

Simple CMV transient infection stochastic model simulations

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Generate some example time series, look and plot some basic characteristics. Also look at some aggregate features of some longer simulations.

```
times = seq(0, 500, 0.1)
cmv_title = expression(paste("Log"[10], " CMV DNA copies/swab"))
general_title = expression(paste("Simulated log"[10], " CMV viral load"))
```

Simulate some examples

Simulate stochastic models with a few different R_0 and initial I values. Also look at deterministic model trajectory. The code for simulation is in this section.

Here, we simulate at 75 day infections for combinations of $R_0 = 1.05$ and 1.5 (determines the β coefficient) and initial I = 1 and 10 (initial infected cells with replicated virus).

```
parms_latent$beta = betas_latent[1] #R0 = 1.05
parms_latent$beta = betas_latent[2]

#print R0
with(parms_latent, beta * K * p/(c * delta *(1+mu/alpha)))

## [1] 1.632113

determ_model = ldply(c(1, 10), function(i0){
  ldply(c(1.05, 1.5), function(r0){
    parms_latent$beta = r0/with(parms_latent, p * K/ (c * delta *(1+mu/alpha)))
    initial = c(S = parms_latent$K, I0 = 0, I = i0, V = 0)
    x = as.data.frame(lsoda(initial, times, CMVModel_latent_ode, parms_latent))
    x$R0 = r0
    x$initI = i0
    x
  })
})

set.seed(10)
example_runs = ldply(c(1, 10), function(i0){
  ldply(c(1.05, 1.5), function(r0){
    ldply(1:50, function(i){
      parms_latent$beta = r0/with(parms_latent, p * K/ (c * delta *(1+mu/alpha)))
      out = stochastic_model_latent_I(75, parms_latent, initI = i0)
      out$run = i
      out$initI = i0
      out$R0 = r0
      out
    })
  })
})
```

```

    })
  })
})

```

Plot the examples

```

example_sim = ggplot(data = example_runs,
                     aes(x = time, y = log10(V + 1))) +
  theme(legend.position = "none") +
  scale_x_continuous("Days", limits = c(0, 50)) +
  scale_y_continuous("general_title", limits = c(0, 8), breaks = 0:9) +
  facet_grid(R0 ~ initI) +
  geom_line(aes(colour = factor(run))) +
  geom_line(data = determ_model, colour = "blue") +
  theme(text = element_text(size = 18),
        strip.background = element_rect(fill = NA),
        axis.line = element_line(colour = "black"),
        plot.margin=unit(c(0, 0, 0, 0), "lines"),
        panel.border = element_rect(colour = "black", fill=NA, size=1))

top_title <- ggdraw() + draw_label(expression(paste("Initial infected cells (I"[0], ")")))
left_title <- ggdraw() + draw_label(expression(paste("R"[0])), angle = 270, hjust = 1)

out1 = plot_grid(example_sim , left_title, ncol=2, rel_widths=c(1, .1))
plot_grid(top_title, out1, ncol=1, rel_heights=c(0.1, 1))

```

