16S rRNA V3-V4 Target Region

Nate Olson

2017-02-23

```
variable_regions <- data_frame(region_id = rep(paste0("V",c(1:9)),2),
                               pos = c(8, 95, 305, 486, 745, 884,
                                       1028, 1179, 1371,
                                       96, 306, 487, 746, 885,
                                           1029, 1180, 1372, 1468))
variable_region_id <- variable_regions %>%
    group_by(region_id) %>% summarise(pos = mean(pos)) %>%
    mutate(y = 0.5)


primer_df <- data_frame(region_type = "amplicon",
                        region_id = c("341F","806R"),
                        pos_str = c(341, 785),
                        pos_end = c(357, 805)) %>%
    gather("str_end","pos", -region_id, -region_type)

read_df <- frame_data(
                ~region_id, ~str_end, ~pos, ~ymin, ~ymax,
                  "F-Read",    "str",  341,     1,     2,
                  "F-Read",    "ovr",  505,     1,     2,
                  "F-Read",    "end",  641,     1,     1,
                  "R-Read",    "str",  505,     2,     2,
                  "R-Read",    "ovr",  641,     1,     2,
                  "R-Read",    "end",  805,     1,     2
)

read_id <- read_df %>% filter(str_end != "ovr") %>%
    group_by(region_id) %>% summarise(pos = mean(pos))
```

```
ggplot(variable_regions) +
    geom_ribbon(data = read_df,
                aes(x = pos, ymin = ymin, ymax = ymax,
                    fill = region_id)) +
    geom_area(data = primer_df,
                aes(x = pos, y = 1, fill = region_id)) +
    geom_area(aes(x = pos, y = 1, group = region_id),
              color = "black", alpha = 0.10) +
    geom_text(data = variable_region_id,
              aes(x = pos, y= y, label = region_id)) +

    geom_text(data = read_id,
              aes(x = pos, y= 1.5, label = region_id)) +
    theme_void() +
    labs(fill = "Primers and Reads")
```

```
ggsave("../img/pcr_target_V34.png", width = 8, height = 3)
```

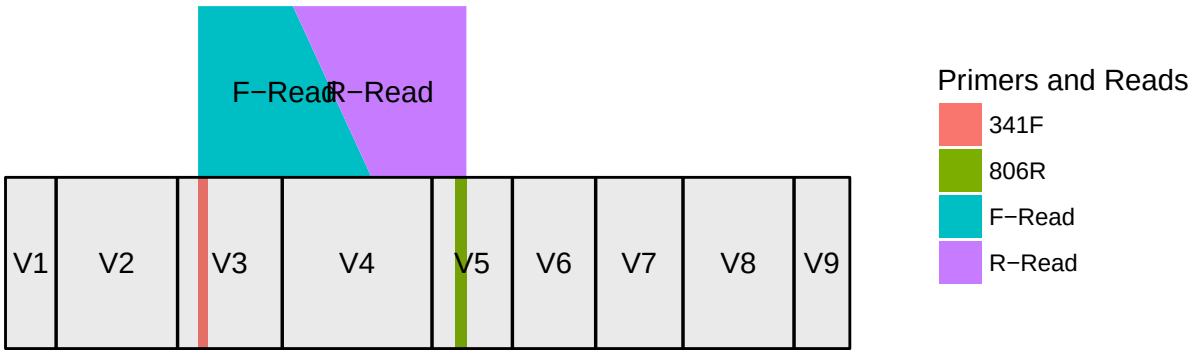

Figure 1: Diagram of forward and reverse reads relative to 16S rRNA variable region. Diagonal in forward and reverse reads represent overlap region. Forward (341F), and reverse (806R) primers indicates by vertical bars in variable regions V3 and V5 respecively.

Session information

```
s_info <- devtools::session_info()
print(s_info$platform)
```

```
##  setting  value
##  version  R version 3.3.2 (2016-10-31)
##  system   x86_64, darwin15.6.0
##  ui       unknown
##  language (EN)
##  collate  en_US.UTF-8
##  tz       America/New_York
##  date     2017-02-23
```

```
s_info$packages %>% filter(`*` == "*") %>% select(-`*`) %>%
      knitr::kable()
```

package	version	date	source
dplyr	0.5.0	2016-06-24	CRAN (R 3.3.2)
ggplot2	2.2.1	2016-12-30	CRAN (R 3.3.2)
purrr	0.2.2	2016-06-18	CRAN (R 3.3.1)
readr	1.0.0	2016-08-03	CRAN (R 3.3.1)
tibble	1.2	2016-08-26	CRAN (R 3.3.1)
tidyr	0.6.1	2017-01-10	CRAN (R 3.3.2)
tidyverse	1.1.1	2017-01-27	CRAN (R 3.3.2)