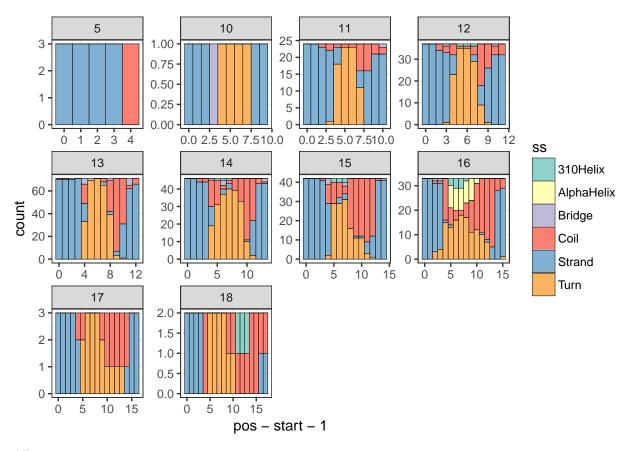
Secondary structure of TCR CDR regions

library(dplyr)

```
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
       intersect, setdiff, setequal, union
library(ggplot2)
Load TCR V-D-J mapping for our PDBs
df.meta = read.table("tcr.annotations.txt", header = T, sep = "\t") %>%
 filter(region %in% c("CDR1", "CDR2", "CDR3"))
Load data processed with STRIDE software, see https://en.wikipedia.org/wiki/STRIDE and https://en.
wikipedia.org/wiki/DSSP_(hydrogen_bond_estimation_algorithm). See DSSP classification section in
https://en.wikipedia.org/wiki/Protein secondary structure for glossary
df.ss = data.frame()
for (f in list.files('data/')) {
  .cmd = paste0('zcat data/', f, ' | grep "^ASG"')
  .df.ss.tmp = read.table(pipe(.cmd), header = F) %>%
               select(V2, V3, V5, V7, V11)
  colnames(.df.ss.tmp) = c("res", "pdb_chain_id", "pos", "ss", "pdb_id")
  .df.ss.tmp$pdb_id = tolower(.df.ss.tmp$pdb_id)
  df.ss = rbind(df.ss, .df.ss.tmp)
df.ss$pos = as.integer(df.ss$pos)
Merge with CDR1-3 mapping
df.ss.1 = merge(df.meta, df.ss, by = c("pdb_id", "pdb_chain_id"), all.y = T) %>%
filter(pos >= start+1 & pos <= end)</pre>
df.ss.1$len_tcr = with(df.ss.1, end - start)
Distribution of various secondary structure classifications for CDR3
ggplot(df.ss.1 %>% filter(region=="CDR3"), aes(x=pos - start - 1, fill = ss)) +
  geom_histogram(binwidth = 1, color = "black", size = 0.1) +
  facet_wrap(~len_tcr, scales = "free") +
  scale_fill_brewer(palette = "Set3") +
  theme_bw()
```



All regions

```
ggplot(df.ss.1, aes(x=pos - start - 1, fill = ss)) +
  geom_histogram(binwidth = 1, color = "black", size = 0.1) +
  facet_wrap(~len_tcr, scales = "free") +
  scale_fill_brewer(palette = "Set3") +
  theme_bw()
```

