user
- id INT(10)
- lastname VARCHAR(30)
- firstname VARCHAR(30)
- mi VARCHAR(30)
- agency VARCHAR(100)
- username VARCHAR(20)
- password VARCHAR(200)
- email VARCHAR(50)
- address VARCHAR(200)
- country VARCHAR(50)
- status TINYINT(1)
- role VARCHAR(20)
- active TINYINT(1)
- dateregistered TIMESTAMP
- Indexes

program
- id INT(10)
- userid INT(10)
- name VARCHAR(100)
- objective VARCHAR(200)
- coordinator VARCHAR(100)
- leadinginstitute VARCHAR(200)
- collaborator VARCHAR(100)
- Indexes

project
- id INT(10)
- userid INT(10)
- programid INT(10)
- name VARCHAR(100)
- objective VARCHAR(200)
- pi VARCHAR(100)
- leadinginstitute VARCHAR(100)
- collaborators VARCHAR(200)
- fundingagency VARCHAR(100)
- Indexes

study
- id INT(10)
- userid INT(10)
- programid INT(10)
- projectid INT(10)
- name VARCHAR(100)
- description VARCHAR(200)
- studytypeid INT(5)
- startyear VARCHAR(4)
- endyear VARCHAR(4)
- remarks VARCHAR(200)
- shared TINYINT(1)
- datecreated DATETIME
- datelastmodified DATETIME
- Indexes

studygermplasmcharacteristics
- id INT(10)
- studygermplasmid INT(10)
- germplasmname VARCHAR(50)
- attribute VARCHAR(30)
- value VARCHAR(30)
- Indexes

germplasm
- id INT(11)
- gid INT(10)
- germplasmname VARCHAR(50)
- othername VARCHAR(50)
- breeder VARCHAR(50)
- germplasmtypeid INT(5)
- irnumber VARCHAR(30)
- ircross VARCHAR(20)
- parentage VARCHAR(50)
- femaleparent VARCHAR(50)
- maleparent VARCHAR(50)
- selectionhistory VARCHAR(50)
- source VARCHAR(50)
- remarks VARCHAR(200)
- userid INT(10)
- Indexes

germplasmcharacteristics
- id INT(10)
- germplasmname VARCHAR(50)
- attribute VARCHAR(30)
- keyvalue VARCHAR(30)
- Indexes

extensiondata
- id INT(10)
- programid INT(5)
- projectid INT(5)
- germplasmname VARCHAR(50)
- yearextension VARCHAR(8)
- locationextension VARCHAR(50)
- countryextension VARCHAR(100)
- area DOUBLE(10,2)
- datasource VARCHAR(200)
- yearrelease VARCHAR(4)
- countryrelease VARCHAR(100)
- seedavailability INT(10)
- userid INT(10)
- Indexes

releaseinfo
- id INT(10)
- programid INT(5)
- projectid INT(5)
- germplasmname VARCHAR(30)
- datasource VARCHAR(200)
- yearrelease VARCHAR(4)
- countryrelease VARCHAR(100)
- seedavailability INT(10)
- userid INT(10)
- Indexes

keymajorgenes
- id INT(10)
- value VARCHAR(20)
- Indexes

studyagronomy
- id INT(10)
- studysiteid INT(10)
- plantingtypeid INT(5)
- sowingdate DATE
- harvestdate DATE
- fertilization VARCHAR(50)
- density VARCHAR(50)
- Indexes

studygermplasm
- id INT(11)
- gref INT(10)
- studyid INT(10)
- dataset INT(11)
- userid INT(10)
- Indexes

germplasmreleaseinfo
- id INT(10)
- germplasmname VARCHAR(50)
- attribute VARCHAR(50)
- value VARCHAR(100)
- Indexes

studyvariable
- id INT(10)
- variablecode VARCHAR(100)
- description VARCHAR(255)
- property VARCHAR(255)
- method VARCHAR(255)
- scale VARCHAR(255)
- applytofilter ENUM('Yes','No')
- defaultcolumn ENUM('Yes','No')
- datatype ENUM('N','C')
- category VARCHAR(50)
- Indexes

keyabiotic
- id INT(10)
- value VARCHAR(20)
- Indexes

country
- cntryid INT(11)
- isonum INT(11)
- isotwo VARCHAR(2)
- isothree VARCHAR(3)
- faothree VARCHAR(3)
- fips VARCHAR(2)
- wb VARCHAR(3)
- isofull VARCHAR(50)
- isoabbr VARCHAR(25)
- cont VARCHAR(10)
- scntry INT(11)
- ecntry INT(11)
- cchange INT(11)
- Indexes

studyderiveddata
- id INT(10)
- studyid INT(10)
- dataset INT(10)
- datarow INT(10)
- datacolumn VARCHAR(20)
- datavalue VARCHAR(150)
- shared TINYINT(1)
- userid INT(10)
- Indexes

studydatacolumn
- id INT(10)
- studyid INT(10)
- dataset INT(10)
- columnheader VARCHAR(20)
- datatype ENUM('dd','rd')
- Indexes

studyfile
- id INT(10)
- userid INT(10)
- studyid INT(10)
- filename VARCHAR(100)
- filenamegen VARCHAR(200)
- filepath VARCHAR(200)
- typeofdata ENUM('dd','rd','gd')
- Indexes

studydesign
- id INT(10)
- studyid INT(10)
- studysiteid INT(10)
- treatmentstructure VARCHAR(50)
- designstructure VARCHAR(50)
- plotsize VARCHAR(20)
- designfactor1 VARCHAR(20)
- designfactor2 VARCHAR(20)
- designfactor3 VARCHAR(20)
- designfactor4 VARCHAR(20)
- Indexes

studyrawdata
- id INT(10)
- studyid INT(10)
- dataset INT(10)
- datarow INT(10)
- datacolumn VARCHAR(20)
- datavalue VARCHAR(150)
- shared TINYINT(1)
- userid INT(10)
- Indexes

germplasmtype
- id INT(10)
- germplasmtype VARCHAR(20)
- description VARCHAR(50)
- Indexes

distributionandextension
- id INT(10)
- programid INT(5)
- projectid INT(5)
- germplasmname VARCHAR(50)
- yearextension VARCHAR(8)
- locationextension VARCHAR(50)
- countryextension VARCHAR(100)
- plantingarea DOUBLE(10,2)
- datasource VARCHAR(200)
- seedavailability INT(10)
- amountseeddistributed INT(10)
- numfarmersadopted INT(10)
- amountseedsproduced DOUBLE(10,2)
- userid INT(10)
- Indexes

studylocation
- id INT(5)
- studyid INT(10)
- dataset INT(11)
- locationid INT(11)
- Indexes

soiltype
- id INT(10)
- type VARCHAR(30)
- Indexes

studysite
- id INT(10)
- studyid INT(10)
- dataset INT(11)
- year VARCHAR(4)
- season VARCHAR(10)
- sitename VARCHAR(100)
- sitelocation VARCHAR(200)
- locationid INT(50)
- ecotypeid INT(5)
- soiltype VARCHAR(50)
- soilph VARCHAR(50)
- Indexes

plantingtype
- id INT(10)
- planting VARCHAR(20)
- Indexes

location
- id INT(10)
- locationname VARCHAR(100)
- country VARCHAR(50)
- province VARCHAR(100)
- region VARCHAR(100)
- altitude VARCHAR(50)
- latitude VARCHAR(50)
- weatherstation VARCHAR(50)
- userid INT(50)
- Indexes

keygrainquality
- id INT(10)
- value VARCHAR(20)
- Indexes

designstructure
- id INT(5)
- design VARCHAR(50)
- Indexes

studytype
- id INT(10)
- studytype VARCHAR(20)
- Indexes

ecotype
- id INT(10)
- ecotype VARCHAR(50)
- Indexes

keybiotic
- id INT(10)
- value VARCHAR(20)
- Indexes

studydataset
- id INT(255)
- studyid INT(255)
- title VARCHAR(255)
- datatype VARCHAR(100)
- Indexes

georef
- locid INT(11)
- llpn INT(11)
- lat DOUBLE
- lon DOUBLE
- alt DOUBLE
- llsource INT(11)
- ll_fmt INT(11)
- ll_datum INT(11)
- ll_uncert DOUBLE
- llref INT(11)
- lldate INT(11)
- lluid INT(11)
- Indexes