

Introduction:

COWDUDE assumes you have access to and sufficient privileges 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 multiple IDs, but each ID has only one accession. For naming schemes for more complex situations (field collections, selfed lines), see [here](#).

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

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

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").

### 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 `germianted_by` and today as the `germinated_date` for all IDs added. If you do not, it will insert the IDs with no additional information.

**\*\*NOTE:** COWDUDE v1.0 will not accept certain badly formatted ID numbers.

**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.

**\*\*NOTE:** COWDUDE v1.0 starts all numbering at 1. If RIMPA0056.1 already exists, you risk overwriting it with a new insert or update.

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

### III. 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.