# Glycimic Index

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## Loading libraries

```r
library(ggplot2)
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
```

## Loading data

Control, with white bread, which has a known glycemic index of 75%:

```r
t_control <- read.csv("control.csv")
names(t_control) <- c("t", names(t_control)[-1])
t_control$Gemiddeld <- NULL
knitr::kable(t_control)
```

| t | X1 | X2 | X3 | X4 | X5 | X6 | X7 | X8 | X9 |
|----|--------|--------|--------|--------|--------|-------|-------|--------|--------|
| 15 | 0.000 | -0.013 | 0.075 | -0.013 | 0.175 | 0.088 | 0.163 | 0.050 | 0.125 |
| 30 | 0.013 | 0.113 | 0.225 | 0.263 | 0.575 | 0.288 | 0.413 | 0.225 | 0.363 |
| 45 | 0.025 | 0.113 | 0.225 | 0.675 | 0.775 | 0.425 | 0.550 | 0.288 | 0.375 |
| 60 | 0.163 | -0.100 | 0.125 | 0.750 | 0.425 | 0.275 | 0.550 | 0.025 | 0.313 |
| 75 | 0.225 | -0.038 | -0.100 | 0.475 | 0.038 | 0.250 | 0.413 | -0.213 | 0.225 |
| 90 | 0.087 | 0.013 | -0.225 | 0.350 | -0.087 | 0.413 | 0.225 | -0.163 | 0.000 |
| 105 | -0.025 | -0.013 | -0.125 | 0.450 | -0.113 | 0.425 | 0.163 | -0.087 | -0.138 |
| 120 | -0.088 | 0.013 | -0.050 | 0.325 | -0.087 | 0.425 | 0.138 | -0.062 | -0.150 |

Treatment, with Jimmy Joy's Plenny Shake, of which the glycemic index needs to be determined:

```r
t_jj <- read.csv("jj.csv")
names(t_jj) <- c("t", names(t_jj)[-1])
t_jj$Gemiddeld <- NULL
knitr::kable(t_jj)
```

| t | X1 | X2 | X3 | X4 | X5 | X6 | X7 | X8 | X9 |
|---|----|----|----|----|----|----|----|----|----|
| 15 | 0.050 | 0.113 | 0.088 | 0.138 | 0.063 | 0.038 | 0.100 | 0.050 | 0.050 |
| 30 | 0.175 | 0.200 | 0.213 | 0.250 | 0.200 | 0.138 | 0.138 | 0.200 | 0.275 |
| 45 | 0.175 | 0.013 | 0.200 | 0.150 | 0.313 | 0.225 | 0.063 | 0.238 | 0.338 |
| 60 | 0.088 | -0.138 | 0.075 | 0.000 | 0.350 | 0.087 | 0.088 | 0.050 | 0.138 |
| 75 | 0.025 | -0.063 | 0.013 | -0.050 | 0.300 | -0.050 | 0.175 | -0.050 | 0.125 |
| 90 | -0.100 | 0.063 | -0.013 | -0.025 | 0.213 | -0.025 | 0.188 | 0.075 | 0.087 |
| 105 | -0.163 | 0.038 | -0.013 | -0.062 | 0.100 | 0.037 | 0.138 | 0.063 | 0.087 |
| 120 | -0.113 | -0.075 | 0.013 | -0.062 | 0.038 | 0.175 | 0.125 | 0.013 | 0.150 |

## Convert data to long form

```
t_control_long <- tidyr::pivot_longer(
  t_control,
  cols = starts_with("X"),
  names_to = "person_id"
)
t_control_long$treatment <- "control"

t_jj_long <- tidyr::pivot_longer(
  t_jj,
  cols = starts_with("X"),
  names_to = "person_id"
)
t_jj_long$treatment <- "jj"
t <- rbind(t_control_long, t_jj_long)
knitr::kable(head(t))
```

| t | person_id | value | treatment |
|----|-----------|-------|-----------|
| 15 | X1 | 0.000 | control |
| 15 | X2 | -0.013 | control |
| 15 | X3 | 0.075 | control |
| 15 | X4 | -0.013 | control |
| 15 | X5 | 0.175 | control |
| 15 | X6 | 0.088 | control |

## AUC per person in time

```
t$person_id <- as.factor(t$person_id)
ggplot(
  t,
  aes(x = t, y = value, color = treatment)
) + geom_point() + geom_smooth() +
  scale_y_continuous("AUC of blood glucose concentration") +
  scale_x_continuous("time (minutes)") +
  ggtitle("AUCs in time") +
  facet_grid(person_id ~ .) +
  ggsave("aucs_in_time_pp.png", width = 7, height = 49)

## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```
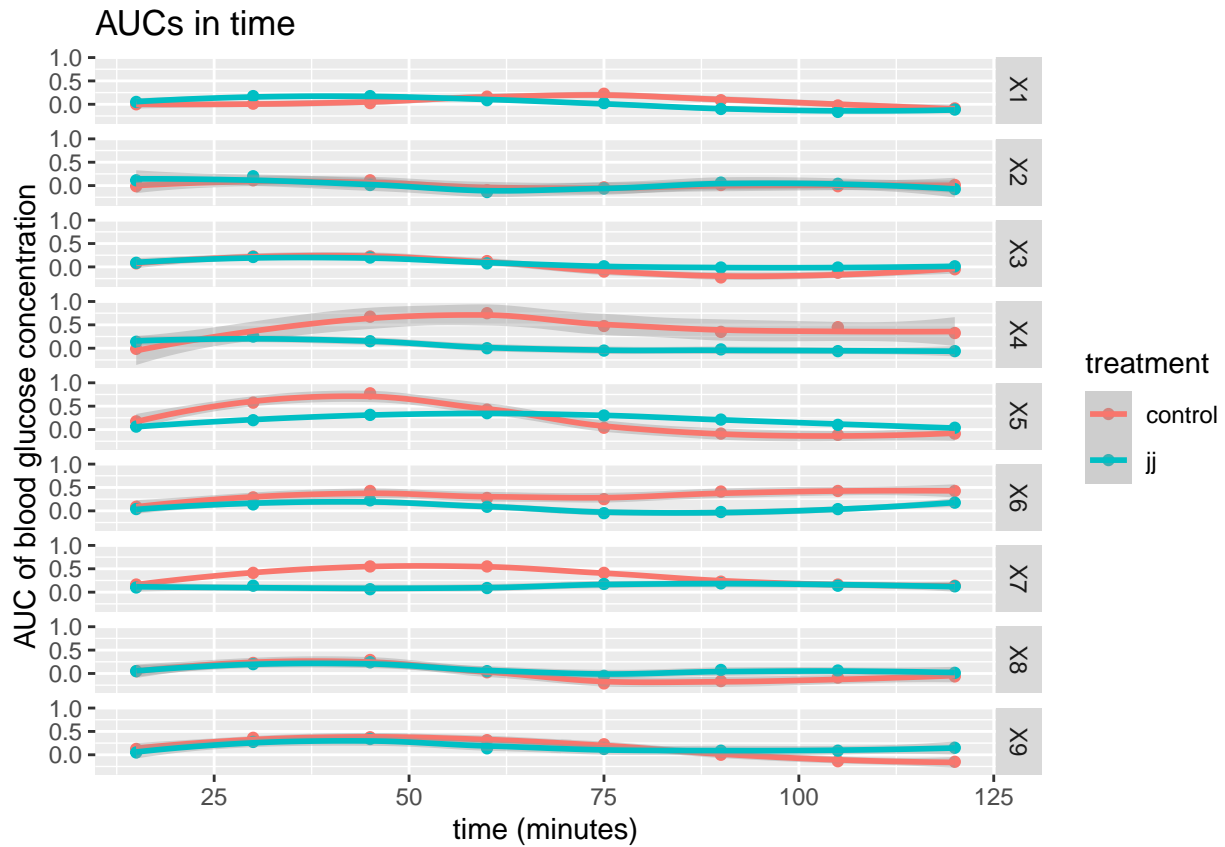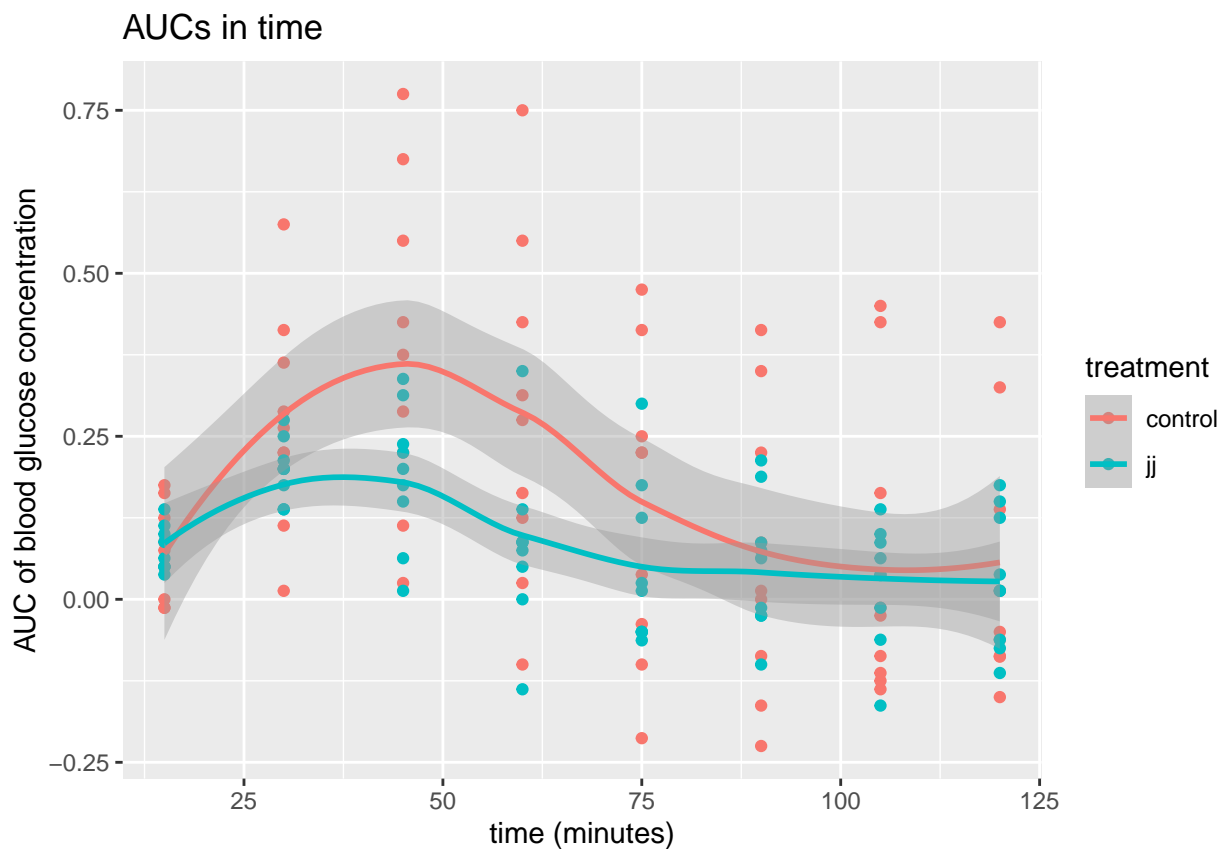
AUCs in time

## Average AUC in time

```
ggplot(
  t,
  aes(x = t, y = value, color = treatment)
) + geom_point() + geom_smooth() +
  scale_y_continuous("AUC of blood glucose concentration") +
  scale_x_continuous("time (minutes)") +
  ggtitle("AUCs in time") +
  ggsave("aucs_in_time.png", width = 7, height = 7)
```

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

## AUCs in time



## Calculate the glycemic index

### Calculate the average concentrations (again)

```
t_summary <- t %>% dplyr::group_by(t, treatment) %>% dplyr::summarise(mean = mean(value), .groups = "dr
knitr::kable(t_summary)
```

| t | treatment | mean |
|---|---|---|
| 15 | control | 0.0722222 |
| 15 | jj | 0.0766667 |
| 30 | control | 0.2753333 |
| 30 | jj | 0.1987778 |
| 45 | control | 0.3834444 |
| 45 | jj | 0.1905556 |
| 60 | control | 0.2806667 |
| 60 | jj | 0.0820000 |
| 75 | control | 0.1416667 |
| 75 | jj | 0.0472222 |
| 90 | control | 0.0681111 |
| 90 | jj | 0.0514444 |
| 105 | control | 0.0596667 |
| 105 | jj | 0.0250000 |
| 120 | control | 0.0515556 |
| 120 | jj | 0.0293333 |

**Approximate the area in the two-hour curve**

Simply sum the values

```r
t_gi <- t_summary %>% dplyr::group_by(treatment) %>% dplyr::summarise(sum = sum(mean), .groups = "drop")
knitr::kable(head(t_gi))
```

| treatment | sum |
|-----------|-----------|
| control | 1.332667 |
| jj | 0.701000 |

**Correct values**

We know the control (white bread) has a glycemic index of 75%.

```r
control_row <- which(t_gi$treatment == "control")
control_sum <- t_gi$sum[control_row]
conversion <- 75 / control_sum
testthat::expect_equal(control_sum * conversion, 75)
jj_row <- which(t_gi$treatment == "jj")
jj_sum <- t_gi$sum[jj_row]
gi <- jj_sum * conversion
cat(paste("The glycemic index of Jimmy Joy's Plenny shake is", gi))
```

```
## The glycemic index of Jimmy Joy's Plenny shake is 39.4509754877439
```

The glycemic index of Jimmy Joy's Plenny shake is approximately 40%, which is classified as a low glycemic index.