:** Convert the imputed values  $\hat{x}_{ij}$  back to their original scale:

$$x_{ij}^{\text{imputed}} = \hat{x}_{ij} \cdot s_j + \bar{x}_j$$

**Step 6:** Repeat steps 2 to 5 until the imputations achieve stability. If  $n \le p$ , transpose the matrix before conducting the iterations.

# Regularized Version of the GabrielEigen

Regularization is employed to prevent overfitting, ensuring higher quality imputations and more reliable parameter estimation. To enhance the original GabrielEigen imputation system, a regularized Singular Value Decomposition is used, effectively creating a regularized version of the method.

#### Algorithm

Let  $X_{11}$  denote the matrix  $(n-1 \times p-1)$  and m the desired rank. The algorithm is as follows:

**Step 1:** Initially, a  $V(p-1 \times m)$  matrix is obtained with random entries from a uniform distribution (0,1).

**Step 2:** The matrix  $U(n-1 \times m)$  is calculated as:

$$U = X_{11}V(V^TV + \lambda I_m)^+$$

where  $I_m$  represents the identity matrix  $(m \times m)$  and (+) represents a generalized inverse and  $\lambda$  is the regularization parameter.

**Step 3:** The matrix *V* is updated through:

$$V = X_{11}^T U (U^T U + \lambda I_m)^+$$

**Step 4:** The value of the regularized objective function is calculated by:

$$J = ||X_{11} - UV^T||_F^2 + \lambda(||U||_F^2 + ||V||_F^2)$$

.

**Step 5:** Steps 2, 3 and 4 are repeated iteratively until reaching convergence in the value of *J*.

**Step 6:** The standard SVD is calculated over  $UV^T$  to obtain the corresponding regularized eigenvalues and eigenvectors.

**Step 7:** The imputation equation of the regularized GabrielEigen becomes:

$$x_{ij}^{(m)} = x_i^T U_{\text{reg}} D_{\text{reg}}^+ V_{\text{reg}}^T x_j$$

where  $U_{\text{reg}} V_{\text{reg}}^T$  represents the regSVD of  $X_{11}$ .

## Skoltech

#### **Validation**

- ➤ Utilized Kaggle's datasets for Breast and Prostate cancer.
- ➤ Introduced missing values randomly at 5%, 15%, and 30% ratios.
- ➤ Varied lambda values for comprehensive analysis.
- ➤ Evaluation Metrics including mean absolute error and correlation coefficient used..

#### Mean Absolute Error

The Mean Absolute Error (MAE) is a metric used to quantify the average magnitude of errors between predicted and actual values. The formula for calculating MAE is as follows:

$$MAE = \frac{1}{n} \sum_{i=1}^{n} |x_i - \hat{x}_i|$$

where  $x_i$  and  $\hat{x}_i$  represents the actual and predicted value of  $i^{th}$  observation respectively.

MAE is a straightforward and interpretable metric. A smaller MAE indicates better agreement between the predicted and actual values, with each absolute difference contributing equally to the overall error.

#### **Correlation Coefficient**

The correlation coefficient between two variables, denoted as r, is a statistical measure of the strength and direction of their linear relationship. The formula for calculating the correlation coefficient between two variables X and Y is given by:

$$r = \frac{\sum_{i=1}^{n} (X_i - \bar{X})(Y_i - \bar{Y})}{\sqrt{\sum_{i=1}^{n} (X_i - \bar{X})^2 \sum_{i=1}^{n} (Y_i - \bar{Y})^2}}$$

A correlation close to 1 indicates a strong positive linear relationship, while a correlation close to -1 indicates a strong negative linear relationship. A correlation close to 0 suggests a weak or no linear relationship.

In red, the minimised values of the statistics by regularised GabrielEigen in each percentage considered.  $\lambda$ =0 represents the original GabrielEigen. In red, the minimised values of the statistics by regularised GabrielEigen in each percentage considered.  $\lambda$ =0 represents the original GabrielEigen.

# Skoltech

#### Summary of study on the breast cancer dataset

	Missing Ratio	λ = 0	λ = 0.1	λ = 0.2	λ = 0.3	λ = 0.4	λ = 0.5
Mean absolute error	5%	0.3748	0.3376	0.3255	0.52993	0.4000	0.2791
	15%	1.0597	1.3509	0.9963	0.9978	0.9927	1.0414
	30%	2.9354	2.6785	3.0909	3.2415	2.8780	3.4083
Correlation	5%	0.9994	0.9996	0.9994	0.9981	0.9991	0.9997
	15%	0.9972	0.9956	0.9985	0.9987	0.9986	0.9985
	30%	0.9922	0.9941	0.9921	0.9902	0.9930	0.9885

In red, the minimised values of the statistics by regularised GabrielEigen in each percentage considered.  $\lambda = 0$  represents the original GabrielEigen.

### Skoltech

#### Summary of study on the prostate cancer

	Missing Ratio	λ = 0	λ = 0.1	λ = 0.2	λ = 0.3	λ = 0.4	λ = 0.5
Mean absolute error	5%	0.92694	0.7487	1.9829	1.5997	0.8035	1.2669
	15%	3.6482	3.9415	1.6656	2.1878	2.9213	3.1672
	30%	5.6748	6.1363	5.1481	2.0581	6.4935	6.5073
	5%	0.9989	0.9984	0.9963	0.9972	0.9991	0.9981
Correlation	15%	0.9929	0.9924	0.9986	0.9965	0.9951	0.9963
	30%	0.9910	0.9912	0.9899	0.9806	0.9907	0.9905

In red, the minimised values of the statistics by regularised GabrielEigen in each percentage considered.  $\lambda=0$  represents the original GabrielEigen.

## Skoltech

#### Conclusion

- ➤ A generalization of the GabrielEigen imputation method has been proposed using regularized SVD.
- ➤ The regularized version is flexible and can be applied to any data matrix, making it suitable for non-parametric imputation for multivariate data.
- ➤ The method proved to be quite adaptable across different types of interaction, matrix dimensions, and percentages of missing data.
- ➤ The method has potential for use with methodologies for obtaining robust and multiple imputations.

#### **Future Research**

- > Exploring different mechanisms of data absence and their impact on the proposed method.
- Investigating the effects of various probability distributions on the efficiency and effectiveness of the method.
- > Further research on the optimal choice of the regularization parameter, particularly in different data scenarios.
- Integrating the proposed methodology with existing robust and multiple imputation methods to enhance its applicability and effectiveness.

#### Thank you for your attention

Daniyal Asif; conceptualization, software, validations, project administration, supervision, visualization, writing—original draft.

Hassan Maqsood; conceptualization, software, visualization, and writing—original draft.

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#### Questions?

