Server/Database Set Up:

Java
If not installed already, install the Java JDK, which can be downloaded from:
http://www.oracle.com/technetwork/java/javase/downloads/index.html

MySQL
Download and install a MySQL server from the following URL.
http://dev.mysql.com/downloads/mysql/

Apache Tomcat Server
Download an apache tomcat server from the following URL:
http://tomcat.apache.org/

Configuration of the tomcat server is described below:

Jdbc connector
To connect the MySQL database to the tomcat server, download the JDBC connector from http://dev.mysql.com/downloads/connector/j/ and place the jar file (ex: mysql-connector-java-5.1.34-bin.jar) into the lib folder of the server. Note: If the server is set up in an IDE (ie: eclipse), be sure to configure the server configuration found within the workspace.

SSL cert
QuIN is initially configured to be used with a secure connection, which can be changed by re-configuring the web.xml file. If this is not changed, then a certificate will need to be created by running `keytool -genkey` in a terminal.

Resource Configuration:

Add the following resource in the context.xml file located in the conf directory, providing the necessary database information in brackets. The database port may also need to be modified depending on the MySQL server configuration:

```
<Resource name="jdbc/chinqtdb" auth="Container" type="javax.sql.DataSource"
    maxActive="100" maxIdle="30" maxWait="10000"
    username="<db username>" password="<db password>"
    driverClassName="com.mysql.jdbc.Driver"
    url="jdbc:mysql://localhost:3306/<database name>" testOnBorrow="true"
    validationQuery="SELECT 1"/>
```

Server Configuration:

If using the secure connection/not modifying the web.xml configuration:

Modifying the default port 8080 connector to redirect to port 8443:

```
<Connector port="8080" protocol="HTTP/1.1" connectionTimeout="20000"
    redirectPort="8443" />
```

Then add a connector on port 8443, providing the details on the SSL certificate:

```
<Connector port="8443" protocol="org.apache.coyote.http11.Http11Protocol"
    maxThreads="150" SSLEnabled="true" scheme="https" secure="true"

    ciphers="TLS_ECDHE_RSA_WITH_AES_128_CBC_SHA256,TLS_ECDHE_RSA_WITH_AES_128_CBC_
    SHA,TLS_ECDHE_RSA_WITH_AES_256_CBC_SHA384,TLS_ECDHE_RSA_WITH_AES_256_CBC_SHA,T
    LS_RSA_WITH_AES_128_CBC_SHA256,TLS_RSA_WITH_AES_128_CBC_SHA,TLS_RSA_WITH_AES_2
    56_CBC_SHA256,TLS_RSA_WITH_AES_256_CBC_SHA"

    clientAuth="false" sslProtocol="TLS" keystoreFile="<keystore file>"
    keystorePass="<keystorepass>"/>
```

R
R can be downloaded from the following site:
https://www.r-project.org/

Once downloaded three packages will need to be installed:

1) *topGO*
    Install topGO using the instructions found here:
    http://www.bioconductor.org/packages/release/bioc/html/topGO.html

2) *vioPlot*

    ```
    install.packages("vioplot")
    ```

3) *RServe*

    ```
    install.packages("Rserve")
    ```

Database Import:

1) Schema Set Up
First set up the database schemas by running the database_setup.sql file provided.

2) dbSNP
QuIN does not use the entire dbSNP database, and only uses the information of where the SNPs are located on the genome. For this reason, the chromosome reports are used for importing this information and can be found in the chr_rpts directory of the latest human GRCh37 build for hg19 SNPs found here: ftp://ftp.ncbi.nih.gov/snp/organisms/

Once the files are found perform the following steps:

1) Create a new folder for storing the chromosome reports.
2) Download the the reports for the desired chromosomes (ex: chr1-chr22, chrX, chrY)
3) Run the following command in a terminal, with the file path information in brackets:

```
java –jar "<directory containing setup jars>/dbSNPImport.jar" GRCh37p13 "<your
    download path of all files>/" true
```

3) UCSC Refflat
The following steps are used to import the hg19 gene information from UCSC.

1) Set the database to UCSC using

```
USE ucsc;
```

2) Download the table creation script from
ftp://hgdownload.cse.ucsc.edu/goldenPath/hg19/database/refFlat.sql

and run the script in MySQL after which there should be a table labeled "refFlat" in the ucsc database/schema.

3) Rename the refFlat table to hg19 using

```
ALTER TABLE `ucsc`.`refFlat` RENAME TO  `ucsc`.`hg19` ;
```

4) Download the data from
ftp://hgdownload.cse.ucsc.edu/goldenPath/hg19/database/refFlat.txt.gz

and load the data into the database using the following command in a terminal, with the file path information in the brackets.

```
java –jar "<directory containing setup jars>/UCSCRefFlatImport.jar"
    "ucsc.hg19" "<your download path>/refFlat.txt.gz"
```

4) NCBIGene2GO/Gene2Refseq
The NCBI Gene2GO and Gene2Refseq data is used for performing GO enrichment analysis. To import this data into the database, first download the following files from NCBI:

ftp://ftp.ncbi.nih.gov/gene/DATA/gene2go.gz
ftp://ftp.ncbi.nih.gov/gene/DATA/gene2refseq.gz

Once downloaded, run the following command to import the data.

```
java –jar  "<directory containing setup jars>/NCBIGene2GOImport.jar" "<path to
    gene2go file>/gene2go.gz" "<path to gene2refseq>/gene2refseq.gz"
```

5) GWAS Catalog
The GWAS catalog is used for associating curated diseases/traits with SNPs. To import this data into the database, first download tsv file for the full GWAS catalog from:

http://www.ebi.ac.uk/gwas/docs/downloads

Once downloaded, import the data using the following command in a terminal, replacing the file paths in brackets:

```
java –jar "<directory containing setup jars>/GWASCatalogImport.jar" "<directory
    containing setup jars>/GWASCatalogImport.jar" "<your download path>"
```

6) ClinVar
For additional disease to SNP associations, the ClinVar database is imported. To import this database, first download the XML file found here:

ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/xml/ClinVarFullRelease_00-latest.xml.gz

Once downloaded, unzip the file and import the data by running the following command and replacing the file paths in brackets.

```
java – jar "<directory containing setup jars>/ClinVarImport.jar" "<download
    path>/ClinVarFullRelease_00-latest.xml"
```

Pushing QuIN to Tomcat:

Finally, once all the data has been imported into the database, add the project to the apache tomcat server in your preferred IDE or generate a WAR file and add it to the "webapps" directory of the tomcat filepath.

Starting Rserve:
Rserve needs to be started in R before methods using Rserve will function correctly. To start Rserve run the following commands:

```
library(Rserve)
Rserve(args='--no-save')
```