Extraction
APCL18_001 - APCL18_094
2018-06-19

This is a script for adding samples that are not in the laboratory database and have not been extracted
source("scripts/lab_helpers.R")

obtain a list of all clownfish sample ids from the Leyte database

```
# connect to leyte fieldwork db
leyte <- read_db("Leyte")
# import fish table
# select down to only sample_id numbers and remove any rows without a sample
fish <- leyte %>% tbl("clownfish") %>%
  select(sample_id) %>%                    # select only the column sample_id
  filter(!is.na(sample_id)) %>%            # remove any non-sample observations
  distinct(sample_id) %>%                      # remove any repeat sample_ids (this should not be ne
  collect()

# make sure each sample_id is only represented once
fish <- distinct(fish)
```

Because we are targeting a known range of fin clips, going to comment out the following portion and select the range

```
work <- fish %>%
  filter(sample_id >= "APCL18_001", sample_id <= "APCL18_094")
```

This is set up to handle one plate at a time.

```
# define wells
plate <- data.frame(row = rep(LETTERS[1:8], 12), col = unlist(lapply(1:12, rep, 8))) %>%
  mutate(sample_id = ifelse(row == "G" & col == 2, "XXXX", NA), #normally this one is D2 but I forgot t
    sample_id = ifelse(row == "E" & col == 8, "XXXX", sample_id))

samples <- plate %>%
  filter(is.na(sample_id)) %>%
  select(-sample_id)

plate <- anti_join(plate, samples, by = c("row", "col"))

samples <- cbind(samples, work)

plate <- rbind(plate, samples)


#### make a plate map of sample IDs (for knowing where to place fin clips) ####
  platemap <- as.matrix(reshape2::acast(plate, plate[,1] ~ plate[,2]), value.var = plate[,3])
```

```
## Using sample_id as value column: use value.var to override.
```

```r
knitr::kable(platemap, booktabs = T) %>%
  kable_styling(latex_options = "scale_down")
```

	1	2	3	4	5	6	7	8	9	10	11	12
A	APCL18_001	APCL18_009	APCL18_016	APCL18_024	APCL18_032	APCL18_040	APCL18_048	APCL18_056	APCL18_063	APCL18_071	APCL18_079	APCL18_087
B	APCL18_002	APCL18_010	APCL18_017	APCL18_025	APCL18_033	APCL18_041	APCL18_049	APCL18_057	APCL18_064	APCL18_072	APCL18_080	APCL18_088
C	APCL18_003	APCL18_011	APCL18_018	APCL18_026	APCL18_034	APCL18_042	APCL18_050	APCL18_058	APCL18_065	APCL18_073	APCL18_081	APCL18_089
D	APCL18_004	APCL18_012	APCL18_019	APCL18_027	APCL18_035	APCL18_043	APCL18_051	APCL18_059	APCL18_066	APCL18_074	APCL18_082	APCL18_090
E	APCL18_005	APCL18_013	APCL18_020	APCL18_028	APCL18_036	APCL18_044	APCL18_052	XXXX	APCL18_067	APCL18_075	APCL18_083	APCL18_091
F	APCL18_006	APCL18_014	APCL18_021	APCL18_029	APCL18_037	APCL18_045	APCL18_053	APCL18_060	APCL18_068	APCL18_076	APCL18_084	APCL18_092
G	APCL18_007	XXXX	APCL18_022	APCL18_030	APCL18_038	APCL18_046	APCL18_054	APCL18_061	APCL18_069	APCL18_077	APCL18_085	APCL18_093
H	APCL18_008	APCL18_015	APCL18_023	APCL18_031	APCL18_039	APCL18_047	APCL18_055	APCL18_062	APCL18_070	APCL18_078	APCL18_086	APCL18_094

ONLY DO THIS ONCE ### generate extract numbers for database

```r
lab <- read_db("Laboratory")
extracted <- lab %>% tbl("extraction") %>%
  summarise(last = max(extraction_id)) %>%
  collect() %>%
  mutate(last = substr(last, 2,5))

plate <- plate %>%
  mutate(well = 1:nrow(plate)) %>%
  mutate(extraction_id = paste("E", well + as.numeric(extracted$last), sep = "")) %>%
  mutate(well = paste(row, col, sep = "")) %>%
  mutate(notes = "lysed 2018-06-19",
    method = "DNeasy96",
    final_vol = "200")

plate_name <- plate %>%
  summarise(first = min(extraction_id),
    last = max(extraction_id))

# make a platemap with extraction ids ####
map <- plate %>%
  select(row, col, extraction_id)
  platemap <- as.matrix(reshape2::acast(map, map[,1] ~ map[,2]), value.var = map[,3])
```

```
## Using extraction_id as value column: use value.var to override.
```

```r
knitr::kable(platemap, booktabs = T) %>%
  kable_styling()
```

	1	2	3	4	5	6	7	8	9	10	11	12
A	E4553	E4561	E4568	E4576	E4584	E4592	E4600	E4608	E4615	E4623	E4631	E4639
B	E4554	E4562	E4569	E4577	E4585	E4593	E4601	E4609	E4616	E4624	E4632	E4640
C	E4555	E4563	E4570	E4578	E4586	E4594	E4602	E4610	E4617	E4625	E4633	E4641
D	E4556	E4564	E4571	E4579	E4587	E4595	E4603	E4611	E4618	E4626	E4634	E4642
E	E4557	E4565	E4572	E4580	E4588	E4596	E4604	E4551	E4619	E4627	E4635	E4643
F	E4558	E4566	E4573	E4581	E4589	E4597	E4605	E4612	E4620	E4628	E4636	E4644
G	E4559	E4552	E4574	E4582	E4590	E4598	E4606	E4613	E4621	E4629	E4637	E4645
H	E4560	E4567	E4575	E4583	E4591	E4599	E4607	E4614	E4622	E4630	E4638	E4646

```
plate <- plate %>%
  mutate(plate = paste(plate_name$first, plate_name$last, sep = "-")) %>%
  select(-row, -col)
```

import the extract_list into the database

Make sure you have created your output PDF for this labwork before sending to the database

```
rm(lab)
lab <- write_db("Laboratory")
```

Loading required package: DBI

```
# dbWriteTable(lab, "extraction", plate, row.names = F, overwrite = F, append = T)

dbDisconnect(lab)
```

[1] TRUE

```
rm(lab)
```