Extraction plan for APCL18_565-APCL18_658

2018-07-26

This is a script for adding samples that are not in the laboratory database and have not been extracted. This is set up to handle one plate at a time.

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

```r
# 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 only the column sample_id
  select(sample_id) %>%
  # remove any non-sample observations
  filter(!is.na(sample_id)) %>%
  distinct(sample_id) %>%
  # remove any repeat sample_ids (this should not be needed)
  collect()

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

Select the range of samples in the plate

```r
work <- fish %>%
  filter(sample_id >= params$first, sample_id <= params$last)

# define wells
plate <- data.frame(row = rep(LETTERS[1:8], 12), col = unlist(lapply(1:12, rep, 8))) %>%
  mutate(sample_id = ifelse(row == "D" & col == 2, "XXXX", NA),
    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) %>%
  arrange(col, row)
```

Make a plate map of sample IDs (for knowing where to place fin clips)

```r
platemap <- as.matrix(reshape2::acast(plate, plate[,1] ~ plate[,2]), value.var = plate[,3])
knitr::kable(platemap, booktabs = T) %>%
  # use scale_down to get map to fit within the bounds of the pdf
  kable_styling(latex_options = "scale_down")
```

	1	2	3	4	5	6	7	8	9	10	11	12
A	APCL18_565	APCL18_573	APCL18_580	APCL18_588	APCL18_596	APCL18_604	APCL18_612	APCL18_620	APCL18_627	APCL18_635	APCL18_643	APCL18_651
B	APCL18_566	APCL18_574	APCL18_581	APCL18_589	APCL18_597	APCL18_605	APCL18_613	APCL18_621	APCL18_628	APCL18_636	APCL18_644	APCL18_652
C	APCL18_567	APCL18_575	APCL18_582	APCL18_590	APCL18_598	APCL18_606	APCL18_614	APCL18_622	APCL18_629	APCL18_637	APCL18_645	APCL18_653
D	APCL18_568	XXXX	APCL18_583	APCL18_591	APCL18_599	APCL18_607	APCL18_615	APCL18_623	APCL18_630	APCL18_638	APCL18_646	APCL18_654
E	APCL18_569	APCL18_576	APCL18_584	APCL18_592	APCL18_600	APCL18_608	APCL18_616	XXXX	APCL18_631	APCL18_639	APCL18_647	APCL18_655
F	APCL18_570	APCL18_577	APCL18_585	APCL18_593	APCL18_601	APCL18_609	APCL18_617	APCL18_624	APCL18_632	APCL18_640	APCL18_648	APCL18_656
G	APCL18_571	APCL18_578	APCL18_586	APCL18_594	APCL18_602	APCL18_610	APCL18_618	APCL18_625	APCL18_633	APCL18_641	APCL18_649	APCL18_657
H	APCL18_572	APCL18_579	APCL18_587	APCL18_595	APCL18_603	APCL18_611	APCL18_619	APCL18_626	APCL18_634	APCL18_642	APCL18_650	APCL18_658

ONLY DO THIS ONCE

Generate extract numbers for database

```
lab <- read_db("Laboratory")
extracted <- lab %>% tbl("extraction") %>%
  summarise(last = max(extraction_id, na.rm = T)) %>%
  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(method = "DNeasy96",
    final_vol = "200")

plate_name <- plate %>%
  summarise(first = min(extraction_id),
    last = max(extraction_id, na.rm = T))
```

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.
```

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

	1	2	3	4	5	6	7	8	9	10	11	12
A	E5127	E5135	E5143	E5151	E5159	E5167	E5175	E5183	E5191	E5199	E5207	E5215
B	E5128	E5136	E5144	E5152	E5160	E5168	E5176	E5184	E5192	E5200	E5208	E5216
C	E5129	E5137	E5145	E5153	E5161	E5169	E5177	E5185	E5193	E5201	E5209	E5217
D	E5130	E5138	E5146	E5154	E5162	E5170	E5178	E5186	E5194	E5202	E5210	E5218
E	E5131	E5139	E5147	E5155	E5163	E5171	E5179	E5187	E5195	E5203	E5211	E5219
F	E5132	E5140	E5148	E5156	E5164	E5172	E5180	E5188	E5196	E5204	E5212	E5220
G	E5133	E5141	E5149	E5157	E5165	E5173	E5181	E5189	E5197	E5205	E5213	E5221
H	E5134	E5142	E5150	E5158	E5166	E5174	E5182	E5190	E5198	E5206	E5214	E5222

```
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)
```

```
## [1] TRUE
```

```
dbDisconnect(lab)
```

```
## [1] TRUE
```

```
rm(lab)
```

Load fin clips