

● **Input**

- A: Adjacent matrix of PPI network;
- F: Function profile for all proteins;
- K: Maximum number of possible complexes;
- λ : Rate parameter of exponential distribution;
- τ : Threshold parameter for obtaining protein complex candidates.

● **Output**

- ψ : Complex-function preference matrix;
- θ : Protein-complex membership matrix;
- θ^* : Resultant protein-complex membership indication matrix;
- s : Value of the objective function (10).

● **Main algorithm**

1. Initialize matrices θ and ψ randomly;
2. Update θ according to Equation (11);
3. Update ψ according to Equation (12);
4. Calculate the value s of the objective function (10);
5. Repeat Steps 2, 3 and 4 until the relative change of s is less than 10^{-6} or times of iteration reach 400;
6. Normalize θ such that $\sum_{k=1}^K \theta_{ik} = 1$;
7. Obtain the resultant protein-complex membership indication matrix θ^* according to Equation (13);
8. Treat each connected subnetwork of a complex candidate as a single complex;
9. Filter out detected complexes which contain less than three proteins;
10. Return ψ , θ , θ^* , and s.