Columns of gene expression matrix are highly sparse in the DCT domain. Hence, we propose to recover missing data column-wise, i.e., by

\[ \min_{\mathbf{x}_i} \max_w \left( \| \mathbf{x}_i - \hat{\mathbf{x}} \|_2^2 + \lambda_2 \mathbf{w}^T \mathbf{A} \mathbf{x}_i \right) \]  

where \( \mathbf{w}_i \) is an auxiliary vector such that

\[ \| \mathbf{x}_i \|_1 = \max_{\mathbf{w}_i} \left( \mathbf{w}_i^T \mathbf{x}_i \right) \]

TV denoising problem is minimized using iterative clipping algorithm with update equations as given in algorithm where,

\[ \mathbf{w}(0) = 0 \text{ and } \alpha = \max \text{eig}(\mathbf{A}^T \mathbf{A}) \]

**Algorithm**

1. **Stage-1 - Matrix Recovery**  
   Input: \( Y \) (Input incomplete matrix), DCT matrix \( \mathbf{D} \)  
   for loop from \( i = 1, \ldots, n \)  
   1. Calculate \( \hat{\mathbf{x}}_i \) for all \( i \) using \( \mathbf{y}_i \)  
   2. while converge:  
      \( \mathbf{z}_i \leftarrow \text{soft} \left( \mathbf{z}_i + \frac{1}{\lambda_2} (\mathbf{D}^T \mathbf{D})^{-1} (\mathbf{y}_i - \hat{\mathbf{x}}_i \mathbf{D}^T) \right) \)  
   3. end while  
   4. \( \hat{\mathbf{x}}_i \leftarrow \mathbf{D} \mathbf{z}_i \)  
   5. end for  
   6. Obtain \( \mathbf{X} \) from \( \hat{\mathbf{x}}_i \)  
   7. Output: \( \mathbf{X} \) (Recovered Matrix)

2. **Stage-2 - Denoising**  
   Input: \( X/\text{Noisy matrix} \), \( \Lambda \) (Difference Operator)  
   for loop from \( i = 1, \ldots, n \)  
   1. while converge:  
      \( \mathbf{x}_i \leftarrow \text{clip} \left( \mathbf{x}_i + \Lambda \mathbf{w}_i \right) \)  
   2. end while  
   3. Obtain \( \mathbf{X} \) from \( \mathbf{x}_i \)  
   4. Output: \( \mathbf{X} \) (Recovered Matrix)

**Conclusion**

- In this study, we have presented novel TV-DCT method that is a 2-stage matrix imputation method and we have investigated the performance of our proposed method at low as well as high observability of data.
- The comparative performance of TV-DCT method is observed to be superior to three state-of-the-art matrix completion methods in terms of NRMSE and classification accuracy.

**References**


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