In silico prediction methods of self-interacting proteins: An empirical and academic survey

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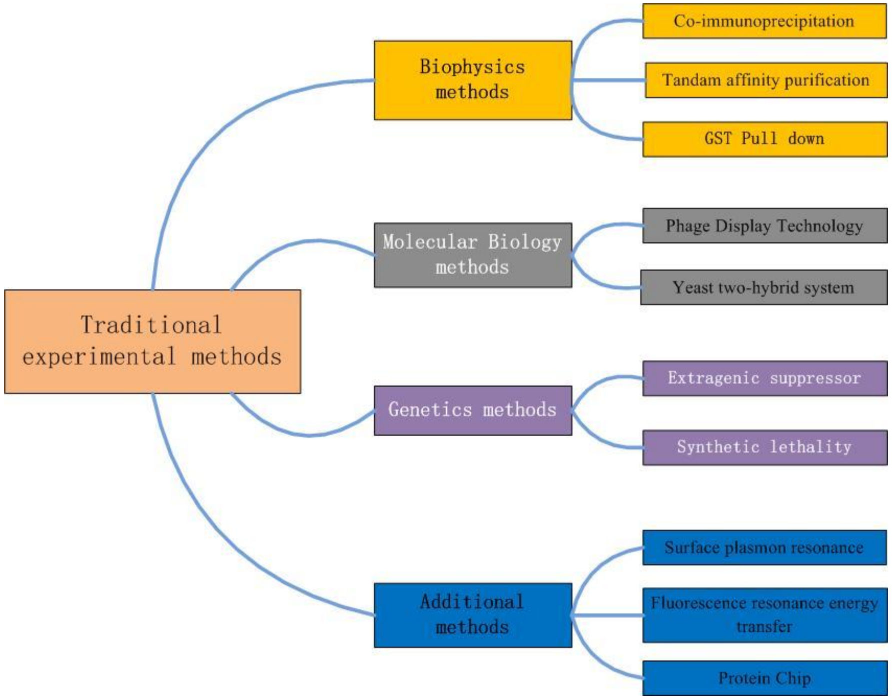
Problems & Ideas

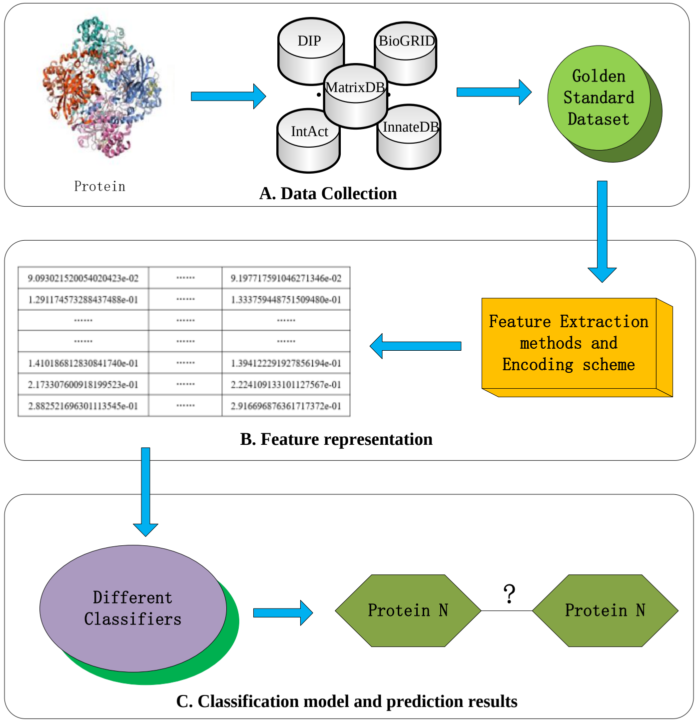
- Problems of traditional biological wet-lab experiments in SIPs:
  - high cost.
  - labor intensive.
- Ideas: to sum up a comprehensive overview of the recent literature with the computational SIPs prediction, to provide important references for actual work in the future.



The traditional biological prediction methods

Main Contributions

- Contributions:
  - Many computational feature extraction methods are briefly described and extracted the useful characteristics based on these techniques as much as possible before analyzing and training these data;
  - Some relatively comprehensive and popular state-of-the-art methods are counted for predicting self-interacting proteins in recent years;



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The flowchart of SIPs prediction model