Preparator and catalog owner contributions

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Building off Jessie's approach, let's sum preparator and catalog owner contributions to the "full" (multitaxa) blood dataset.

We start by loading libraries, set our working directory, and read in the data:

```
library(tidyverse, quietly = TRUE)
setwd("~/Dropbox/andean_range_limits/data/")
full <- read.csv("blood_data.csv")
```

Next, we'll count up the total number specimens each contributor has assigned to their name as 1) catalog owner and 2) preparator:

```
cat.num.count <- full %>% group_by(`Cat.owner`) %>% summarise(count = length(`Cat.owner`))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
prep.num.count <- full %>% group_by(`Preparator`) %>% summarise(count = length(`Preparator`))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

We'll sort this in descending order, and merge dataframes so each row totals catalog specimens and prepared specimens for a single person:

```
cat.num.count <- cat.num.count %>% arrange(desc(count))
prep.num.count <- prep.num.count %>% arrange(desc(count))
colnames(cat.num.count) <- c("name", "catalog_specimen_count")
colnames(prep.num.count) <- c("name", "prepared_specimen_count")
export <- inner_join(cat.num.count, prep.num.count, by = "name")
```

What does this file look like?

```
head(export)
```

```
## # A tibble: 6 x 3
##   name                catalog_specimen_count prepared_specimen_count
##   <chr>                                <int>                   <int>
## 1 Emil Bautista O.                      1762                    1810
## 2 Donna C. Schmitt                       367                     366
## 3 C. Jonathan Schmitt                    340                     300
## 4 Dora Susanibar C.                      329                     320
## 5 Andrew B. Johnson                      319                     209
## 6 Phred M. Benham                        258                     264
```

Last, we'll write it out as a .csv file for Chris:

```
write.csv(export, "~/Dropbox/andean_range_limits/data/total_blood_data_contributions.csv")
```