Model analysis

Non Linear Dynamics

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LAC Operon Model analysis

Based on Yildirim et al. 2004.

See repository for more information.

Setup

```
library(tidyverse)
## -- Attaching packages -
                                                 ----- tidyverse 1.3.1 --
## v ggplot2 3.3.6
                    v purrr
                             0.3.4
## v tibble 3.1.7
                    v dplyr
                             1.0.9
## v tidyr
          1.2.0
                   v stringr 1.4.0
## v readr
           2.1.2
                    v forcats 0.5.1
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                  masks stats::lag()
library(broom)
options(scipen=999)
```

Models with one starting condition

Loading simulation results

Loading data into dataframes

```
original = read_csv("results/Original model 2022-11-11 02:41:58.csv")
corrected = read_csv("results/Corrected model 2022-11-11 02:42:02.csv")
```

Combining into one DF

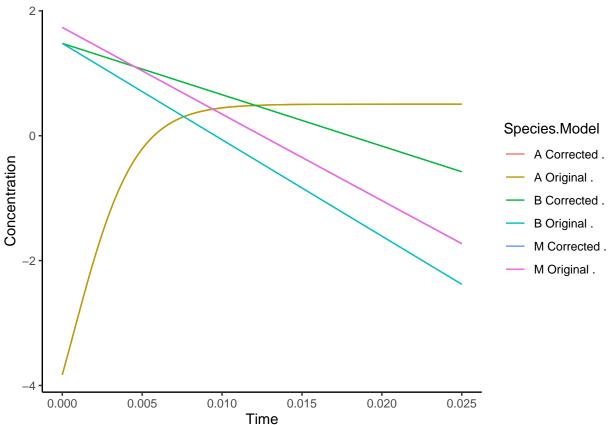
```
data <-
bind_rows(original %>% mutate(Model = "Original"), corrected %>% mutate(Model = "Corrected"))
```

Scaling and pivoting data

```
data <-
  data %>%
  mutate(across(-c(Time, Model), scale)) %>%
  pivot_longer(cols = -c(Time, Model), names_to="Species", values_to="Concentration") %>%
  mutate(across(c(Model, Species), as.factor))
```

Visualising results

```
ggplot(data %>% mutate(Species.Model = paste(Species, Model, delimiter=".")), aes(x=Time, y=Concentrati
geom_line() +
#scale_y_log10() +
theme_classic()
```



Model analysis

<fct>

<dbl>

0.916

1.00

##

1 M

2 B ## 3 A

Checking hypothesis: There is no significant difference between the data measured with either model.

```
data %>%
  group_by(Species) %>%
  nest() %>%
  mutate(F_test = map(data, ~ aov(Concentration ~ Model + Time, data = .x) %>% tidy() %>% pluck("p.valu unnest(F_test) %>%
  select(-data)

## # A tibble: 3 x 2
## # Groups: Species [3]
## Species F_test
```

Models with a scan of starting conditions

Loading simulation results

```
Loading data into dataframes
```

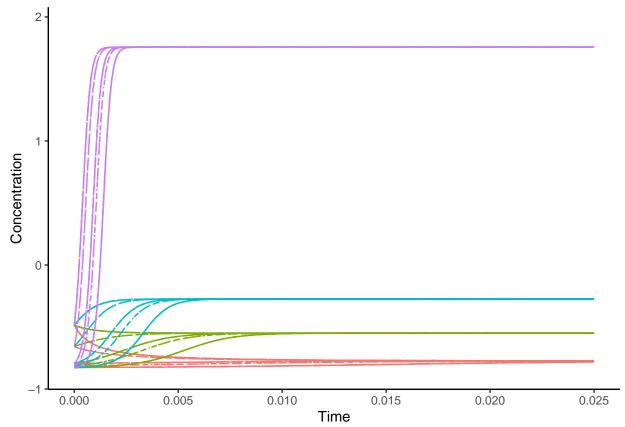
```
data <- read_csv("results/Starting conditions scan 2022-11-11 10:37:22.csv") %>%
  mutate(across(c(Model, Starting_Conditions_Set, L), as.factor))
```

```
Scaling and pivoting data
```

```
pivot_scaled_data <-
  data %>%
  mutate(across(c(M, B, A), scale)) %>%
  pivot_longer(cols = -c(Time, Model, Starting_Conditions_Set, L), names_to="Species", values_to="Concernutate(across(c(Species), as.factor))
```

Visualising results

```
ggplot(pivot_scaled_data %>% filter(Model == "Corrected") %>% mutate(Species.Set = paste(Species, Start
  geom_line(show.legend=F) +
  #scale_y_log10() +
  theme_classic()
```



```
sim_end = max(data$Time)
data %>%
  pivot_longer(cols=c(M, B, A), names_to="Species", values_to="Concentration") %>%
  filter(Time == sim_end) %>%
  group_by(Species, L) %>%
```

```
## `summarise()` has grouped output by 'Species'. You can override using the
## `.groups` argument.
## # A tibble: 12 x 3
## # Groups:
               Species [3]
##
      Species L
                     SteadyState
##
      <chr>
              <fct>
                           <dbl>
   1 A
              10000
                        15876.
##
##
   2 A
              50000
                        81515.
##
   ЗА
              100000
                       161539.
                       752458.
##
   4 A
              500000
##
   5 B
              10000
                            6.62
##
   6 B
              50000
                            6.62
##
  7 B
              100000
                            6.62
```

6.62

11.5

11.5

11.5

11.5

<tibble [251,000 x 5]>

<tibble [251,000 x 5]>

<tibble [251,000 x 5]>

summarize(SteadyState=mean(Concentration))

Model analysis

##

8 B

9 M

10 M

11 M

12 M

1 M

2 B

3 A

500000

10000

50000

100000

500000

Checking hypothesis: There is no significant difference between the data measured with either model.

1.00

1.00

0