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: , , *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*** 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*** 15. ***until*** 17. */\*linearized Bregmans interations\*/* 18. ***if*** ***then break*** 20. ***end for*** 22. ***Return*** *LD\** |

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