Introduction:

COWDUDE assumes you have access to and sufficient priveleges in the lab germplasm database. If you do not know your username and password to this database, COWDUDE will not work except for printing barcodes.

COWDUDE assumes you are using the Ross-Ibarra lab germplasm naming convention.   The basic idea is that each **accession** is named "RI" followed by a species abbreviation followed by 4 numbers, such as RIMPA0056 or RIL0001 or RIMMA0564. Individual samples from an accession are called **ID numbers** or IDs, and are made up of an accession name followed by a decimal and a number without padded zeros, such as RIMPA0056.1, RIMPA0056.11, RIL0001.37, etc. Each accession may have multiuple IDs, but each ID has only one accession. For naming schemes for more complex situations (field collections, selfed lines), see here.

COWDUDE manipulate the Samples table in the germplasm database. The Samples table is made up of the following columns:

ri_accession	accession number
ID	ID number
drybag	bag w/ silica gel where lyophilized tissue is stored
coldbox	box in -80 where extracted DNA is stored
status	**see below**
germinated_by	who germinated the seeds
germinated_date	when seeds were germinated
planted_by	who planted the seeds
planted_date	when seeds were planted
harvested_by	who harvested tissue
harvested_date	when tissue was harvested
lyophilized_by	who lyophilized tissue
lyophilized_date	when tissue was lyophilized
extracted_by	who extracted DNA
extracted_date	when DNA was extracted
ng_ul	ng per uL of DNA
260_280	260/280 quality score reading of DNA
gel_test	genomic band visible on a gel (pass/fail)
notes	any other information

Running COWDUDE:

Cowdude can be opened by double-clicking the cow icon in the /Applications folder. COWDUDE has two command-line options which do not work when double-clicking:

-v shows which version of COWDUDE is being run and exits the program
--toy which allows you to use the "toy" table in the mysql database for testing

When you are done using COWDUDE, it will Moo.

COWDUDE instructions:

I. Barcode

A. Making Barcodes

COWDUDE will print code 128 barcodes to a postscript file on your Desktop called labels.ps. This can be opened in Preview and directly printed on the lab inkjet onto labels. Make sure you use [avery labels 8167](#) (bought from VetMed) or something with identical format. Otherwise the barcodes will not line up on the stickers.

When instructed, paste in your set of labels. Make sure the list does not have an extra whitespace, as whitespace characters will be included in the barcode (e.g. "RIMPA0056 " is not the same as "RIMPA0056".

B. Barcode scanning

You can use the barcode scanner in one of 2 modes:

Plugged in to the dock:

In this case, open up whatever program you want the data to be put in (textwrangler, word, excel), and select that program as if you were going to type in the IDs. Start scanning, and the barcode reader will automatically "type" in the IDs of what you scan.

Mobile:

You can scan barcodes in the greenhouse (or the other side of the lab) and keep them in the scanner memory. However, the scanner memory dumps and is erased as soon as you put the scanner in the cradle. *So it is important that you open a program like excel or textwrangler BEFORE putting the scanner in its cradle or all the scans in memory will be lost.*

II.Insert

The insert option allows you to add new samples to the sample table. Usually this is done when germinating seeds. You have two options, either to paste a list of ID numbers you already have, or to generate ID numbers based on a set of accessions.

Paste. After pasting in your list of accessions COWDUDE will ask if you want to automatically update these to germinated. If you do, it will mark you as the germinated_by and today as the germinated_date for all IDs added. If you do not, it will insert the IDs with no additional information. COWDUDE will not insert IDs that already exist in the database, and will give an error and quit if you try to include certain badly formatted IDs.

Generate. If you only have a list of accessions, COWDUDE can generate the ID list for you. This can be done in **batch** or **individual** modes. In batch mode, all accessions are given the same number of IDs. This is useful if you are germinating say 6 seeds each of 20 different accessions — paste in the accession names, and COWDUDE will do the rest. Individual mode lets you enter a different number of IDs for each accession.

After inserting new IDs, COWDUDE will allow you to automatically generate barcodes for the same IDs.

In either batch or individual cases, COWDUDE will start numbering based on the most recent accession in the database. It is wise to generate barcodes for these immediately so you have a list of the IDs you have created.

III.Query

Query lets you paste in a list of accessions and find out what are the most recent IDs for each accession. It also reports if an accession is not in the database currently.

IV.Update

Update mode in COWDUDE lets you update sample status, or add data on DNA quantity/quality.

A.Sample Status

Samples in the database have one of several possible status labels:

NULL   no information on samples status
DEAD   was germinated/planted but did not survive
GERMINATED   seeds put on petri dishes for germination
PLANTED   seedlings/seeds put in soil after germination
HARVESTED   tissues harvested and placed in -80
LYOPHILIZED   harvested tissue is dried and put in bags for storage
EXTRACTED   dried DNA is extracted and genomic DNA is in -80

You cannot choose the NULL option for updating.

COWDUDE will automatically enter your name and today's date for the _by and _date columns when you update samples to harvested, planted, genotyped, lyophilized, or extracted.

If you choose lyophilized or extracted, COWDUDE will force you to enter information on the whereabouts of the samples. Be prepared to paste in data one bag/box at a time and have that information handy.

If you choose harvested, COWDUDE gives you the option of automatically marking all nonharvested IDs from the same accession as dead.

COWDUDE will alert you if some IDs could not be updated. This is usually due to formatting error with the ID name.

B.DNA data

COWDUDE can let you enter DNA data as well. To do so, you will need to set up a tab-delimited text file. The first row needs to have headers. The first header MUST be "ID". You can include one, two, or three of the following columns: "ng_ul", "260_280", or "gel_test" in any order. COWDUDE may have problems with missing data, so only include samples/columns for which you have data. On each additional line of the file, you need to have the sample ID (in the ID column) and then data for each of the other columns.

COWDUDE will ask you for the name of the file. It must be on your Desktop.