

Effect of IPTG Induction in 3 organism libraries in EZ media

```
library(pacman)
p_load(data.table, ggplot2, RSQLite)

chem_gen_db <- dbConnect(RSQLite::SQLite(), "../chem_gen.db")
Experiments <- data.table(dbReadTable(chem_gen_db, "Experiments"))
Ryan_Strains <- data.table(dbReadTable(chem_gen_db, "Ryan_Strains"))
dbDisconnect(chem_gen_db)

today <- "2022-03-30"

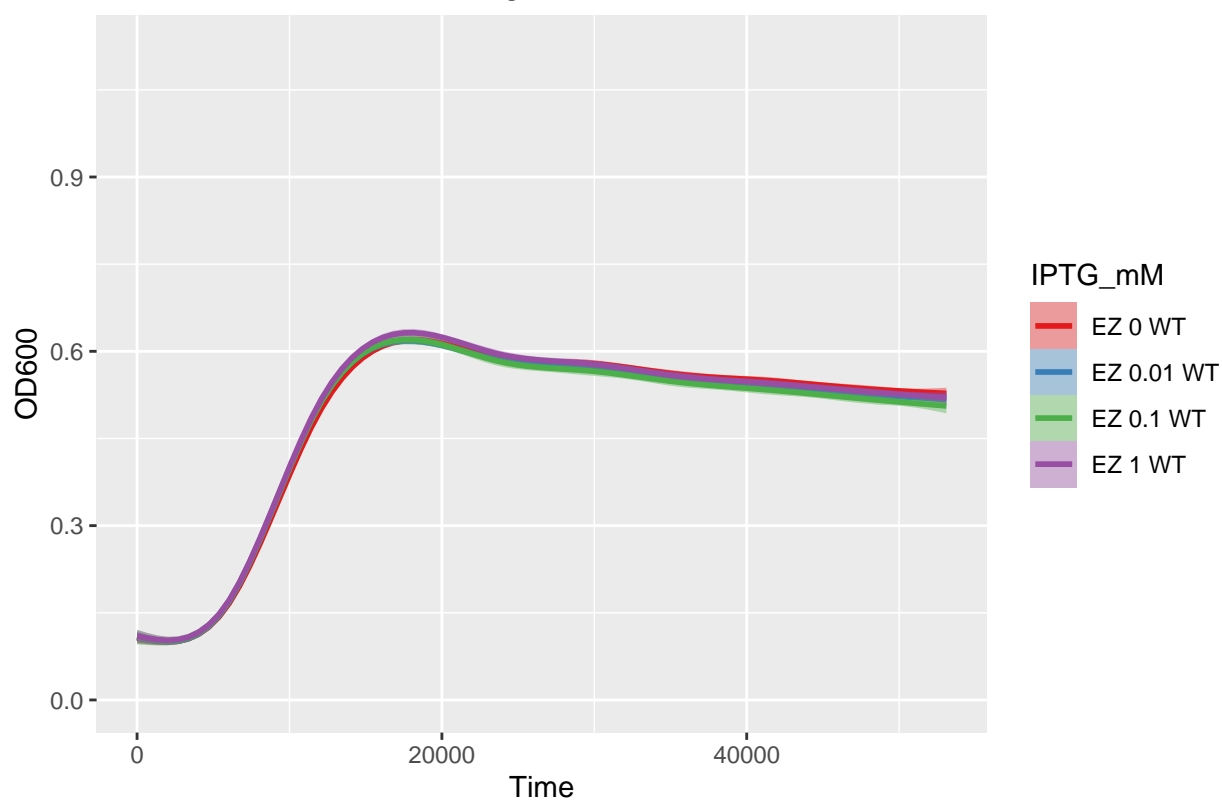
Experiments <- Ryan_Strains[Experiments[Date == today], on = .(Organism)]

for (i in unique(Experiments[!is.na(Species), Species])) {

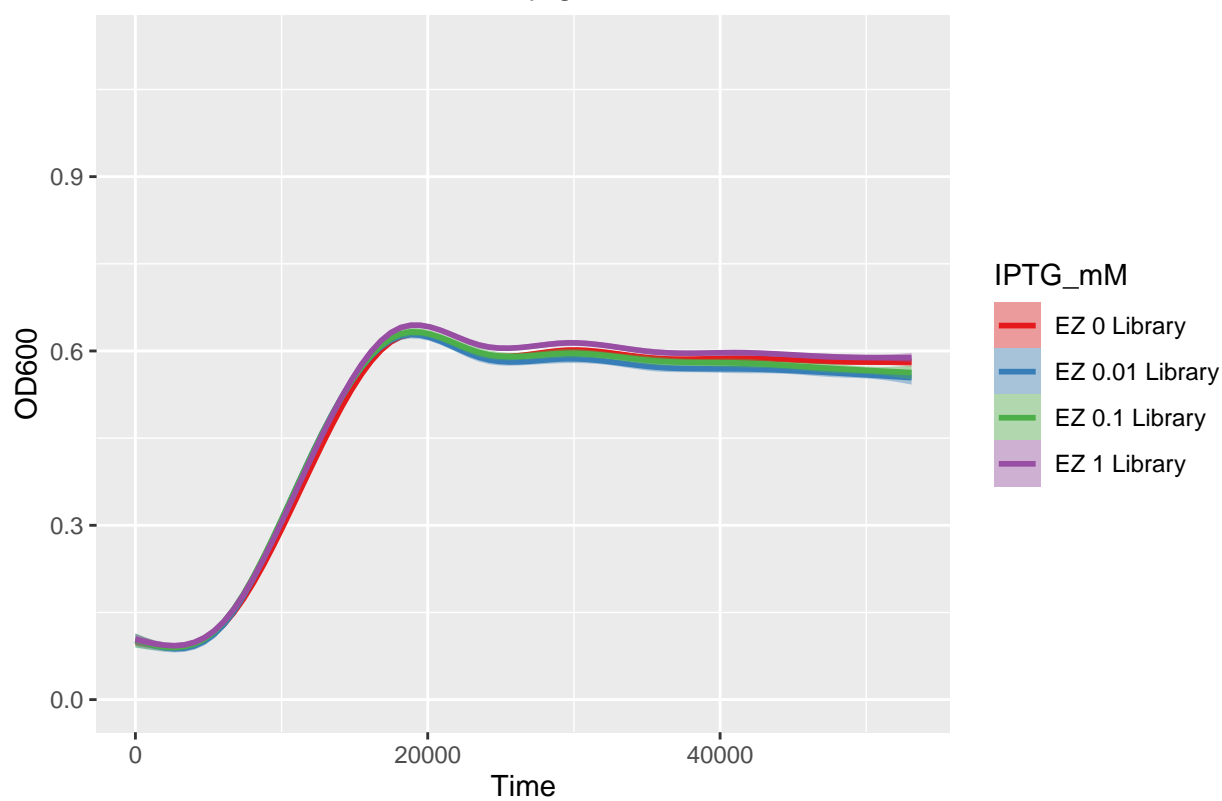
  for (j in unique(Experiments$Remark)){
    this.plot <-
      ggplot(
        Experiments[
          Species == i & Remark == j,
          .(OD600,
            IPTG_mM = paste(Media, Induced, Remark)),
          by = .(Time)],
        aes(x = Time, y = OD600, color = IPTG_mM, fill = IPTG_mM)) +
      ylim(0, max(Experiments$OD600)) +
      geom_smooth(formula = y ~ s(x, bs = "cs"), method = "gam") +
      scale_colour_brewer(palette = "Set1") +
      scale_fill_brewer(palette = "Set1") +
      ggtitle(paste(i, j, "growth curves on", today))

    plot(this.plot)
  }
}
```

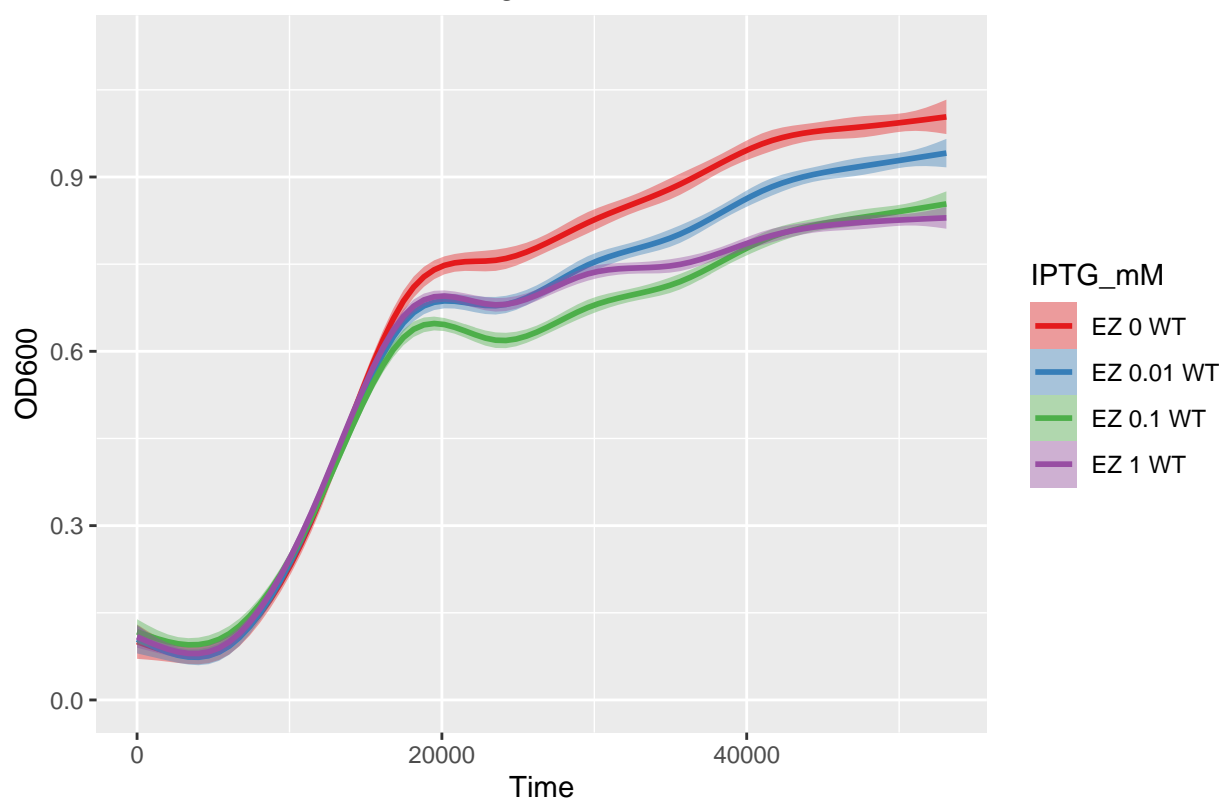
Escherichia coli K-12 WT growth curves on 2022-03-30



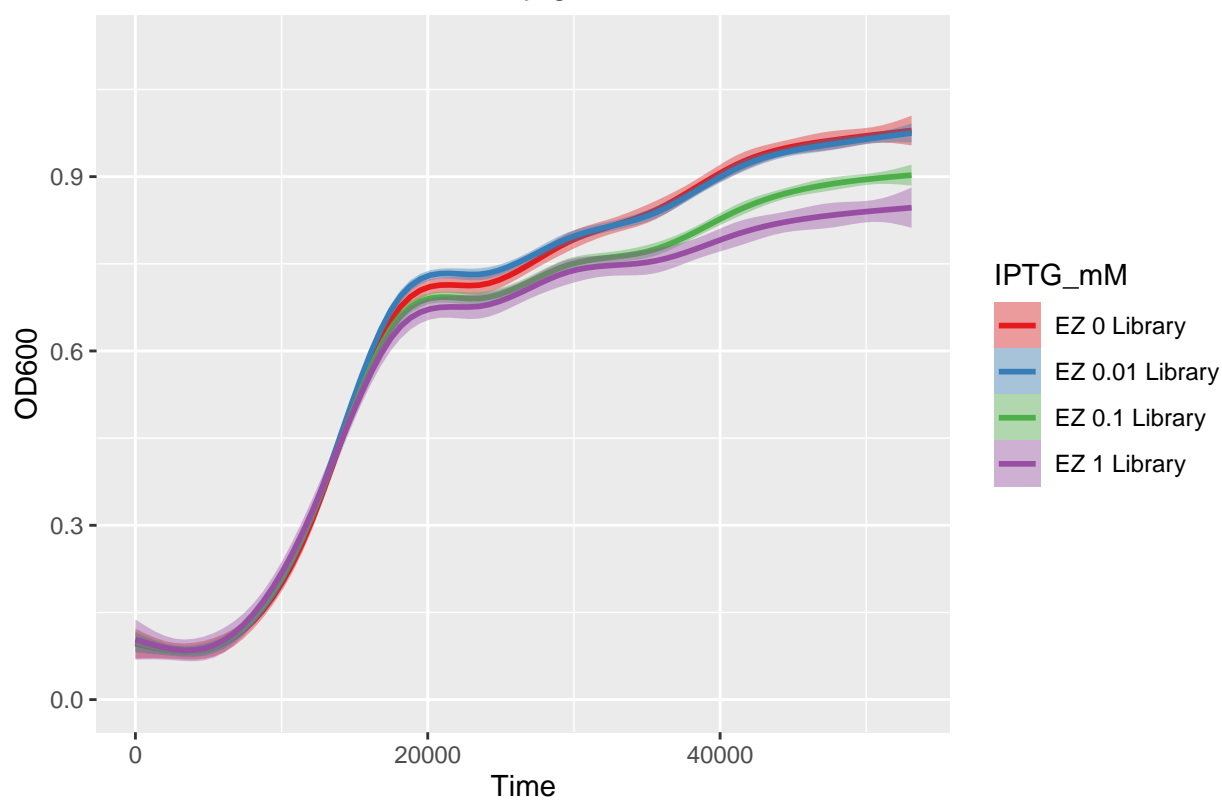
Escherichia coli K-12 Library growth curves on 2022-03-30



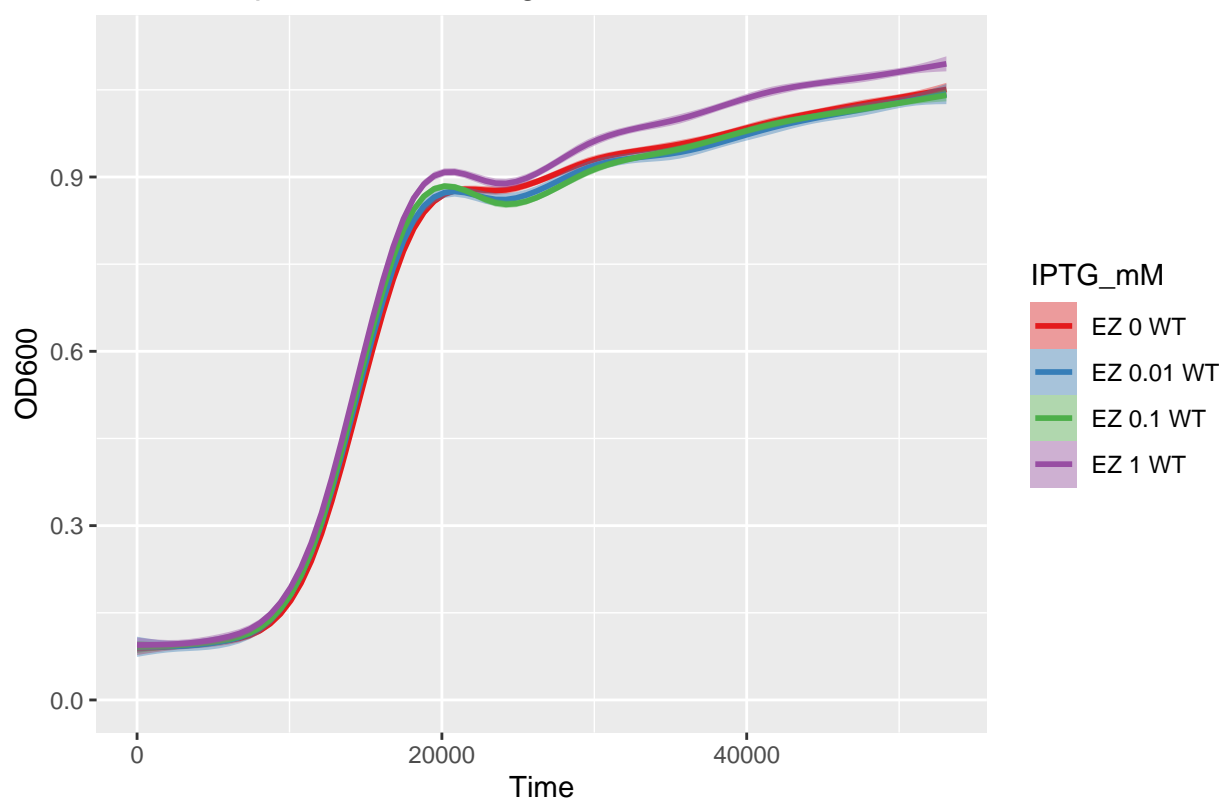
Enterobacter cloacae WT growth curves on 2022-03-30



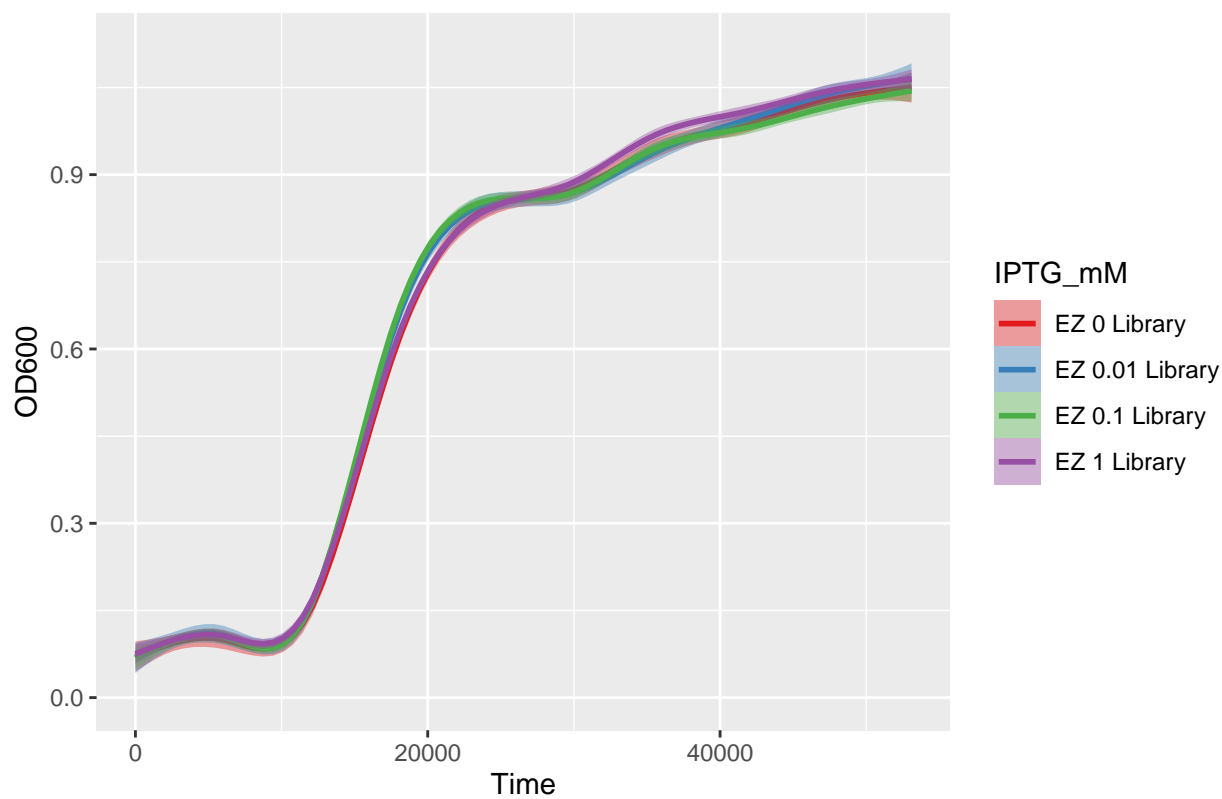
Enterobacter cloacae Library growth curves on 2022-03-30



Klebsiella pneumoniae WT growth curves on 2022-03-30



Klebsiella pneumoniae Library growth curves on 2022-03-30



```

library(pacman)
p_load(data.table, ggplot2, RSQLite)

chem_gen_db <- dbConnect(RSQLite::SQLite(), "../chem_gen.db")
Fitted_Experiments <- data.table(dbReadTable(chem_gen_db, "Fitted_Experiments"))
Ryan_Strains <- data.table(dbReadTable(chem_gen_db, "Ryan_Strains"))
dbDisconnect(chem_gen_db)

today <- "2022-03-30"

Fitted_Experiments <- Ryan_Strains[Fitted_Experiments[Date == today], on = .(Organism)]

for (i in unique(Fitted_Experiments[!is.na(Species), Species])) {
  for (j in unique(Fitted_Experiments$Remark)){

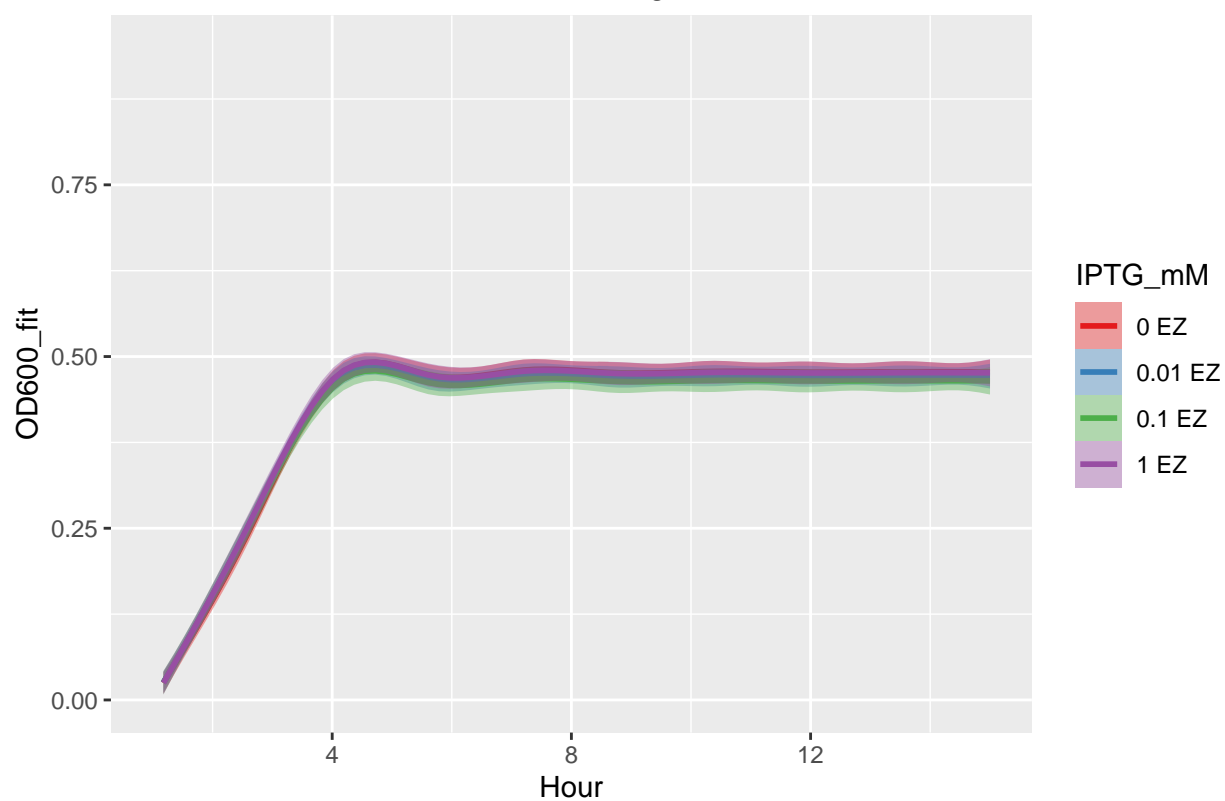
    this.plot <-
      ggplot(
        Fitted_Experiments[
          Species == i & j == Remark,
          .(OD600_fit,
            IPTG_mM = paste(Induced, Media)),
          by = .(Hour)],
        aes(x = Hour, y = OD600_fit, color = IPTG_mM, fill = IPTG_mM)) +
      ylim(0, max(Fitted_Experiments$OD600)) +
      geom_smooth(formula = y ~ s(x, bs = "cs"), method = "gam") +
      scale_colour_brewer(palette = "Set1") +
      scale_fill_brewer(palette = "Set1") +
      ggtitle(paste(i, j, "FITTED growth curves on", today))

    plot(this.plot)
  }
}

```

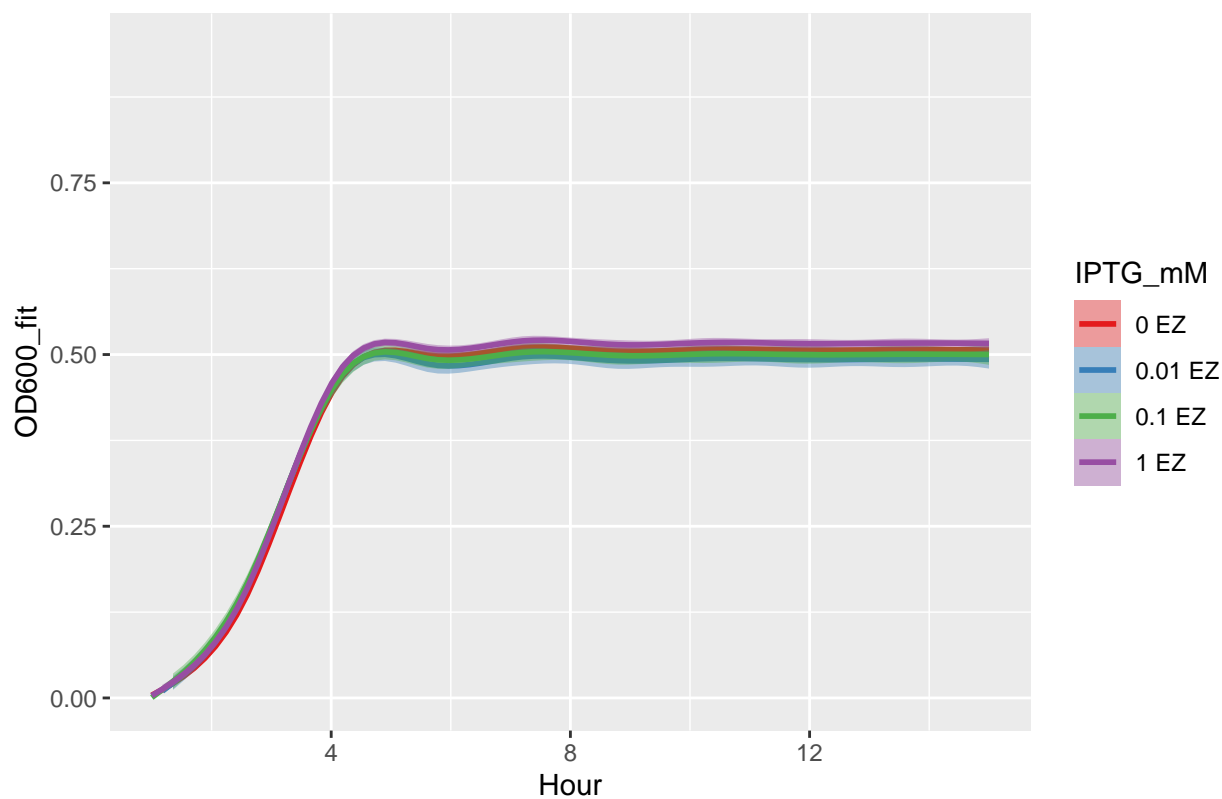
```
## Warning: Removed 4 rows containing missing values (geom_smooth).
```

Escherichia coli K-12 WT FITTED growth curves on 2022-03-30

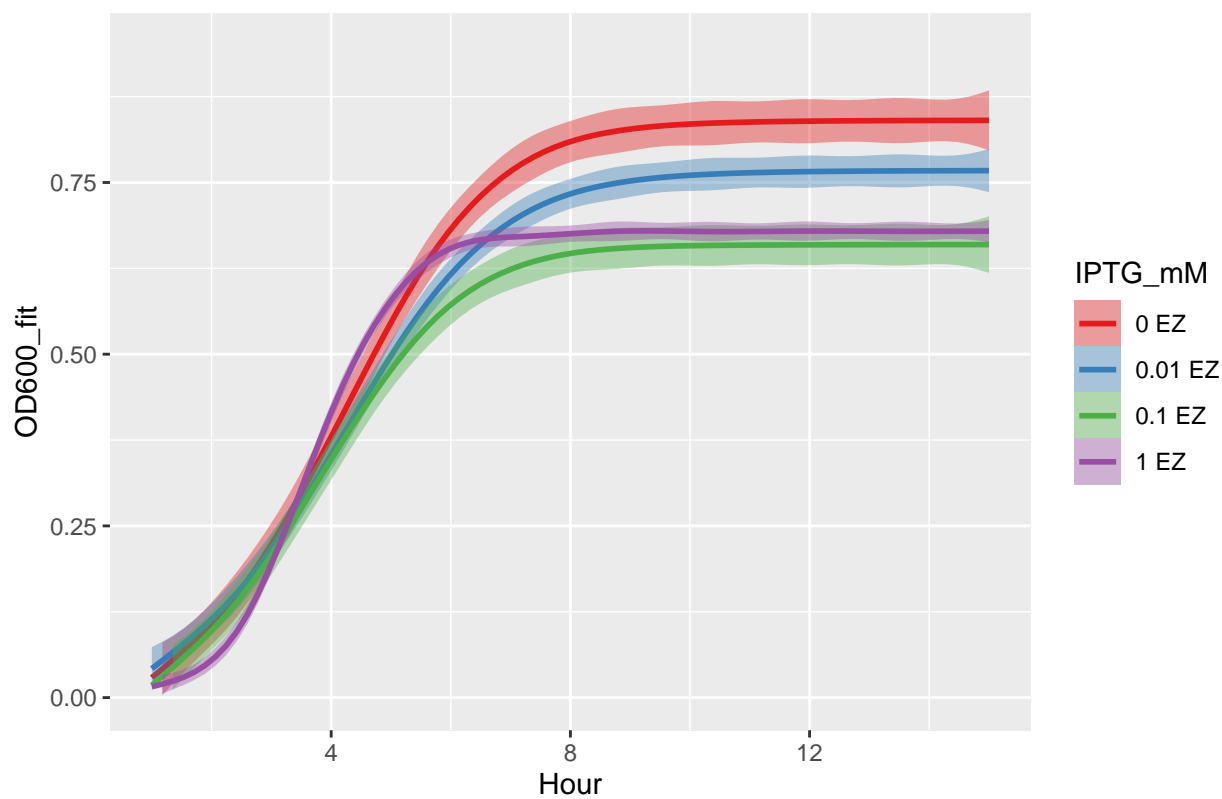


Warning: Removed 1 rows containing missing values (geom_smooth).

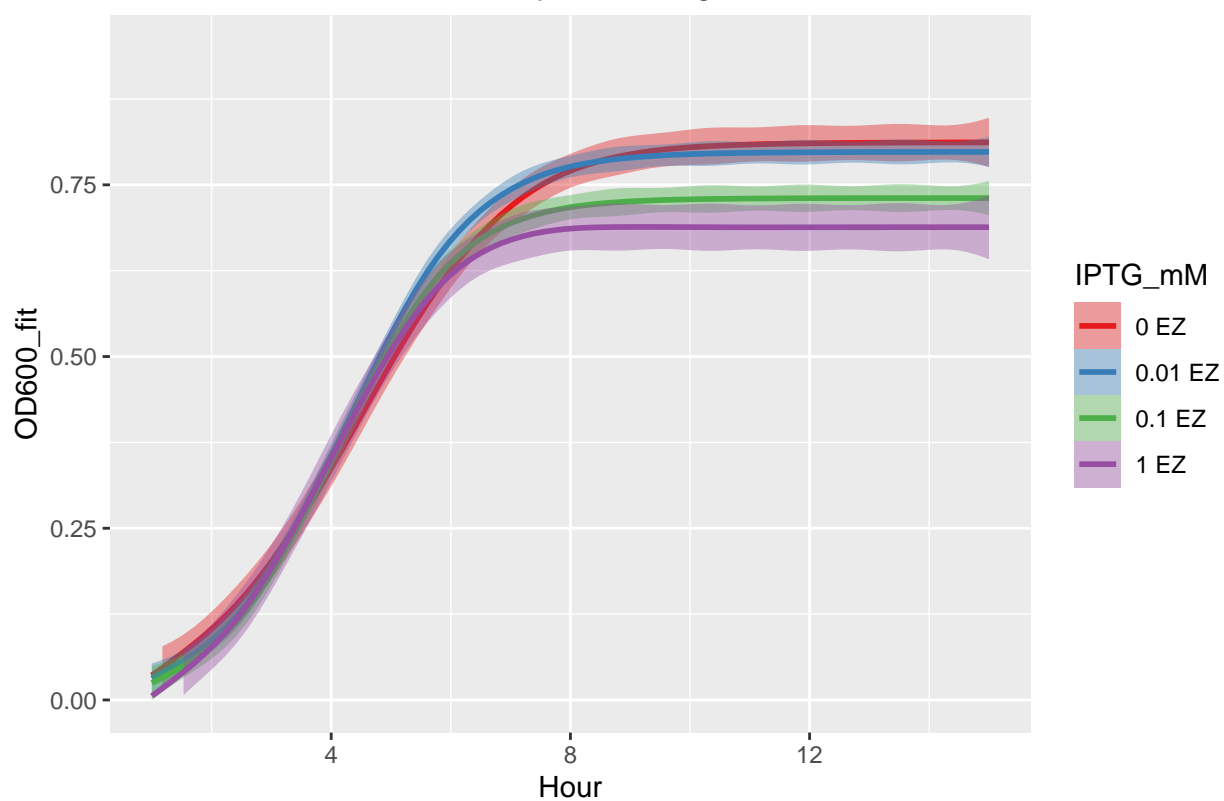
Escherichia coli K-12 Library FITTED growth curves on 2022-03-30



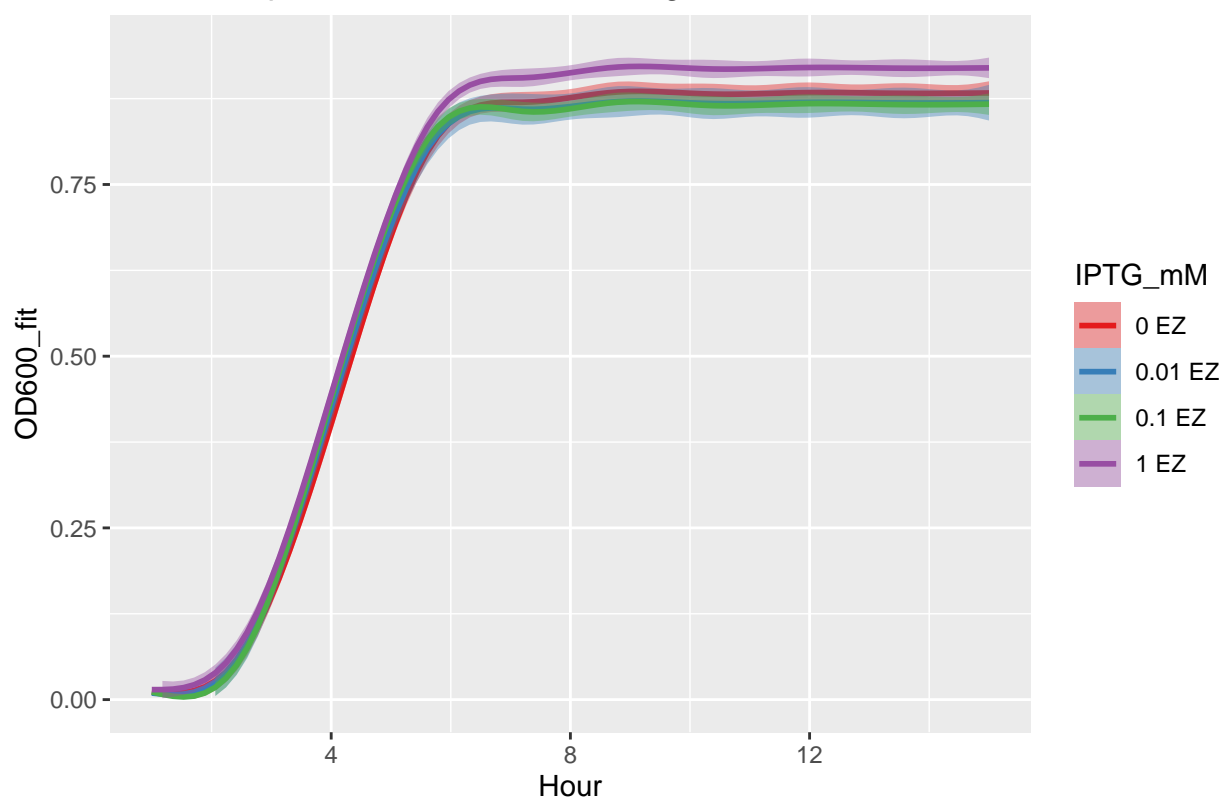
Enterobacter cloacae WT FITTED growth curves on 2022-03-30



Enterobacter cloacae Library FITTED growth curves on 2022-03-30



Klebsiella pneumoniae WT FITTED growth curves on 2022-03-30



Klebsiella pneumoniae Library FITTED growth curves on 2022-03-30

