Supplementary Material

**Inferring Latent Disease-lncRNA Associations by Faster Matrix**

**Completion on a Heterogeneous Network**

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Supplementary Algorithm

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| Algorithm 1 : FRMCLDA algorithm using faster SVT |
| **Input:** lncRNAs similarity matrix *LS*, disease similarity matrix *DS* and incomplete lncRNA-disease association matrix *LD.* Sampling set *Φ*, step size *δ* , the error limit *ε* , Singular value threshold *τ* , increment *l*, max iteration number *i*max.**Output:** Completed lncRNA-disease association matrix *LD*\*1. *Calculate lncRNA integrate similarity LS and disease integrate similarity matrix DS based on the association matrix LD.*
2. *Construct a large sparse adjacent matrix A for heterogeneous network.*
3. Initiation: , $c=\left⌈τ/(δ\left‖Ρ\_{Φ}\left(A\right)\right‖)\right⌉$, *r0 = 0*, *q = 0*, *p = 2*, *l*=5, *imax*=1000.
4. **for** *i = 1,2, · · ·, imax* **do**
5. *ki = ri-1 + l, then regulate the value of p dynamically*
6. **repeat**
7. **if** *i < ireuse* ***or*** *q == qreuse* ***then***
8.
9. *q = 0*
10. ***else***
11. *reuse Q in last round execution of rSVD-BKIr algorithm, and then compute , ,*
12. *q = q + 1;*
13. ***end if***
14.
15. ***until***
16.
17. */\*linearized Bregmans interations\*/*
18. ***if*** ***then break***
19.
20. ***end for***
21.
22. ***Return*** *LD\**
 |

%% where the rSVD-BKI is referenced from the literature: “Faster Matrix Completion Using Randomized SVD”