

# Explore relationships at equilibrium

Here we will explore fundamental relationships in the transmission model, such as the proportion of the population in each model state and the relationship between EIR, prevalence and incidence at equilibrium.

## Proportion in each model state

We can use the equilibrium solution to explore what proportion of the human population are in each model compartment. We will use default parameters:

```
## Loading malariaModelFit

## Warning in setup_ns_exports(pkg, export_all): Objects listed as exports,
## but not present in namespace: breakCoverageTest

age <- default_age()
h <- gq_normal(9)
p <- load_parameters("parameters_Xiaoyu.txt")
```

We will explore a range of EIR (in log space), and several treatment levels:

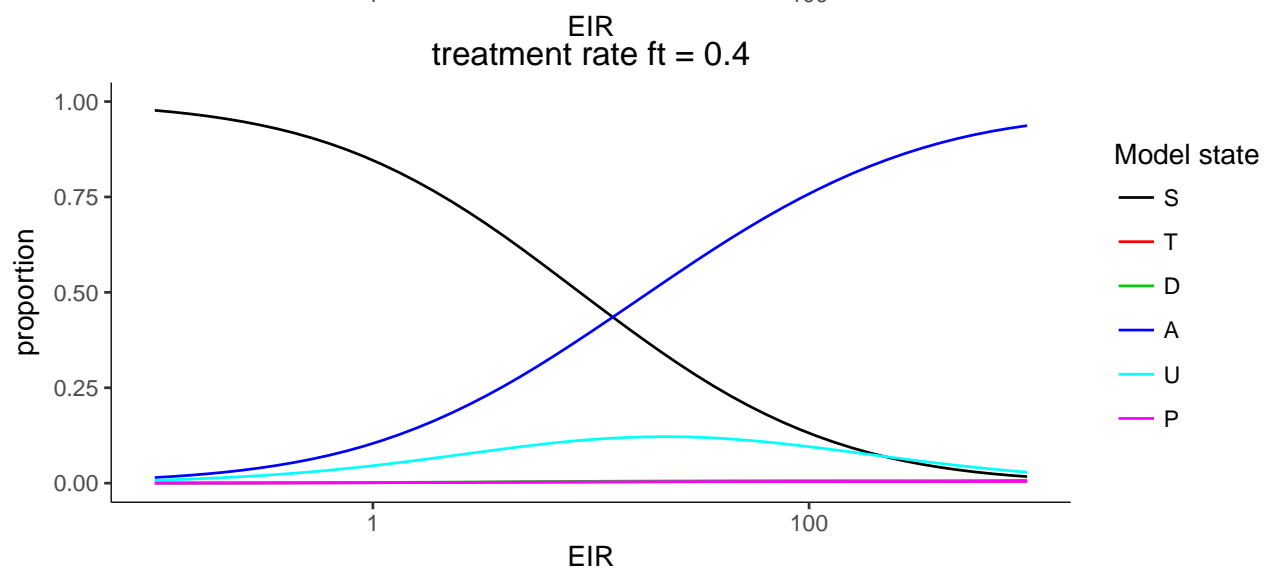
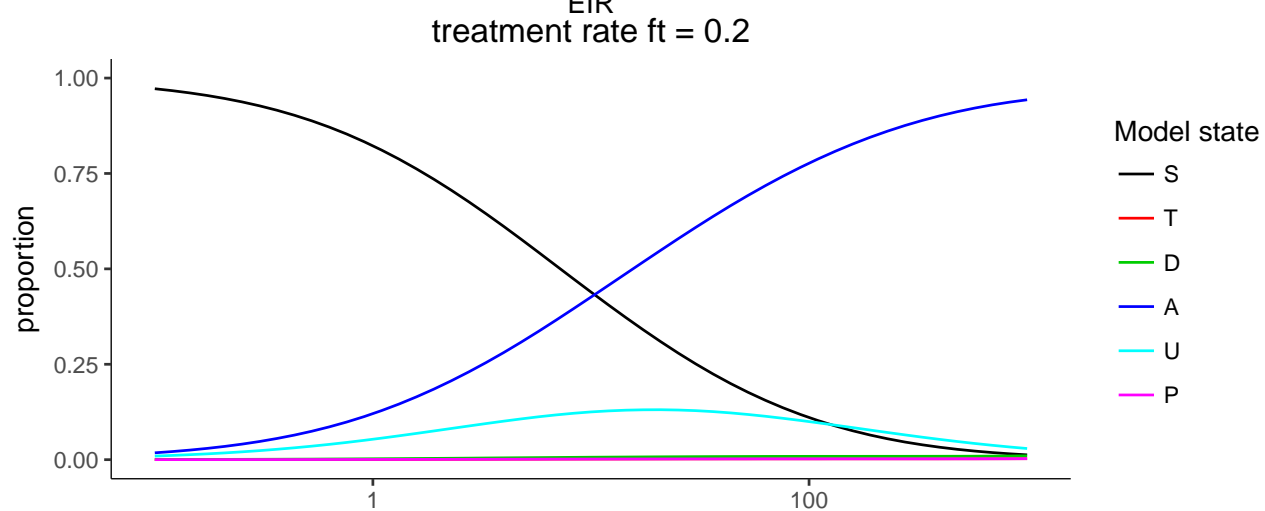
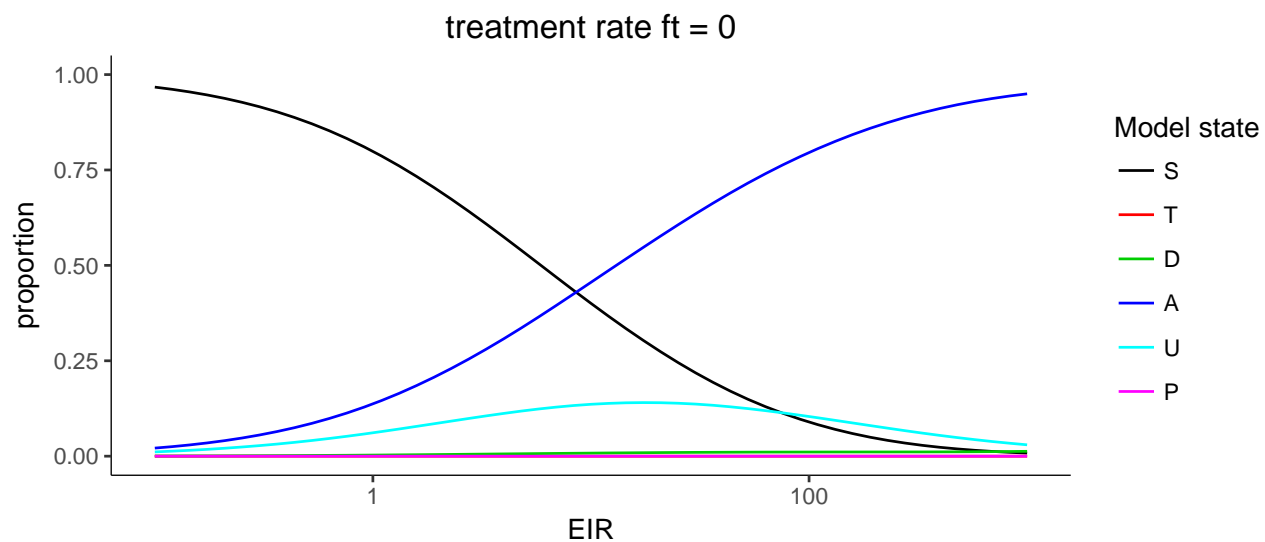
```
# explore a range of EIR and treatment levels
EIR <- exp(seq(log(0.1), log(1000), length=51))
ft <- c(0, 0.2, 0.4, 1)

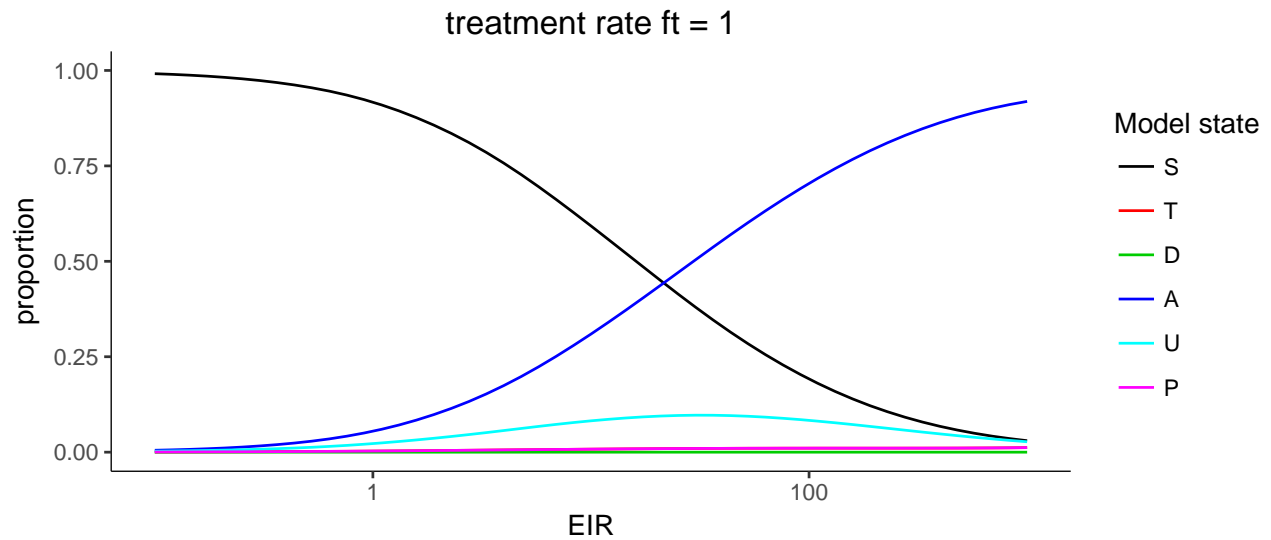
# save solution to list
eqList <- list()
for (i in 1:length(ft)) {
  eqList[[i]] <- list()
  for (j in 1:length(EIR)) {
    eqList[[i]][[j]] <- human_equilibrium_fast(EIR[j], ft[i], p, age, h$nodes, h$weights)
  }
}
```

Save state proportions in array

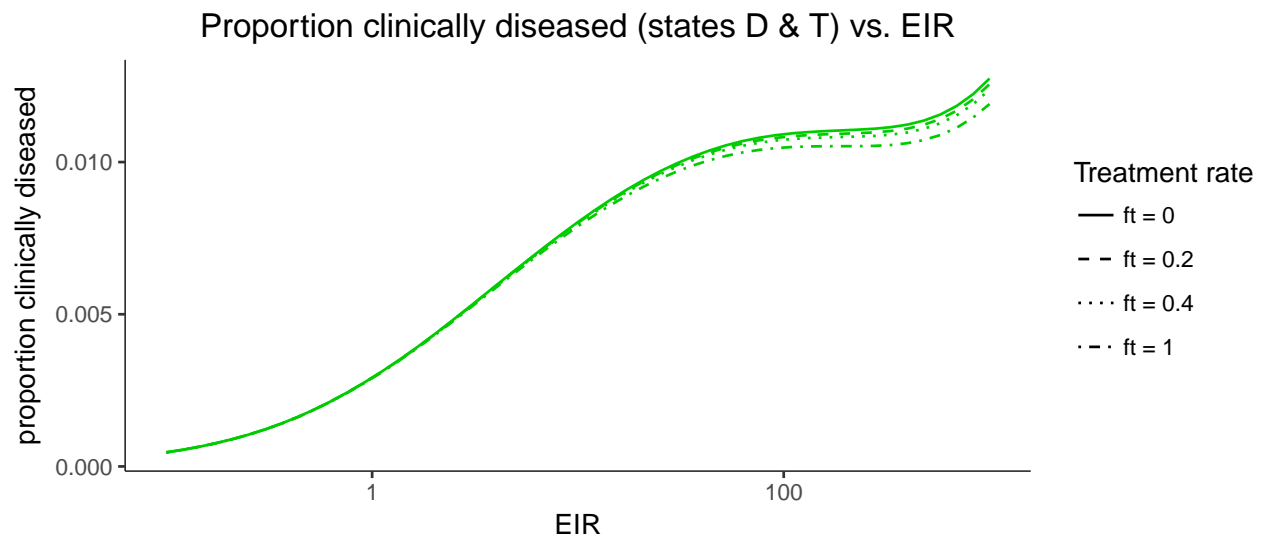
```
# save state proportions in array
stateNames <- c("S", "T", "D", "A", "U", "P")
m <- array(0, dim=c(length(ft), length(EIR), length(stateNames)))
for (i in 1:length(eqList)) {
  for (j in 1:length(eqList[[i]])) {
    m[i,j,] <- colSums(subset(eqList[[i]][[j]]$states, select=stateNames))
  }
}
```

Produce plots





Notice that the greatest proportion of the population is in the susceptible compartment at low EIR, and the asymptomatic compartment at high EIR, with relatively few individuals being clinically infected at any point. We can explore this by focussing on clinically diseased individuals (i.e. those in state D or state T):



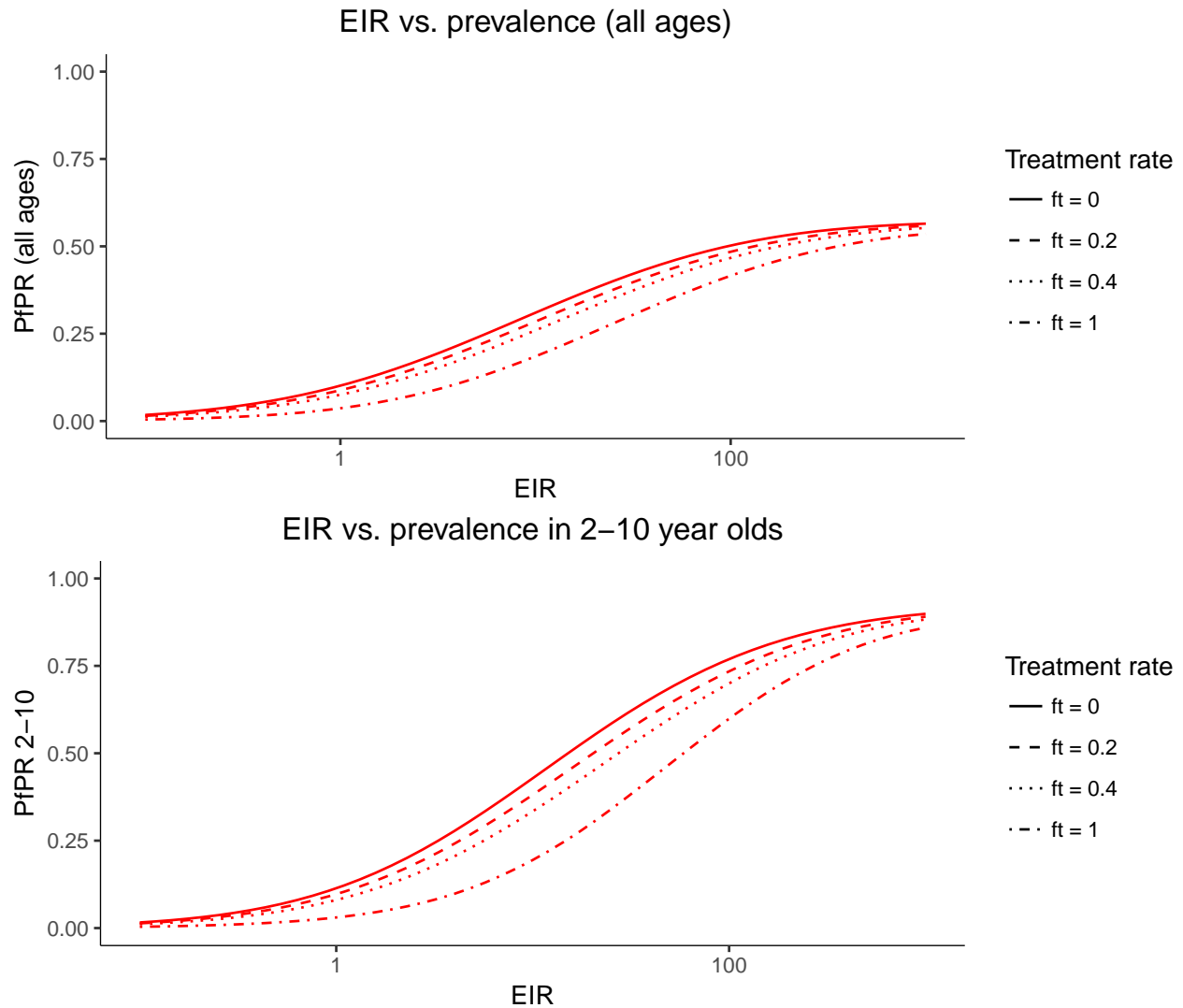
Even at very high transmission the proportion of clinically diseased individuals rarely goes a long way over 1%.

## EIR, prevalence, incidence and R0

Text

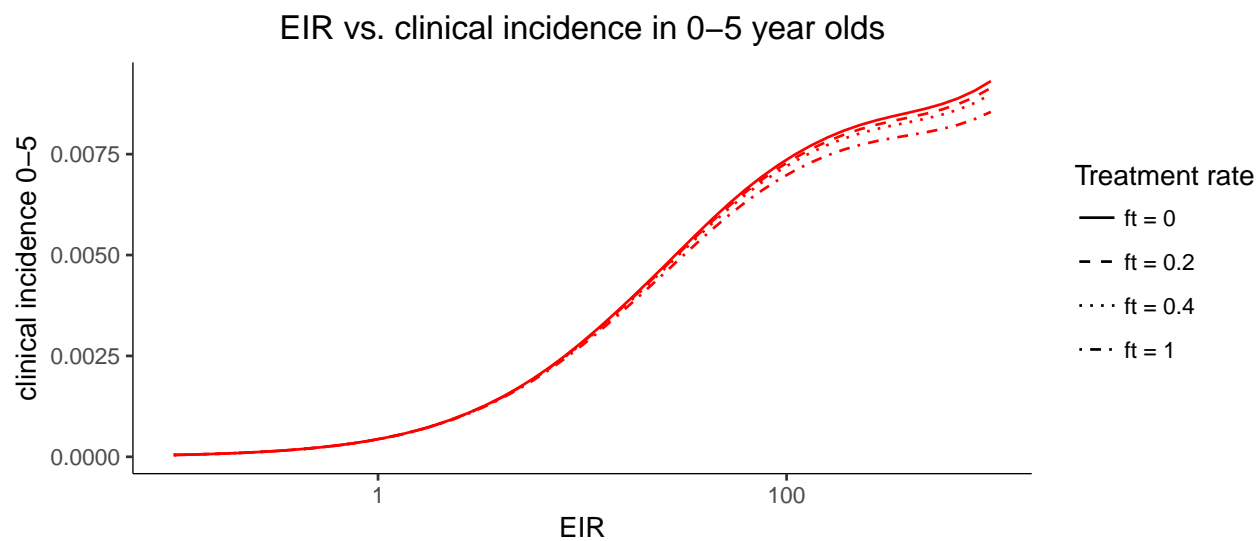
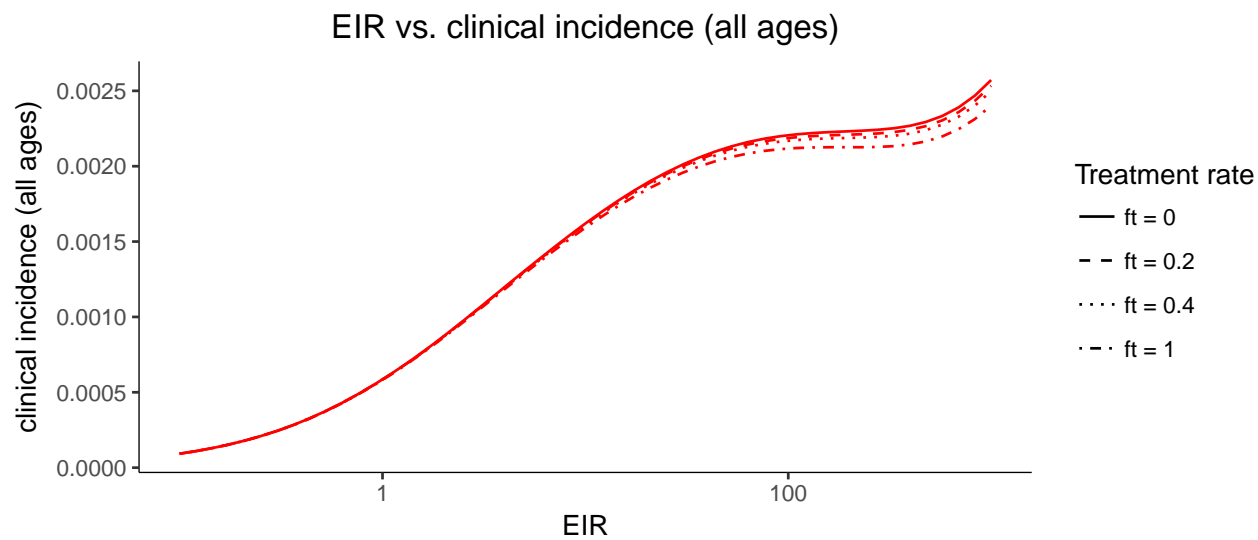
```
# calculate prevalence for a range of treatment rates
prev_allAges <- prev_2_10 <- list()
for (i in 1:length(ft)) {
  prev_allAges[[i]] <- mapapply(find_prev, eqList[[i]], 0, Inf)
  prev_2_10[[i]] <- mapapply(find_prev, eqList[[i]], 2, 10)
}
```

Produce plots



Text

```
# calculate incidence for a range of treatment rates
inc_allAges <- inc_0_5 <- list()
for (i in 1:length(ft)) {
  inc_allAges[[i]] <- mapapply(find_inc, eqList[[i]], 0, Inf)
  inc_0_5[[i]] <- mapapply(find_inc, eqList[[i]], 0, 5)
}
```



Demonstrate why prevalence vs. incidence plots can be confusing.

