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: human_equilibrium_fast, plot_nice1
```

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

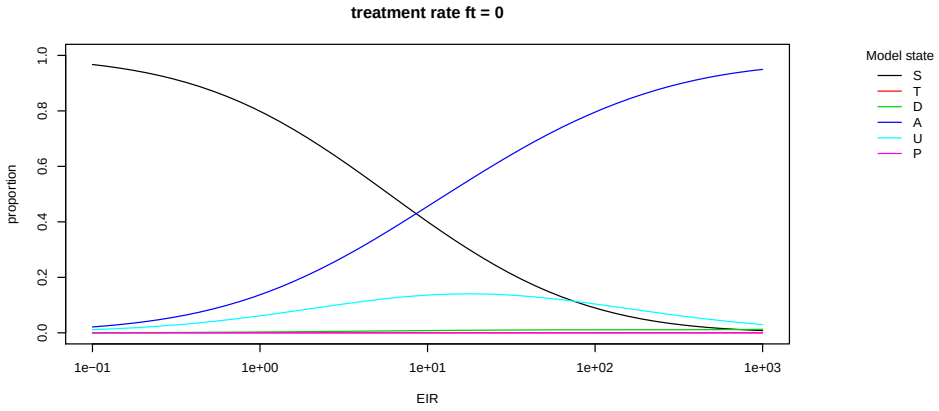
We will explore a range of EIR (in log space), and several treatment levels:

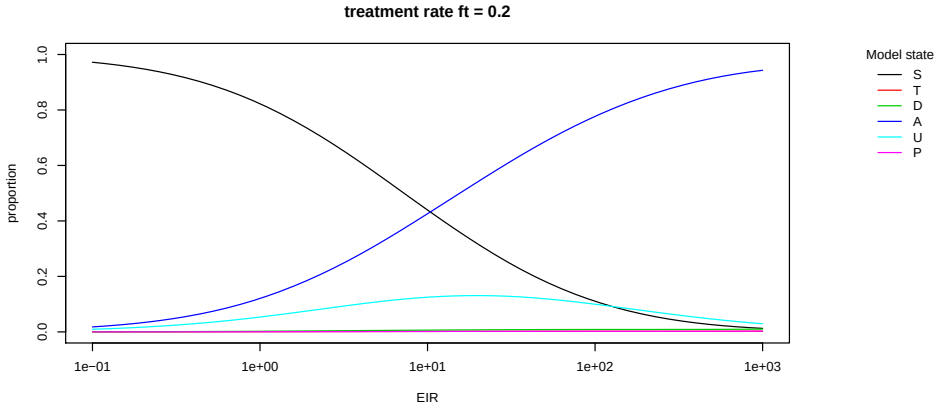
```
# explore a range of EIR and treatment levels
EIR <- exp(seq(log(0.1), log(1000), length=51))
ft <- c(0, 0.2, 0.4, 1)

# 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_cpp(EIR[j], ft[i], p, age, h$nodes, h$weights)
  }
}
```

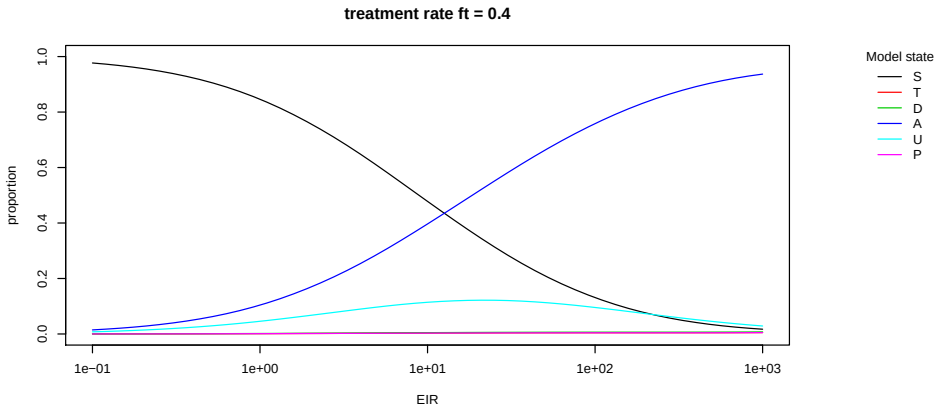
Save state proportions in array

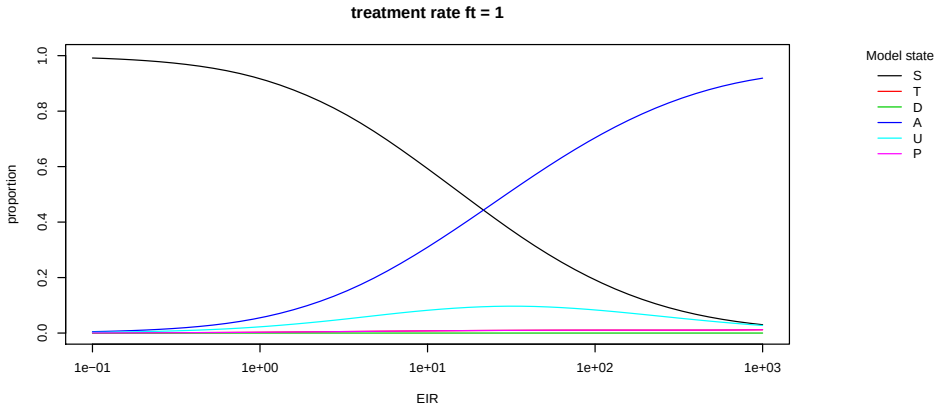
```
# save state proportions in array
stateNames <- c("S", "T", "D", "A", "U", "P")
m <- array(0, dim=c(length(ft), length(EIR), length(stateNames)))
for (i in 1:length(eqList)) {
  for (j in 1:length(eqList[[i]])) {
    m[i,j,] <- colSums(subset(eqList[[i]][[j]]$states, select=stateNames))
  }
}
```

Produce plots

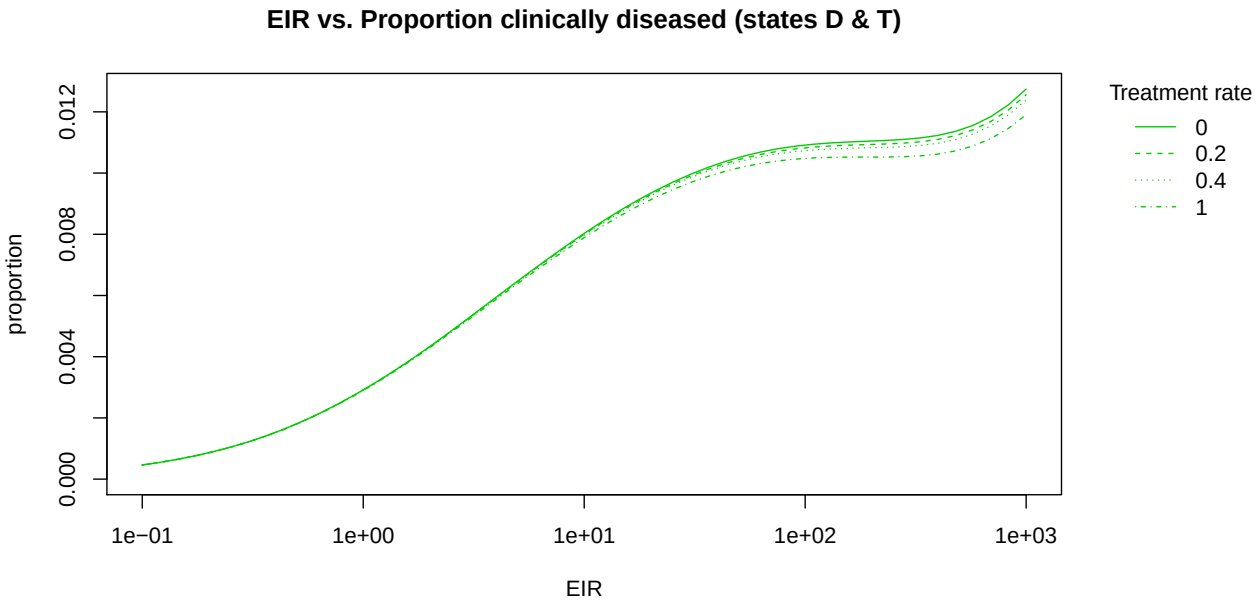

treatment rate ft = 0
proportion
0.0
0.2
0.4
0.6
0.8
1.0
1e−01
1e+00
1e+01
1e+02
1e+03
EIR
Model state
S
T
D
A
U
P


treatment rate ft = 0.2
proportion
0.0
0.2
0.4
0.6
0.8
1.0
1e−01
1e+00
1e+01
1e+02
1e+03
EIR
Model state
S
T
D
A
U
P


treatment rate ft = 0.4
proportion
0.0
0.2
0.4
0.6
0.8
1.0
1e−01
1e+00
1e+01
1e+02
1e+03
EIR
Model state
S
T
D
A
U
P


treatment rate ft = 1
proportion
0.0
0.2
0.4
0.6
0.8
1.0
1e−01
1e+00
1e+01
1e+02
1e+03
EIR
Model state
S
T
D
A
U
P

Notice that the greatest proportion of the population is in the susceptible compartment at low EIR, and in 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):

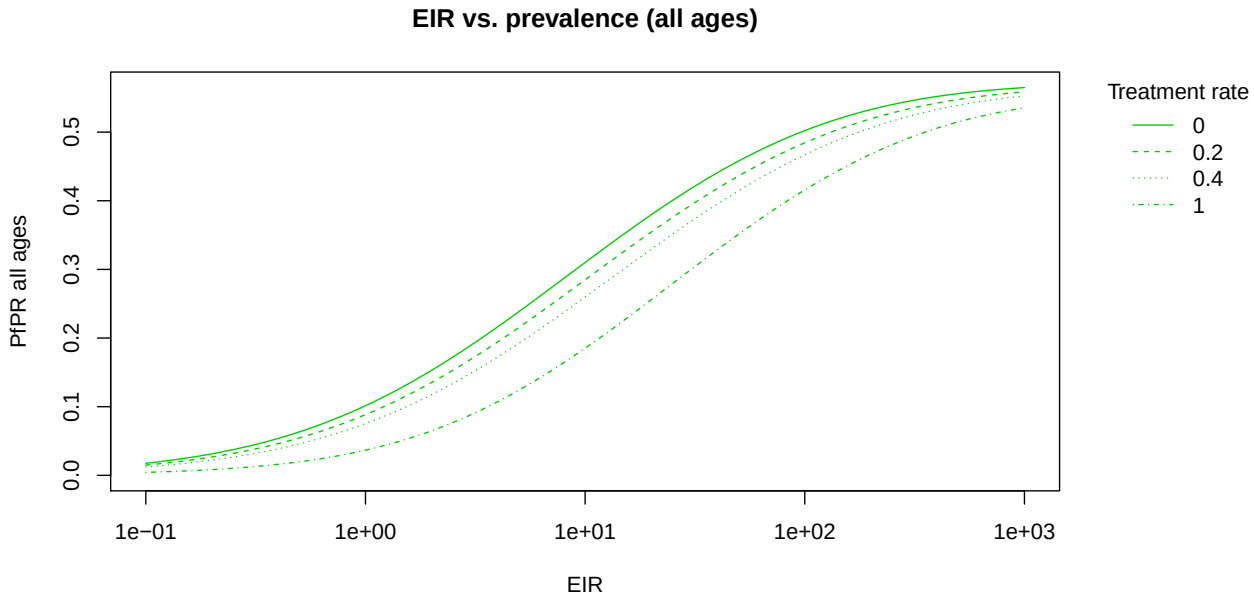


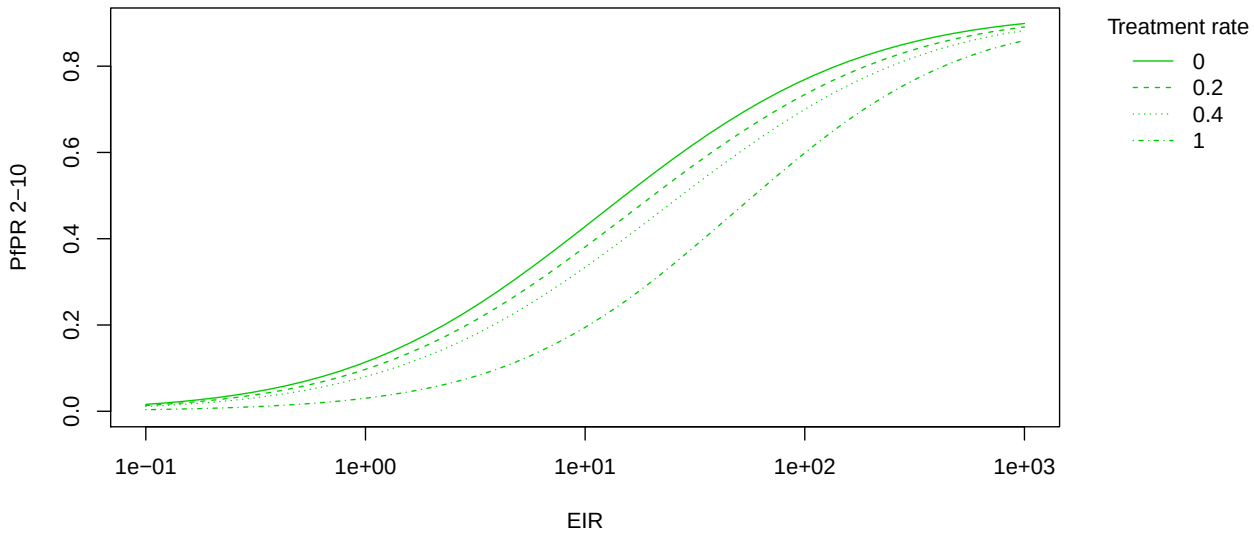
Even at very high transmission the proportion of clinically diseased individuals rarely goes much over 1%. This is due to the buildup of immunity, which causes individuals to become asymptomatically infected later in life.

EIR, prevalence and incidence

We can use the equilibrium model output to calculate prevalence and incidence in any given age bands.

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

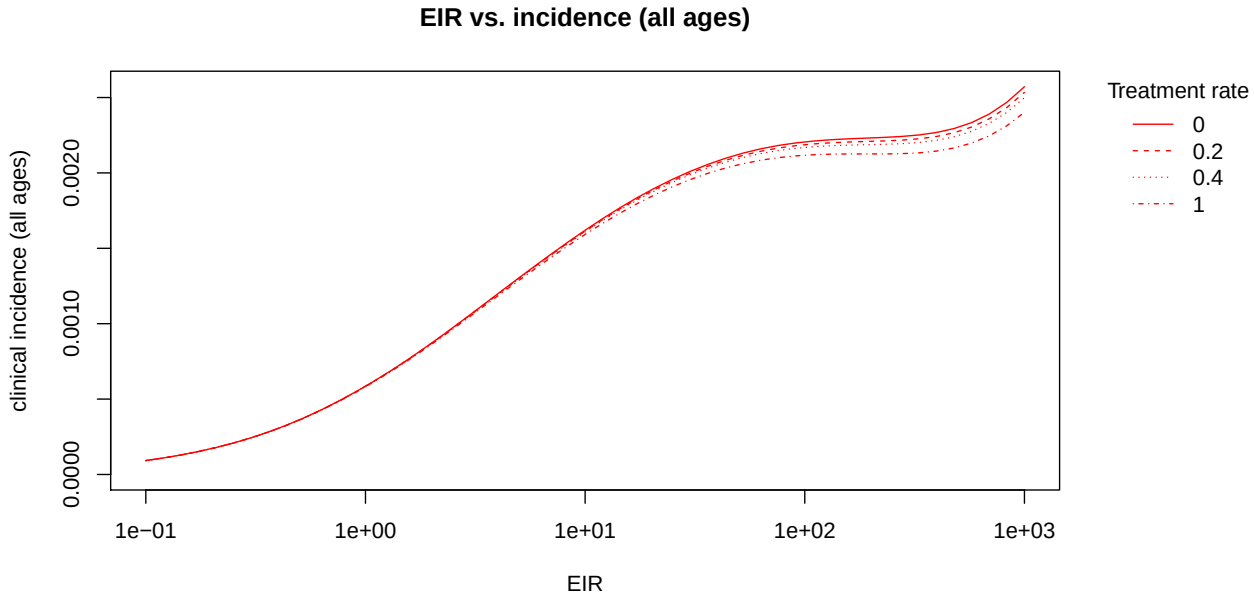


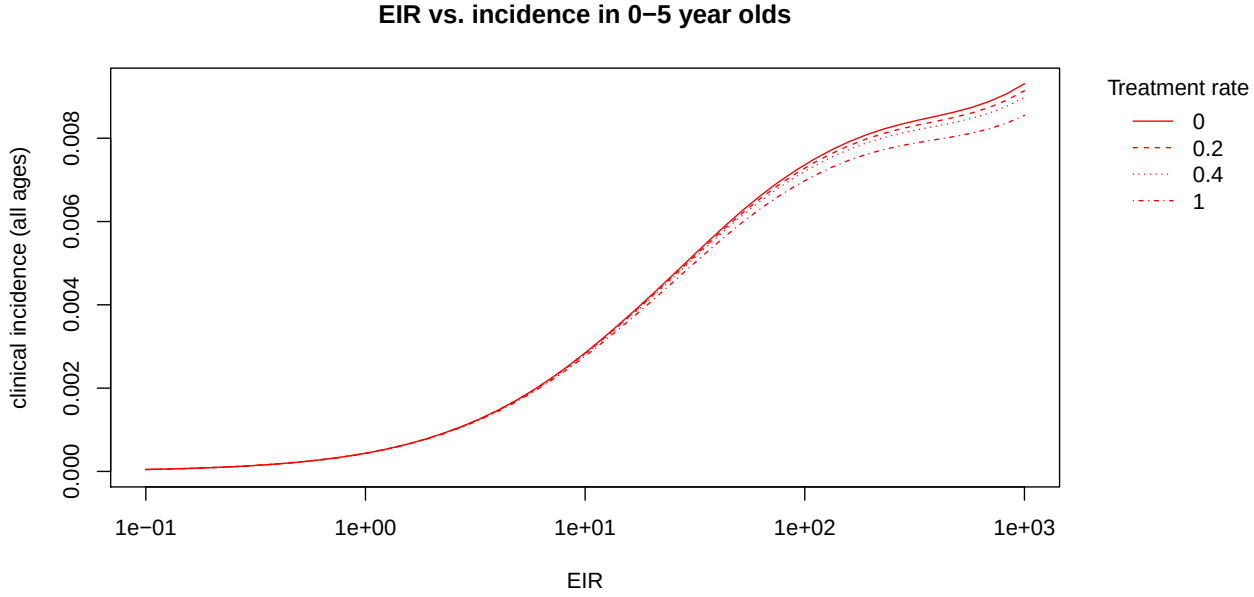


And similarly for incidence:

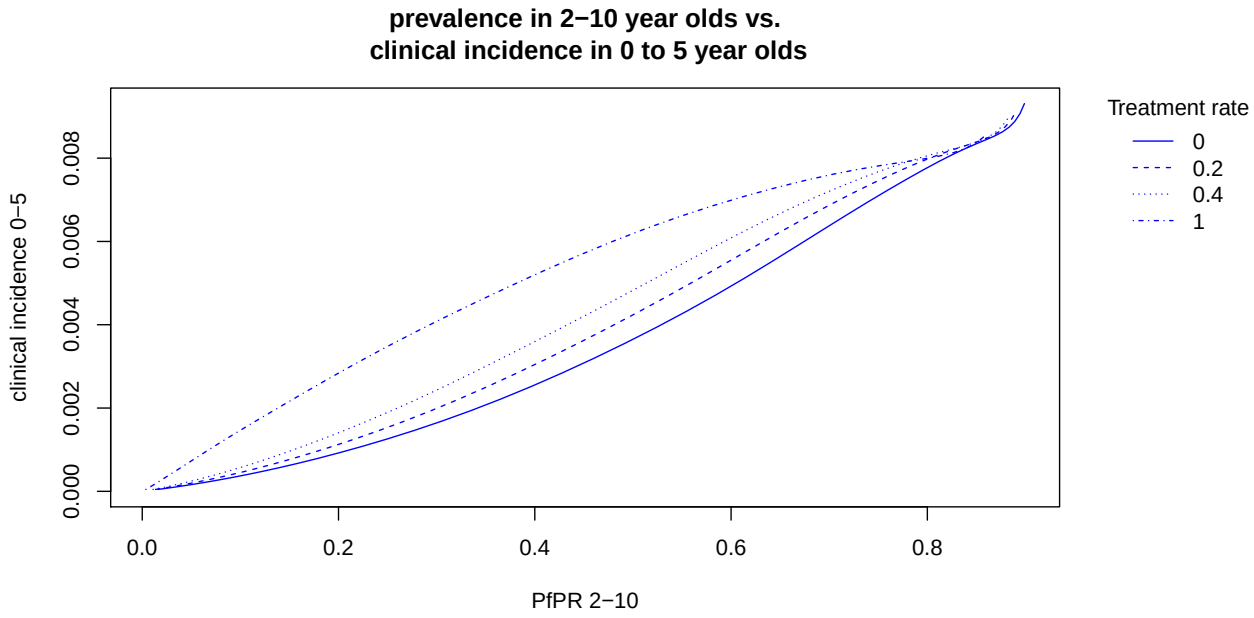
```
# calculate incidence for a range of treatment rates
inc_allAges <- inc_0_5 <- list()
for (i in 1:length(ft)) {
  inc_allAges[[i]] <- mapply(find_inc, eqList[[i]], 0, Inf)
```

```
  inc_0_5[[i]] <- mapply(find_inc, eqList[[i]], 0, 5)
}
```





Note that plots of prevalence vs. incidence can be counter-intunitive at first, because incidence appears to go up with increasing treatment. This is because a prevalence of 50% with high treatment implies that transmission is extremely high to maintain this prevalence, whereas prevalence of 50% with low treatment implies lower transmission, and so lower clinical incidence.



(TO DO - breakdown by age)

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