gasExchangeR

The goal of gasExchangeR is to help exercise physiologist more easily analyze gas exchange data and to provide more directly control when doing so. The overview of the process of analyzing gas exchange data involves importing the data, identifying and removing outliers, interpolating if desired, and finally averaging the data. Afterwards then one can determine ventilatory thresholds, VO2max, and other important values.

Installation

You can install the development version of gasExchangeR from GitHub with:

```
# install.packages("devtools")
devtools::install_github("ahesse2567/gasExchangeR")
```

Development notes

The gasExchangeR package is part of Anton Hesse's PhD dissertation at the University of Minnesota-Twin Cities. Please expect changes and improvements if you use this package, and please submit feedback if you encounter bugs or have suggestions.

Early acknowledgemets and other recommended packages

This package expands on the work by Felipe Mattioni Maturana (https://orcid.org/0000-0002-4221-6104). Specifically, his work on the whippr and lacater packages. gasExchangeR focuses more on graded exercise testing than VO2 kinetics; it also emphasizes ventilatory breakpoint algorithms.

Using this package to find ventilatory thresholds

Many exercise studies require finding the first and second ventilatory thresholds (VT1 & VT2). However, breath-by-breath data is highly variable and requires some cleaning prior to finding these thresholds.

```
# Load libraries
library(gasExchangeR)
library(tidyverse)
library(janitor)
```

Data Processing

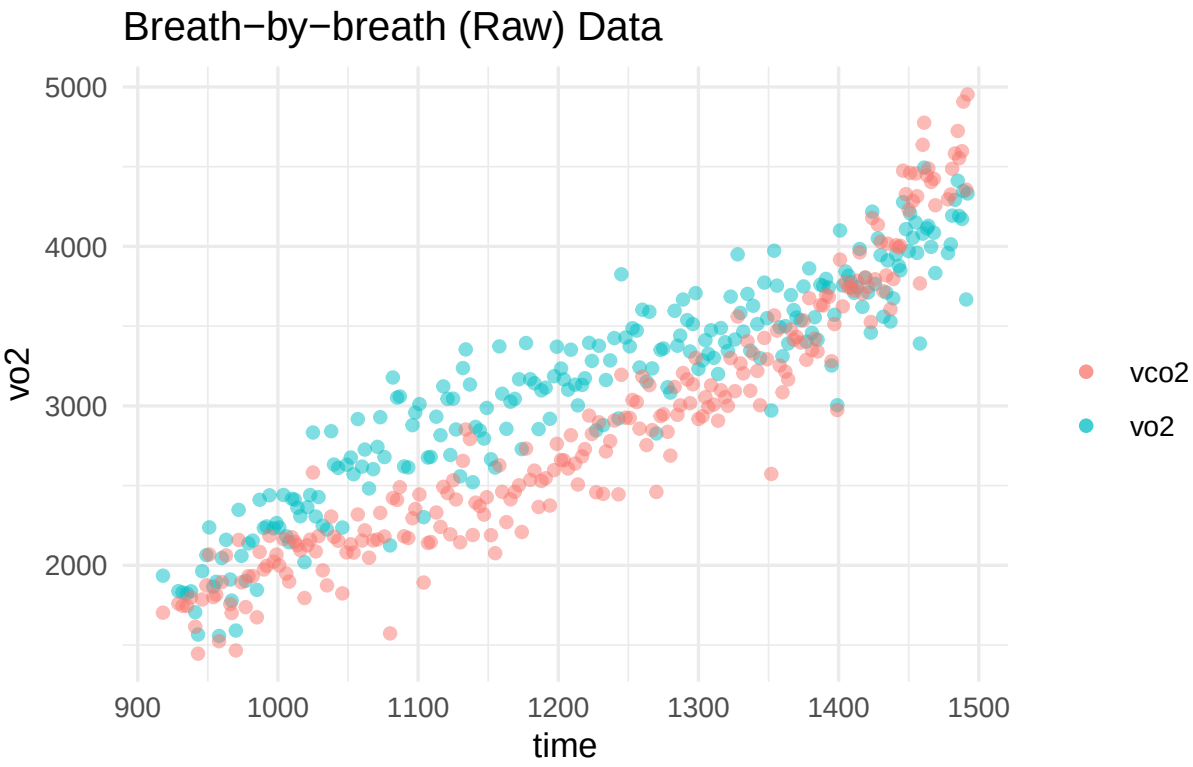
```
# read in raw data
file_lines <- readLines("inst/extdata/Anton_vo2max.txt")
df_raw <- read.table(textConnection(file_lines[-2]), header = TRUE, sep="\t")

# initial data tidying
df_unavg <- df_raw %>%
    as_tibble() %>%
    clean_names() %>%
    separate(`time`, into = c("m1", "s1"), sep = ":") %>%
    separate(ex_time, into = c("m2", "s2"), sep = ":") %>%
    separate(time_clock,
             into = c("h3", "m3", "s3"),
             sep = ":") %>%
    mutate(across(where(is.character), as.numeric)) %>%
    mutate(time = (m1*60 + s1), .keep = "unused") %>%
    mutate(ex_time = (m2*60 + s2 ), .keep = "unused") %>%
    mutate(clock_time = hms::hms(s3, m3, h3), .keep = "unused") %>%
    relocate(contains("time")) %>%
    filter(!is.na(ex_time)) %>%
    filter(speed >= 4.5 & ex_time >= 750) %>%
    select(-time) %>%
    rename(time = ex_time,
           vo2_kg = vo2,
           vo2 = vo2_1,
           ve = ve_btps) %>%
    # calculate common variables
    mutate(ve_vo2 = ve / vo2 * 1000,
           ve_vco2 = ve/vco2*1000,
           excess_co2 = vco2^2 / vo2 - vco2)
```

Plotting the raw data

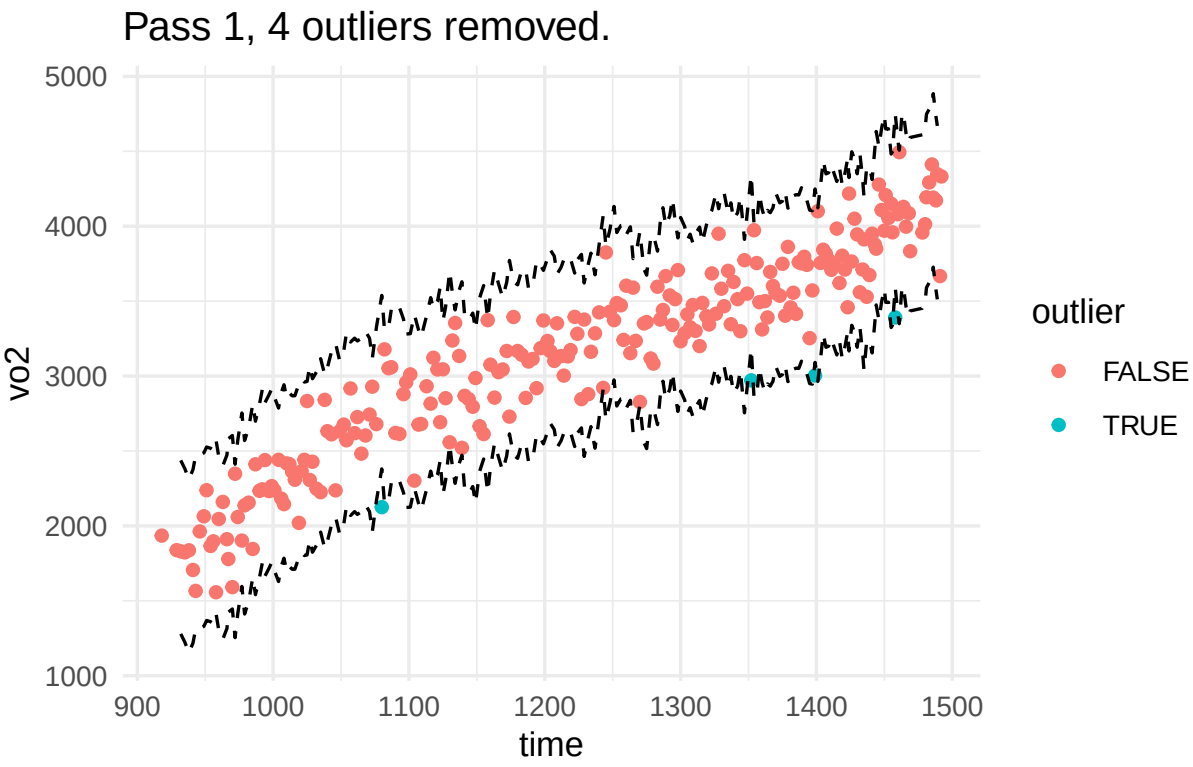
```
ggplot(data = df_unavg, aes(x = time)) +
  geom_point(aes(y = vo2, color = "vo2"), alpha = 0.5) +
  geom_point(aes(y = vco2, color = "vco2"), alpha = 0.5) +
  scale_color_manual(values = c("vo2" = "red", "vco2" = "blue")) +
  theme_minimal() +
  ggtitle("Breath-by-breath (Raw) Data") +
  scale_color_discrete(name = "", labels = c("vo2" = "vo2", "vco2" = "vco2"))
```

```
#> Scale for colour is already present.
#> Adding another scale for colour, which will replace the existing scale.
```



The raw data is obviously noisy. We will first use a rolling-breath average with absolute VO2 values to remove outliers.

```
df_unavg_no_outliers <- df_unavg %>%
    ventilatory_outliers(outlier_cols = "vo2", max_passes = 1,
                         plot_outliers = TRUE)
```

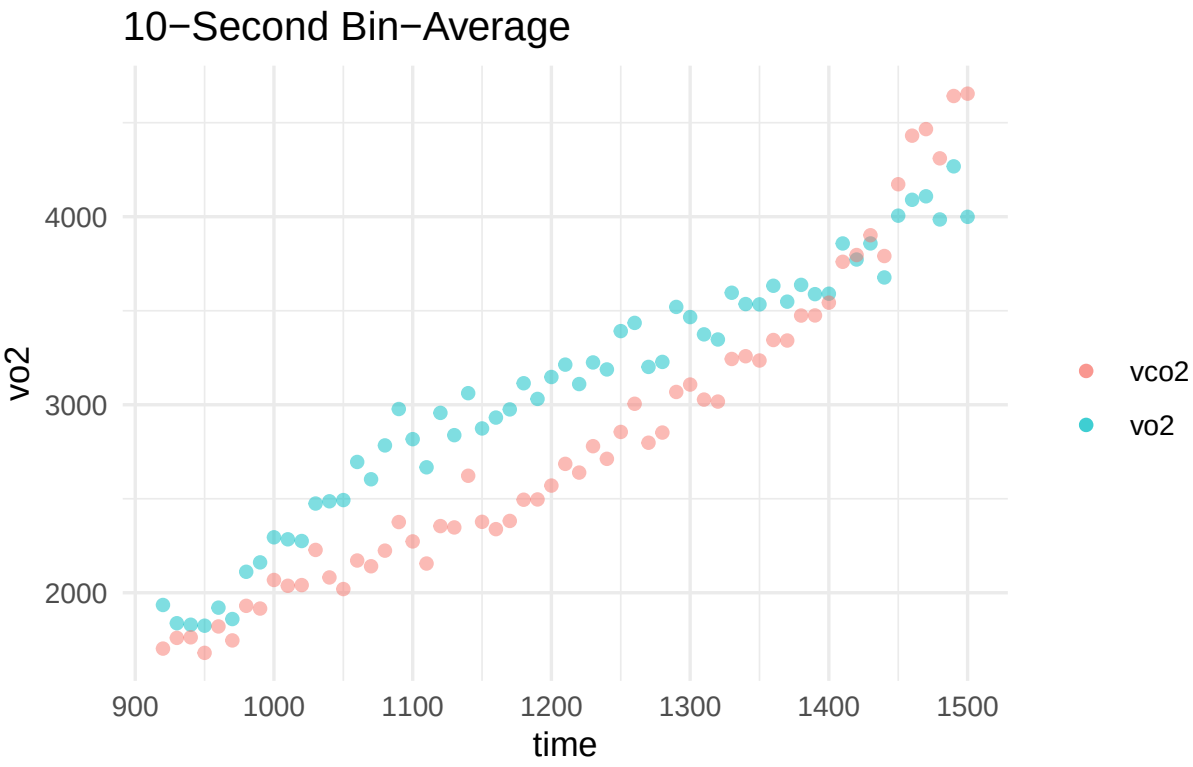



```
#> 4 outliers removed at indicies 62, 170, 193, 225
```

Removing outliers helps, but some averaging is also required.

```
df_avg <- df_unavg_no_outliers %>%
    avg_exercise_test(type = "time", subtype = "bin", bin_w = 10)

ggplot(data = df_avg, aes(x = time)) +
  geom_point(aes(y = vo2, color = "vo2"), alpha = 0.5) +
  geom_point(aes(y = vco2, color = "vco2"), alpha = 0.5) +
  scale_color_manual(values = c("vo2" = "red", "vco2" = "blue")) +
  theme_minimal() +
  ggtitle("10-Second Bin-Average") +
  scale_color_discrete(name = "", labels = c("vo2" = "vo2", "vco2" = "vco2"))
#> Scale for colour is already present.
#> Adding another scale for colour, which will replace the existing scale.
```

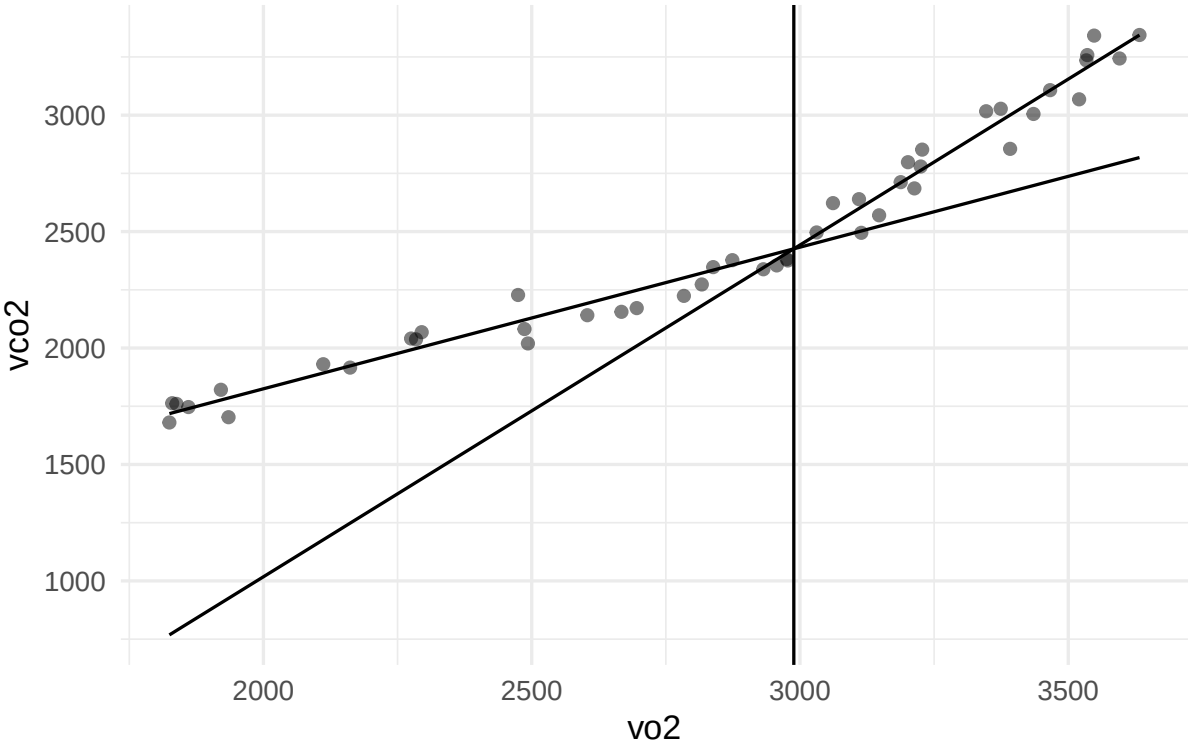


Finding Ventilatory Thresholds

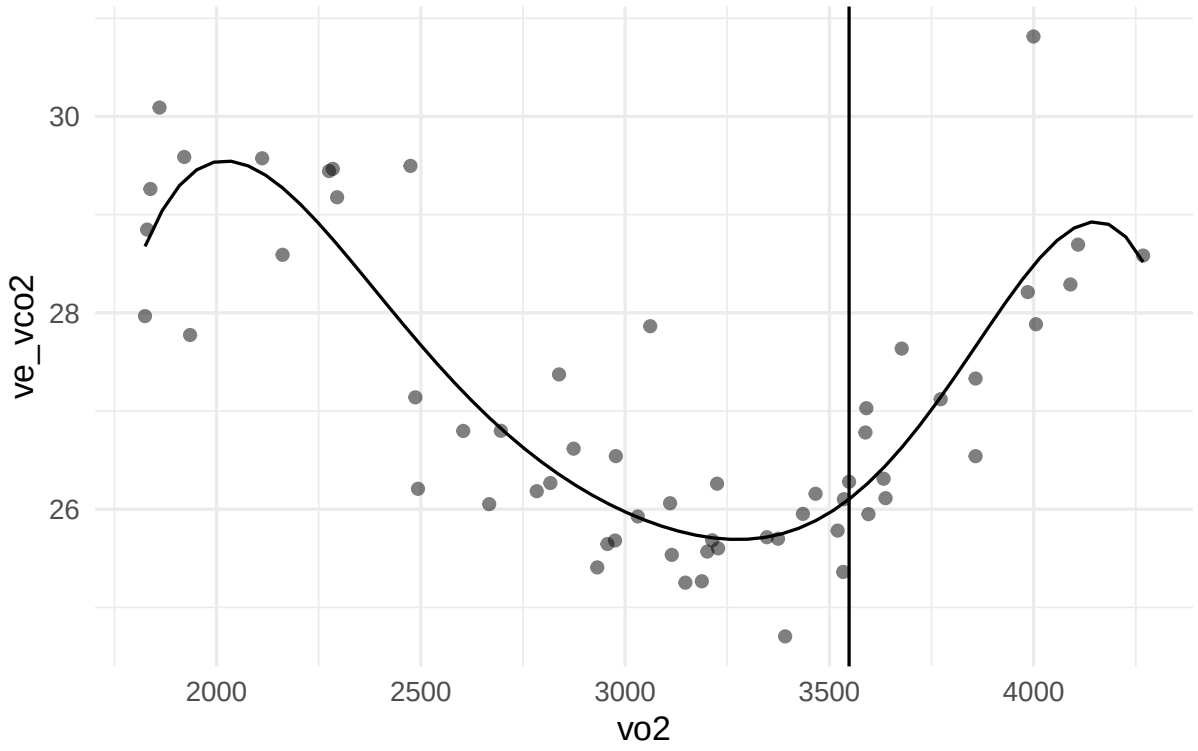
```
bp_dat <- breakpoint(.data = df_avg, method = "v-slope",
                     algorithm_vt2 = "d2_reg_spline_maxima",
                     x_vt2 = "vo2", y_vt2 = "ve_vco2",
                     vo2 = "vo2", vco2 = "vco2", ve = "ve", time = "time",
                     bp = "both", truncate = TRUE, front_trim_vt1 = 60,
                     pos_change = TRUE)
print(bp_dat$bp_dat, width = Inf)
#> # A tibble: 2 x 27
#>   bp    algorithm            x_var y_var   determinant_bp pct_slope_change
#>   <chr> <chr>                <chr> <chr>   <lgl>                      <dbl>
#> 1 vt1   v-slope              vo2   vco2    TRUE                        134.
#> 2 vt2   d2_reg_spline_maxima vo2   ve_vco2 TRUE                         NA
#>   f_stat  p_val_f  time clock_time speed grade vo2_kg   vo2  vco2   rer    rr
#>    <dbl>    <dbl> <dbl>      <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl> <dbl> <dbl>
#> 1   38.7  1.09e-9 1143.     42610.  6.72   1.1   38.1 2988. 2426. 0.804  21.6
#> 2   NA   NA       1342.     42809.  8.82   1.1   45.4 3548. 3271. 0.923  26.9
#>   vt_btps    ve    br peto2 petco2    hr   hrr ve_vo2 ve_vco2 excess_co2
```

```
#>     <dbl> <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl>  <dbl>   <dbl>      <dbl>
#> 1   2873.  61.9  65.1  92.8   40.9  156. 18.8    20.8    25.9      -471.
#> 2   3174.  85.4  51.9  97.7   40.8  178.  7.12   24.1    26.1      -252.
```

```
bp_dat$vt1_dat$bp_plot
```




```
bp_dat$vt2_dat$bp_plot
```


30
28
26
ve_vco2
2000
2500
3000
3500
4000
vo2