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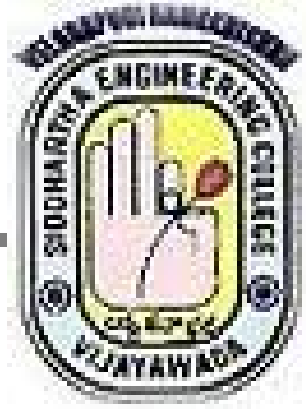
Association analysis of Type 2 Diabetes Proteins Interaction Network



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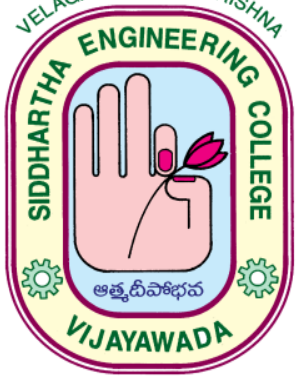

by

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Preamble

- Diabetes is a **chronic disease** that occurs either when the pancreas does not produce enough insulin or when the body cannot effectively use the insulin it produces.
- Diabetes is classified into Type 1 and Type 2
- Type 1 diabetes (previously known as insulin-dependent, childhood-onset) is characterized by deficient insulin production and requires daily administration of insulin
- Type 2 diabetes (formerly called non-insulin-dependent or adult-onset) results from the body's ineffective use of insulin.

Preamble

- Type 2 diabetes comprises 90% of people with diabetes around the world
- 85 to 95 percent of the total number of diabetes cases in developed countries and an even **higher percentage in developing countries.**
- 347 million people worldwide have diabetes .

Insilco approach

- The drug discovery process is labor intensive and expensive in case of *In vitro* and *In vivo*.
- For eradicating such hurdles and paving the way for the drugs of future, *insilico* methods have been envisaged.
- In this regard, study the relation between type 2 diabetes proteins using the advanced concepts of data mining and bioinformatics.
- Identifying the target proteins for a disease like Diabetes, their interactions and associations would lead to find the novel drug for this disease.

The Methodology for Type 2 Diabetes proteins interaction network

- In the present study, Association analysis of Type 2 Diabetes proteins interaction network was implemented in modular manner.

- It was divided into four modules. The procedure is as follows.

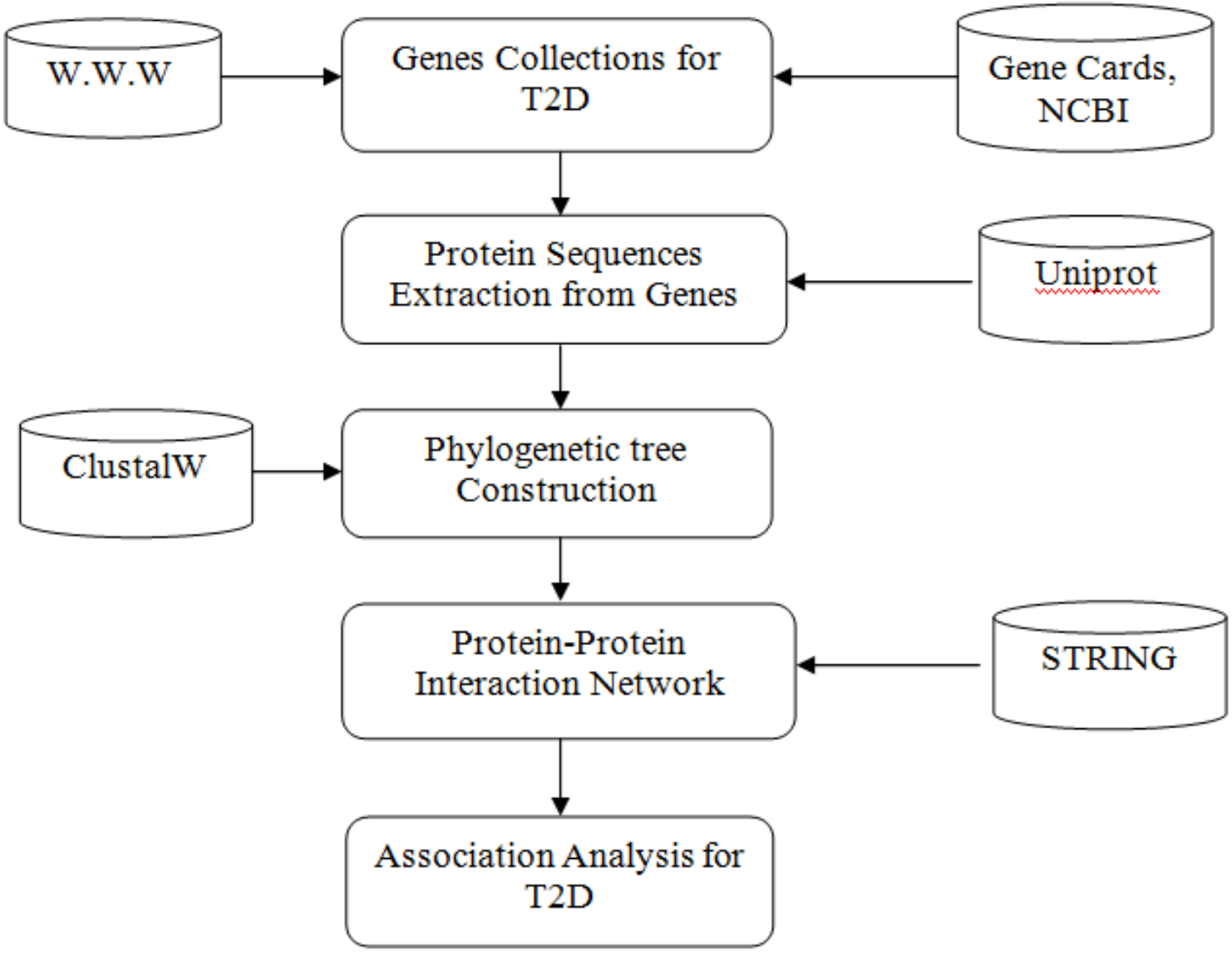
Step 1: Collect the Genes/Proteins responsible for T2D from Biological Databases

Step 2: Construct the Phylogenetic tree for T2D proteins

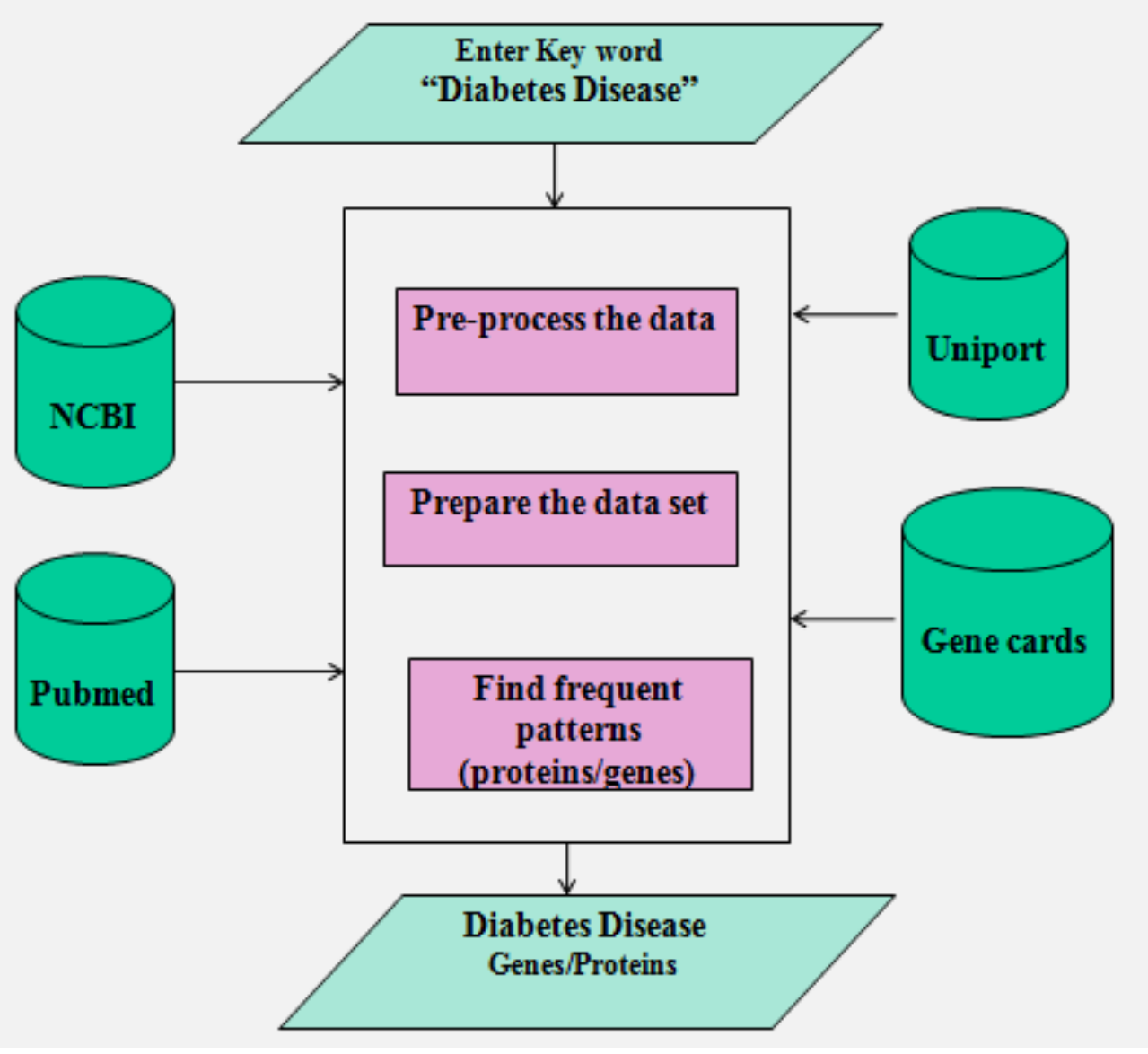
Step 3: Construct the Protein-Protein Interaction network for T2D proteins

Step 4: Identify the association between T2D proteins.

Block diagram of present study



Collection of Diabetes Genes/Proteins

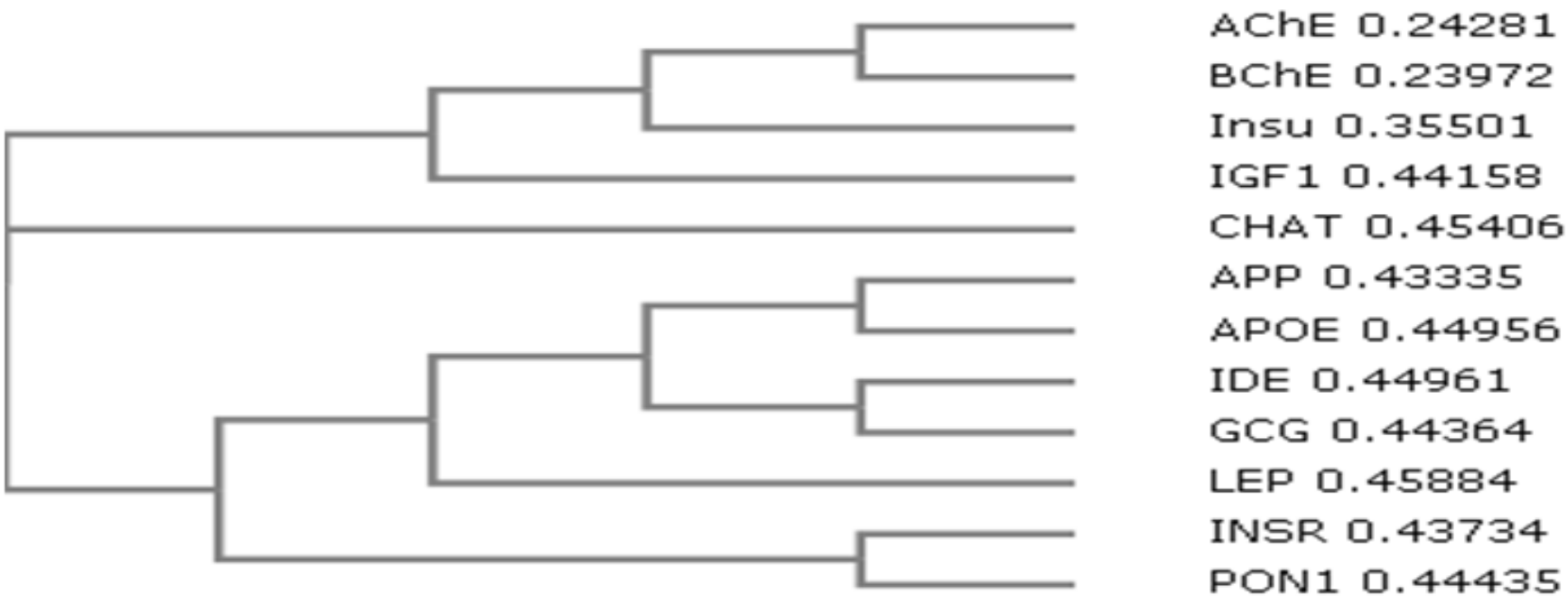


Proteins that have been cause to T2D

➢Selected 12 genes that have been caused for Type 2 Diabetes through Text mining, Literature survey, and protein interaction networks like STRING and Genecards websites

S.No	Ac. No	Gene Name	Protein Name	Sequence length (Amino acids)
1	P01308	INS	Insulin	110 AA
2	P22303	AChE	Acetylcholinesterase	614 AA
3	P06276	BChE	Butyrylcholine esterase	602 AA
4	P06213	INSR	Insulin receptor	1382 AA.
5	P05067	APP	Amyloid beta A4 protein	770 AA.
6	P02649	APOE	Apolipoprotein E	317 AA.
7	P28329	CHAT	Choline O-acetyltransferase	748 AA.
8	P14735	IDE	Insulin-degrading enzyme	1019 AA.
9	P01275	GCG	Glucagon	180 AA.
10	P41159	LEP	Leptin	167 AA.
11	P27169	PON1	Serum paraoxonase/arylesterase 1	355 AA.
12	P05019	IGF1	Insulin-like growth factor I	195 AA.

Phylogenetic Tree for T2D proteins



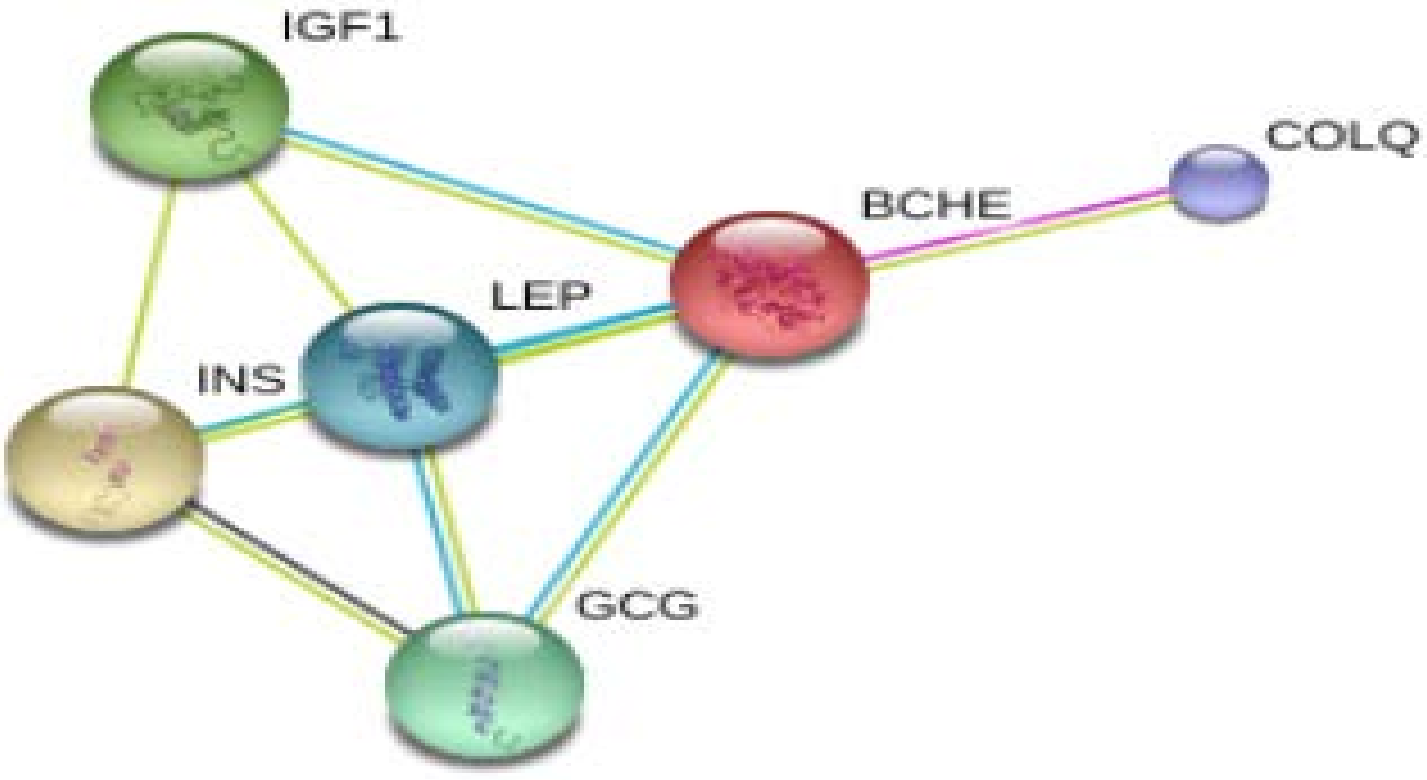
From the Phlogenetic analysis it is observed that

1. LEP and CHAT play significant role in T2D because both proteins have highest scores 0.45884 and 0.45406 respectively.
2. AChE, BChE, and Insulin proteins have close distance and similar sequence
3. APP & APOE, IDE & GCG , and INSR & PON1 have similar protein sequence
4. Finally twelve proteins have to be divided into two classes. One class has AChE, BChE and Insulin proteins and another class has remaining nine proteins.

Protein-Protein Interaction Network

- Protein-protein interaction refers to the association of protein molecules.
- Protein-Protein interaction information is essential for a systems level understanding of cellular behavior and is needed to place the molecular function of individual proteins into their cellular context.
- These networks provide a global view of the interactions between various proteins that are essential for the accomplishment of most protein functions
- Finally this information helpful to find the drug for disease through target proteins and ligand

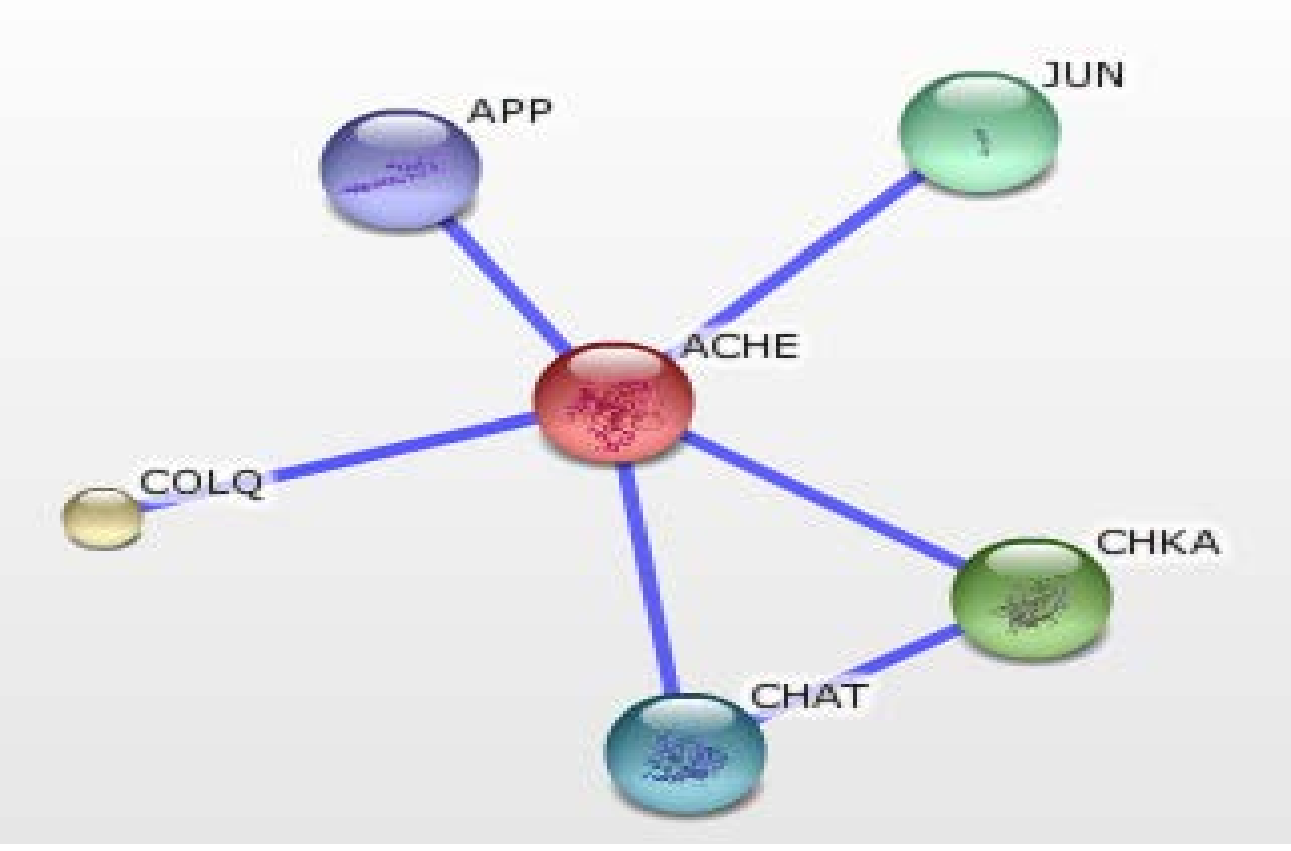
Protein-Protein Interaction Network of BChE



From the above BChE Interaction network diagram, it is observed that

- BChE interact with INS and GCG

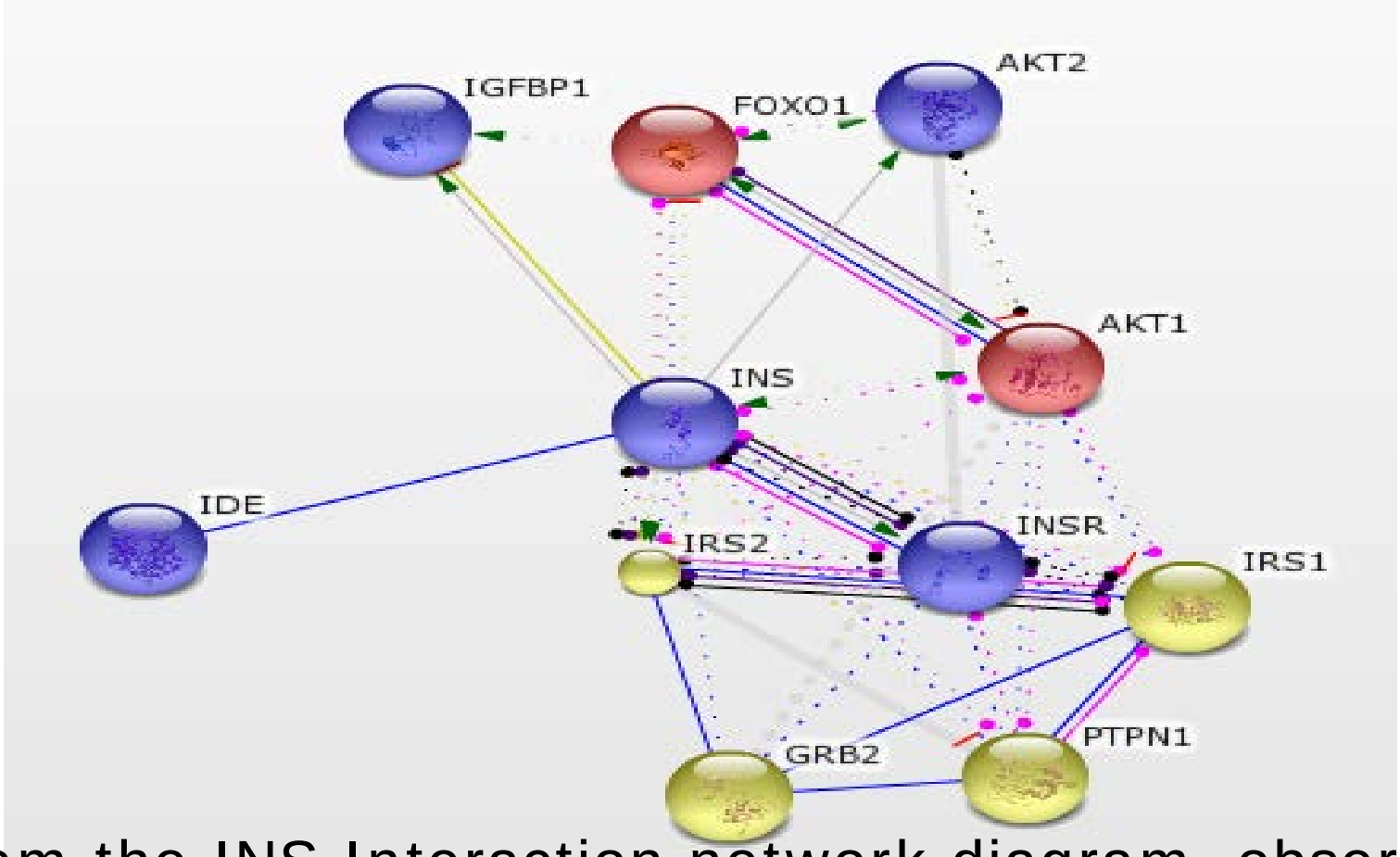
Protein-Protein Interaction Network of AChE



From the AChE Interaction network diagram, it is observed that

- AChE interact with APP and CHAT

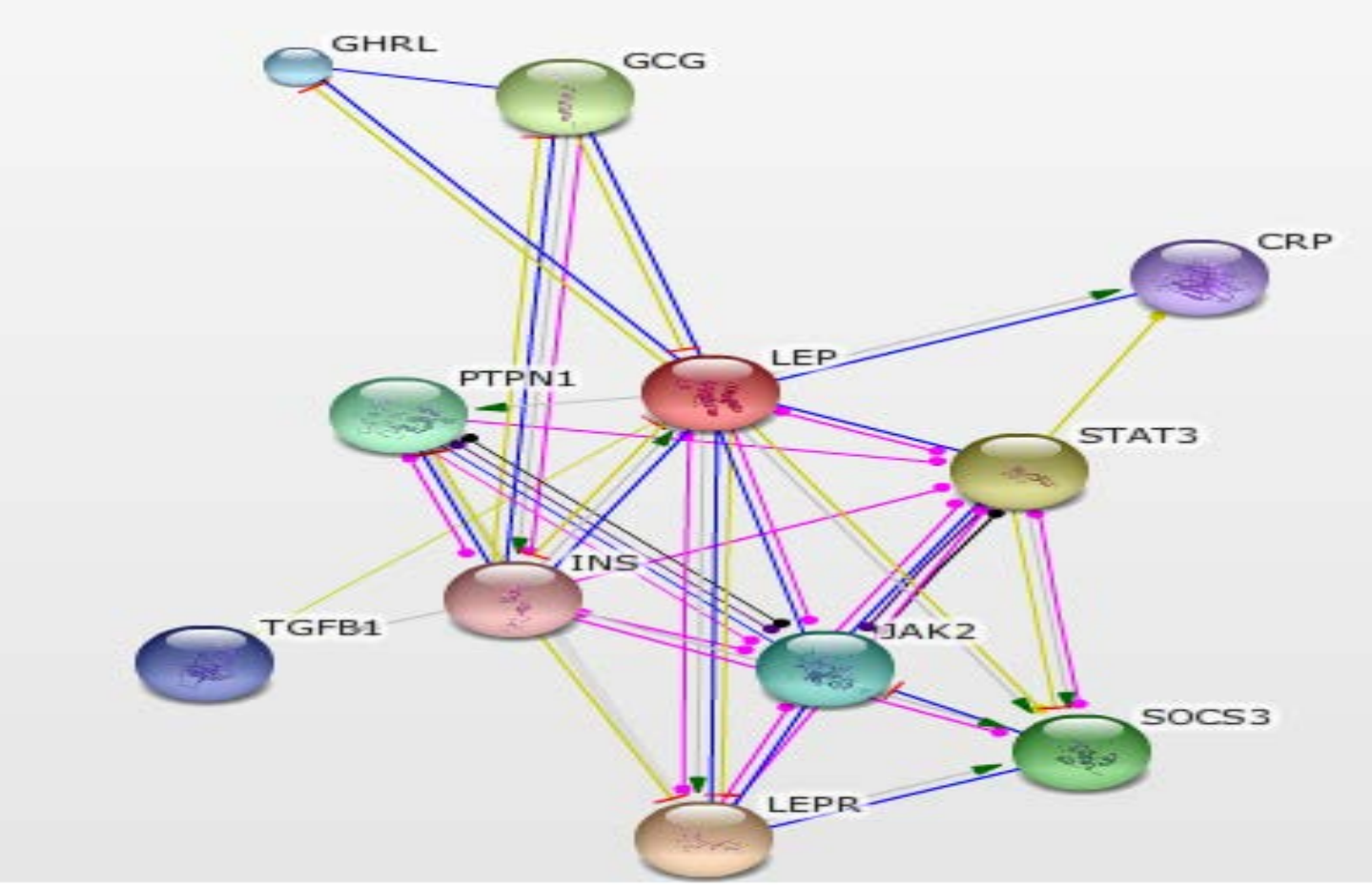
Protein-Protein Interaction Network of INS



From the INS Interaction network diagram, observed that

- INS interact with IDE and INSR

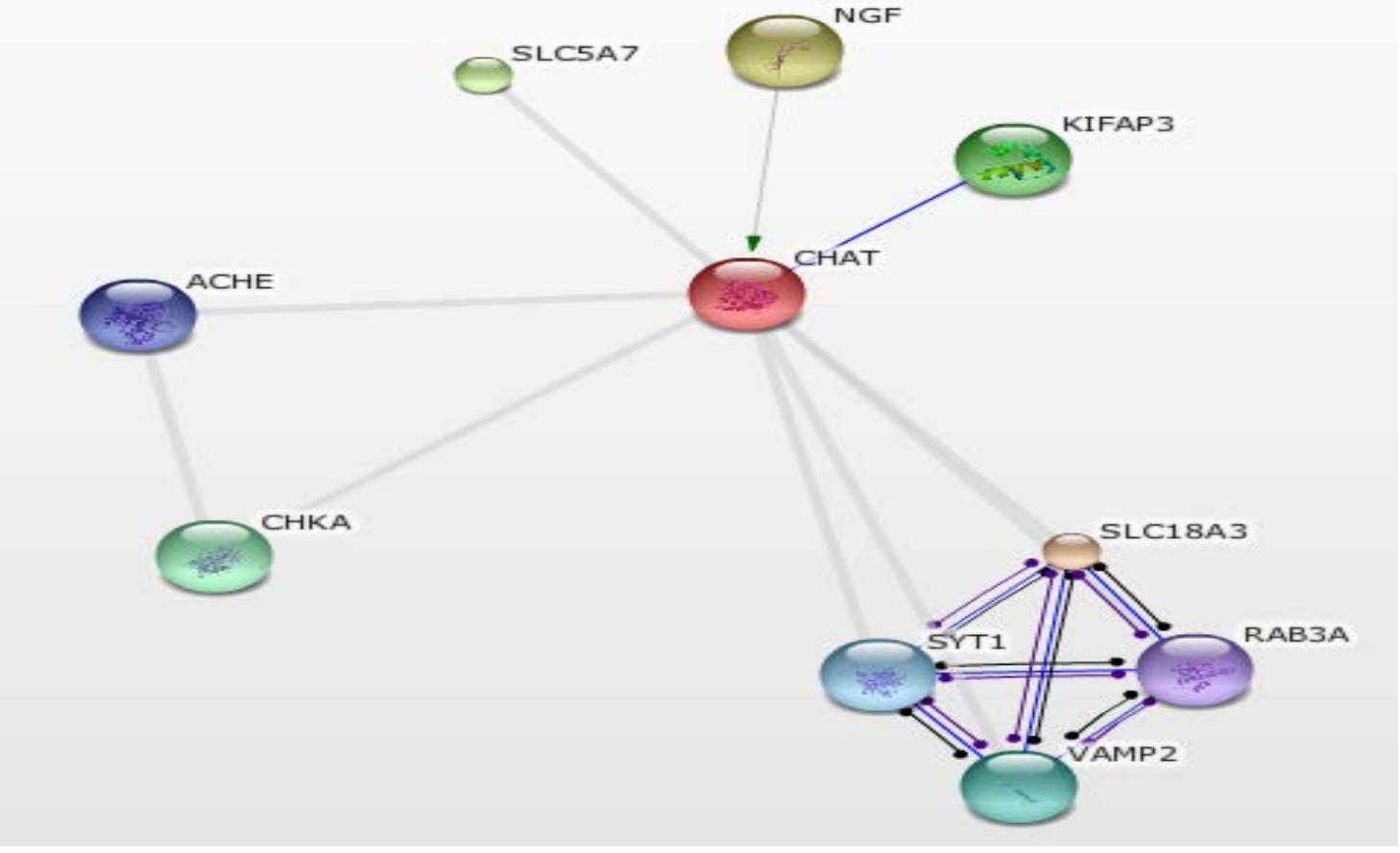
Protein Interaction Network of LEP



From the LEP Interaction network diagram, observed that

- LEP interact with GCG and INS

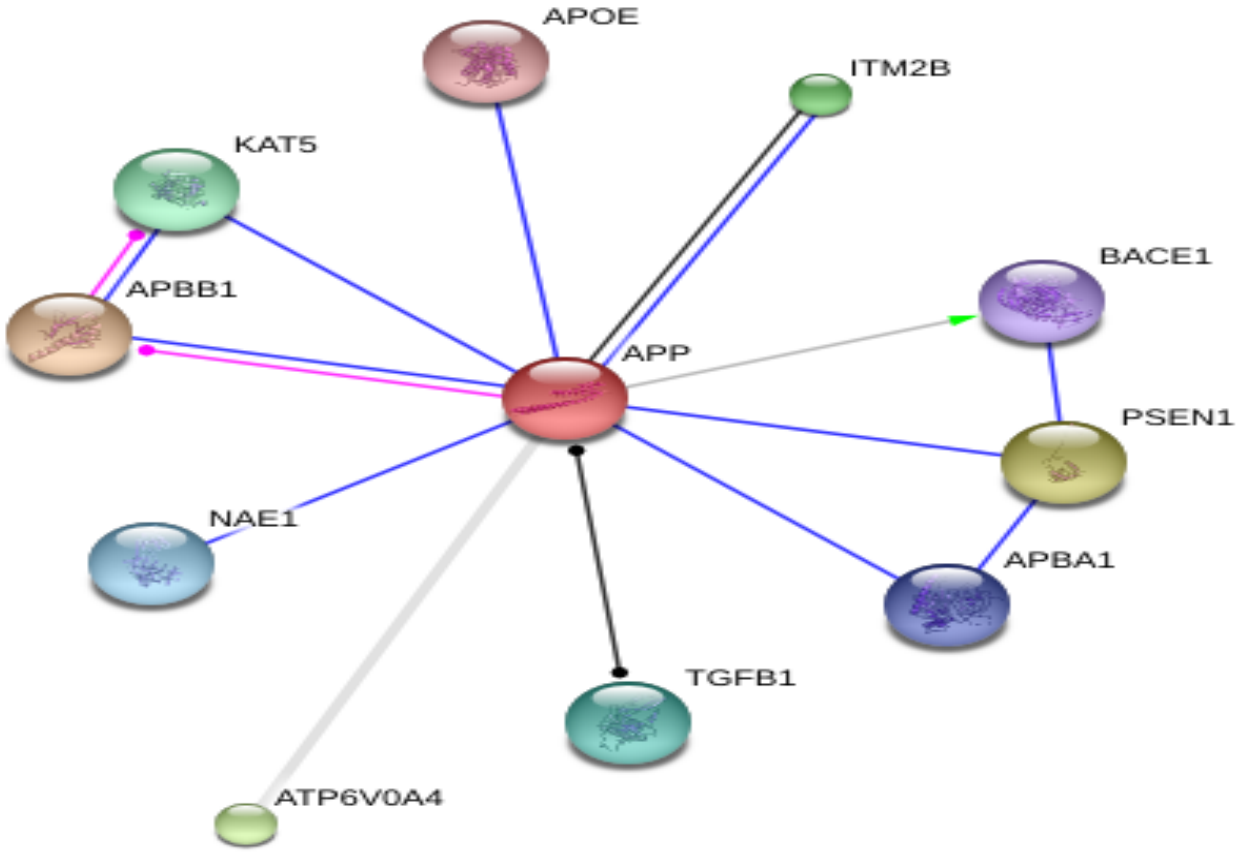
Protein Interaction Network of CHAT



From the CHAT Interaction network diagram, observed that

- CHAT interact with AChE

Protein Interaction Network of APP



From the APP Interaction network diagram, observed that

- APP interact with APOE

Observations from Protein-Protein Interaction Networks

From the above all Protein-Protein Interaction network diagrams, it is observed that

1. BChE interact with INS and GCG
2. AChE interact with APP and CHAT
3. INS interact with IDE and INSR
4. LEP interact with GCG and INS
5. CHAT interact with AChE
6. APP interact with APOE

Conclusion

- In the present work we tried to outline the association analysis that could be performed to arrive at the relationship and association between T2D proteins.
- It is observed that BChE ,Insullin, Chat and LEp are plays key role in T2D diabetes through phylogenetic and proteon protein interaction networks.
- BChE functionality in humans is not clear.
- In future, studies of this nature may pay way for in silico protein-protein interaction experiments that be extended to develop for new therapeutic interventions.

Conclusion

- We will going to develop novel method, which extracts the highly ranked target proteins and most important pathways when given disease genes as input.
- The construction protein-protein interaction by using anther novel new method call dynamic programming approach.
- Finally prune the network and identify the target protein/proteins for specified disease.

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