

T-cell survival: Tem vs Tcm

Fetch metadata

```
meta <- rbind(tibble(fname = list.files("../data/cellpop/d120_data"),
  fpath = paste0("../data/cellpop/d120_data/", fname), subset = "full",
  day = 120), tibble(fname = list.files("../data/cellpop/d60_data"),
  fpath = paste0("../data/cellpop/d60_data/", fname), subset = "full",
  day = 60), tibble(fname = list.files("../data/cellpop/DLI_TemTcm/Tcm_data"),
  fpath = paste0("../data/cellpop/DLI_TemTcm/Tcm_data/", fname),
  subset = "Tcm", day = 0), tibble(fname = list.files("../data/cellpop/DLI_TemTcm/Tem_data"),
  fpath = paste0("../data/cellpop/DLI_TemTcm/Tem_data/", fname),
  subset = "Tem", day = 0)) %>%
mutate(patient = str_split_fixed(fname, "_", 2)[, 1])
```

Load data

```
meta %>%
  group_by(fpath, fname, subset, day, patient) %>%
  group_modify(~read_tsv(.y$fpath)) %>%
  mutate(cdr3 = ifelse(is.na(nSeqCDR3), CDR3.nucleotide.sequence,
    nSeqCDR3), v = ifelse(is.na(bestVGene), V.gene, bestVGene),
    count = ifelse(is.na(cloneCount), Read.count, cloneCount)) %>%
  mutate(tcr_key = paste(v, cdr3)) %>%
  group_by(subset, day, patient, tcr_key) %>%
  summarise(count = sum(count)) %>%
  ungroup -> data
```

Process data: count singletons and doubletons, select pre- and post-transplant datasets and merge them, annotate Tem and Tcm

```
data <- data %>%
  mutate(quantile = case_when(count == 1 ~ "singleton", count ==
    2 ~ "doubleton", .default = "large")) %>%
  mutate(quantile = factor(quantile, levels = c("singleton",
    "doubleton", "large")))

data.pre <- data %>%
  filter(day == 0) %>%
  select(-day, -count)
data.post <- data %>%
  filter(day != 0) %>%
  select(-subset, -count)

data.pre.m <- data.pre %>%
  group_by(subset) %>%
  group_modify(~left_join(.x, data.post %>%
    select(-quantile), by = c("patient", "tcr_key"))) %>%
  mutate(day = ifelse(is.na(day), "Missing", day))
```

```
## Warning in left_join(.x, data.post %>% select(-quantile), by = c("patient", : Each row in `x` is exp
```

```
## i Row 1816 of `x` matches multiple rows.
## i If multiple matches are expected, set `multiple = "all"` to silence this
## warning.

## Warning in left_join(.x, data.post %>% select(-quantile), by = c("patient", : Each row in `x` is expected to match
## i Row 138 of `x` matches multiple rows.
## i If multiple matches are expected, set `multiple = "all"` to silence this
## warning.
```

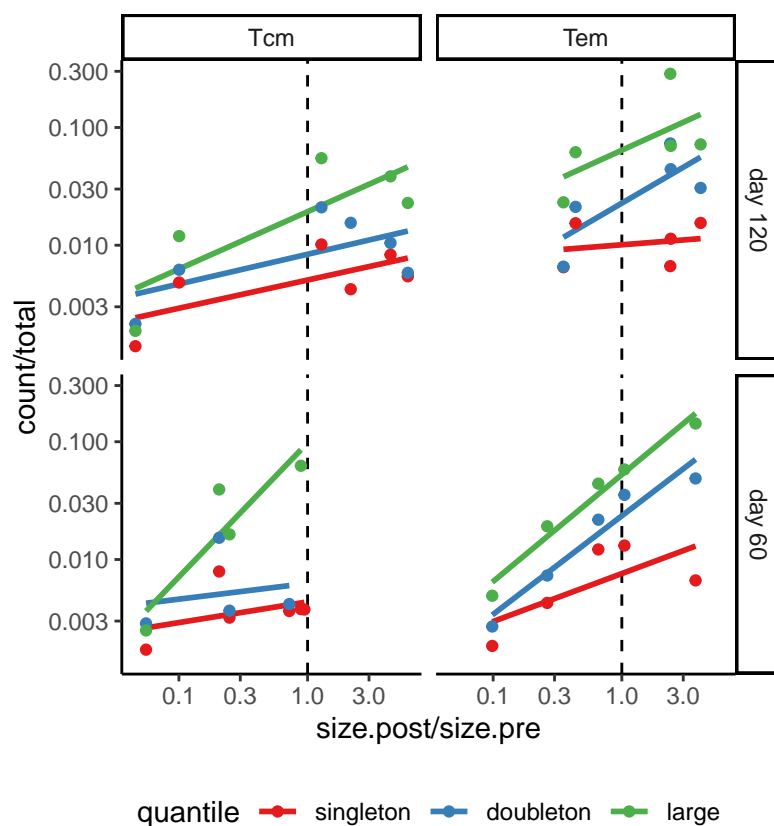
```
data.pre.s <- data.pre.m %>%
  group_by(patient, subset, quantile, day) %>%
  summarise(count = n() + 1) %>%
  left_join(data.pre %>%
    group_by(subset, patient, quantile) %>%
    summarise(total = n() + 1) %>%
    group_by(subset, patient) %>%
    mutate(size.pre = sum(total))) %>%
  left_join(data.post %>%
    group_by(patient, day = as.character(day)) %>%
    summarise(size.post = n() + 1))
```

```
## `summarise()` has grouped output by 'patient', 'subset', 'quantile'. You can
## override using the `.groups` argument.
## `summarise()` has grouped output by 'subset', 'patient'. You can override using
## the `.groups` argument.
## Joining with `by = join_by(patient, subset, quantile)`
## `summarise()` has grouped output by 'patient'. You can override using the
## `.groups` argument.
## Joining with `by = join_by(patient, day)`
```

Linear modelling of fraction donor sampled vs donor/receipient sample size, compare Tem and Tcm

```
data.pre.s %>%
  filter(day != "Missing") %>%
  mutate(day = paste("day", day)) %>%
  ggplot(aes(x = size.post/size.pre, y = count/total, color = quantile,
    group = quantile)) + geom_vline(linetype = "dashed",
    xintercept = 1) + geom_smooth(method = "lm", se = F) + geom_point() +
  scale_color_brewer(palette = "Set1") + facet_grid(day ~ subset) +
  scale_x_log10() + scale_y_log10() + theme_classic() + theme(aspect = 1,
    legend.position = "bottom")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



```
lm(f ~ day + subset + f0, data.pre.s %>%
  filter(day != "Missing") %>%
  mutate(f = log10(count/total), f0 = log10(size.post/size.pre))) %>%
summary
```

```
##
## Call:
## lm(formula = f ~ day + subset + f0, data = data.pre.s %>% filter(day !=
##   "Missing") %>% mutate(f = log10(count/total), f0 = log10(size.post/size.pre)))
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.71290 -0.33466 -0.04139  0.27348  0.96830
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.99515    0.09010  -22.143  < 2e-16 ***
## day60       -0.03146    0.11351   -0.277   0.7827
## subsetTem    0.33094    0.10997    3.009   0.0039 **
## f0           0.40320    0.09047    4.457  3.95e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4179 on 57 degrees of freedom
## Multiple R-squared:  0.4095, Adjusted R-squared:  0.3784
## F-statistic: 13.17 on 3 and 57 DF,  p-value: 1.208e-06
```

Show well-known fact of repertoire reconstitution. Note that not all donors have paired samples

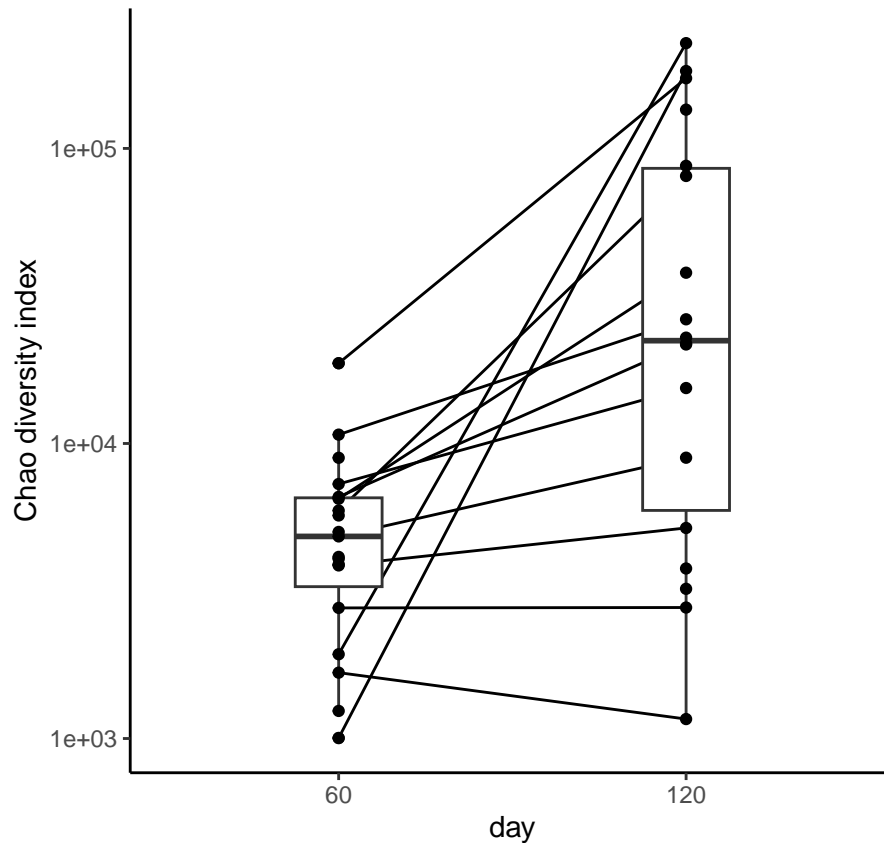
```

data.post.s <- data.post %>%
  group_by(patient, day, quantile) %>%
  summarise(count = n()) %>%
  group_by(patient, day) %>%
  summarise(divChao = sum(count) + count[which(quantile ==
    "singleton")]^2/2/count[which(quantile == "doubleton")])

## `summarise()` has grouped output by 'patient', 'day'. You can override using
## the `.groups` argument.
## `summarise()` has grouped output by 'patient'. You can override using the
## `.groups` argument.

data.post.s %>%
  ggplot(aes(x = as.factor(day), y = divChao)) + geom_line(aes(group = patient)) +
  geom_boxplot(aes(group = day), width = 0.25) + geom_point() +
  scale_y_log10("Chao diversity index") + xlab("day") + theme_classic() +
  theme(aspect = 1)

```



```

t.test(I(log10(divChao)) ~ day, data.post.s)

##
## Welch Two Sample t-test
##
## data: I(log10(divChao)) by day
## t = -3.9501, df = 23.541, p-value = 0.0006149
## alternative hypothesis: true difference in means between group 60 and group 120 is not equal to 0
## 95 percent confidence interval:
## -1.0866824 -0.3403215

```

```
## sample estimates:
## mean in group 60 mean in group 120
##      3.637329      4.350831
# END
```