

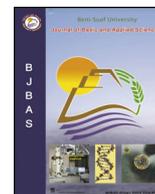
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Full Length Article

## Design regulatory interaction network for anxiety disorders using R: A bioinformatics approach

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## ABSTRACT

Bio-informatics research fields are progressively growing enriched with the incremental use of R tools. Anxiety Disorders can be defined as one of the most common mental disorders. They are tangible psychiatric disorders or a group of mental illnesses thought to be caused by either genetic vulnerability or environmental susceptibility factors. Several studies have revealed that anxiety is associated with an increased risk of Angina, Asthma, Diabetes, Heart Attack and High Blood Pressure. Thus, these five anxiety disorders must have some genetic association among them. Finding the genetic relationship among the above diseases will help to understand the gene linkage and connection association among them which leads to the way to common drug design. Here, after investigating the genetic association of Angina, Asthma, Diabetes, Heart Attack and High Blood Pressure a Regulatory Interaction Network is designed using R. The investigated diseases genes are collected, preprocessed, processed, mined and optimized using R. This research aimed to create a new dimension in the field of drug design.

## 1. Introduction

Bioinformatics analyzes knowledge extracted from biological data and performs some application, calculation or computation, processing of the data to produce a significant result. R, as a great bio-informatics tool, makes the bioinformatics research field more subtle and demanding. Anxiety disorders are a group of mental disorders characterized by significant feelings of anxiety and fear (Diagnostic and Statistical Manual of Mental Disorders). About 12% of people are affected by an anxiety disorder in a given year and between 5 and 30% are affected at some point in their life (Craske and Stein, 2016; Kessler et al., 2007). Angina, Asthma, Diabetes, Heart Attack and High Blood Pressure can be characterized as one kind of Anxiety Disorders. Thus, dealing with anxiety disorders will require analyzing these diseases to find an association relation among them.

Angina is a type of chest pain or pressure, caused when the heart muscle doesn't get enough oxygen-rich blood. Angina can be of two types Stable or Angina Pectoris and Unstable Angina or unexpected chest pain. Unstable angina is responsible for more than 750,000 hospitalizations annually in the United States (National Center for Health Statistics) and thus ranks among the most frequent causes of

hospitalization in this country. Angina is characterized as a symptom of coronary heart disease (CHD), an underlying heart problem rather than a disease. So, there must have a strong association among Angina, Heart Attack, and High Blood Pressure. Finding the association among the diseases will help to find the gene association.

Asthma (AZ-ma) is a chronic (long-term) lung disease that inflames and narrows the airways (Prasad et al., 2010). It is the most common chronic medical condition and a leading health problem, both in prevalence (Sterk et al. 1998; Cunningham et al. 1999; Asher et al. 2000; Weiss et al. 2000), associated social and physical morbidity (Weil et al. 1999), and societal costs (Sterk et al. 1998) in the United States and worldwide (Sterk et al. 1998; Weiss et al. 2000; Mannino et al. 2002). One in 12 people (about 25 million, or 8% of the U.S. population) had asthma in 2009, compared with 1 in 14 (about 20 million, or 7%) in 2001 (Centers for Disease Control and Prevention, 2011). There is evidence that anxiety symptoms are associated with increased severity of asthma (Goodwin). Chest tightness, Shortness of breath etc. are the common symptoms of asthma which indicate that Asthma is also related to Angina, Heart Attack, and High Blood Pressure.

Diabetes is a disease in which the person has high blood glucose or blood sugar. In 2005, it was estimated that more than 20 million people

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```

1. library(rentrez)
2. entrez_dbs()
3. entrez_db_summary("gene")
4. entrez_db_searchable("gene")

5. r_search <- entrez_search(db="gene", term="(angina [ALL] AND Homo
   Sapiens[ORGN]", retmax=700)
6. r_search
7. r_search$ids
8. r_seqs<-entrez_fetch(db="gene", id=r_search$ids, rettype="fasta",retmode="text")
9. r_seqs

```

Fig. 1. R query to collect Angina genes.

```

1. r_search <- entrez_search(db="gene", term="(asthma [ALL] AND Homo
   Sapiens[ORGN]", retmax=700)
2. r_search <- entrez_search(db="gene", term="(diabetes [ALL] AND Homo
   Sapiens[ORGN]", retmax=700)
3. r_search <- entrez_search(db="gene", term="(heart[ALL] AND attack[ALL] AND Homo
   Sapiens[ORGN]", retmax=700)
4. r_search <- entrez_search(db="gene", term="(high blood pressure [ALL] AND Homo
   Sapiens[ORGN]", retmax=700)

```

Fig. 2. Modified R query to collect other disease genes.

```

1. r_seqs1<-write(r_seqs, file="angina.txt")
2. r_seqs1<-write(r_seqs, file="asthma.txt")
3. r_seqs1<-write(r_seqs, file="diabetes.txt")
4. r_seqs1<-write(r_seqs, file="heart_attack.txt")
5. r_seqs1<-write(r_seqs, file="high_bp.txt")

```

Fig. 3. The R query for storing genes in the text file.

```

1. library(tm)
2. filePath <- " FileLocation/angina.txt"
3. text <- readLines(filePath)
4. getTransformations()
5. docs <- Corpus(VectorSource(text))
6. inspect(docs)
7. docs <-docs[-(1:3)]
8. docs <- tm_map(docs, removeWords, c("dd", "dt", "class", "dl","desig","details"))
9. docs <- tm_map(docs, removePunctuation)
10. df<-head(docs,100)
11. inspect(df)
    //Copy and save on a text file and then read the text file into df
12. df<-read.table("FileLocation/angina1.txt",fill=TRUE,header = FALSE)
13. df//Delete unusual columns and rows and keeps the genes only
14. df <-df[,-(3:227)]
15. df <-df[,c(1,2,4:315)]

```

Fig. 4. R query for mining Angina genes.

```

1. filePath <- " FileLocation/asthma.txt"
2. filePath <- " FileLocation/diabetes.txt"
3. filePath <- " FileLocation/heart_attack.txt"
4. filePath <- " FileLocation/high_bp.txt"

```

Fig. 5. Modified R query of Fig. 4 (step 2) for gene mining.

```

1. df<-read.table("FileLocation/asthma1.txt",fill=TRUE,header = FALSE)
2. df<-read.table("FileLocation/diabetes1.txt",fill=TRUE,header = FALSE)
3. df<-read.table("FileLocation/heart_attack1.txt",fill=TRUE,header = FALSE)
4. df<-read.table("FileLocation/high_bp1.txt",fill=TRUE,header = FALSE)

```

Fig. 6. Modified R query of Fig. 4 (step 12) for gene mining.

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