

# TB Vaccination

PDF Version available [here](#).

```
library(data.table)
library(pomp)
library(ggplot2)
library(rstan)

rstan_options(auto_write = TRUE)
options(mc.cores = parallel::detectCores())

#everyone enters on jan 1
#results are for dec 31
newPeople <- data.table(id=1:100,year=2000,age=1,timeNotVax=0,timeWithVax=0,vaccinated=0,ltbi=0,atbi=0)

pomp::bake("data/peopleNoVax.RDS",{
  set.seed(4)
  peopleNoVax <- vector("list",length=17)
  peopleNoVax[[1]] <- newPeople[1,][-1,]
  for(i in 1:17){
    # NO VACCINATIONS
    if(i!=1) peopleNoVax[[i]] <- copy(peopleNoVax[[i-1]])
    peopleNoVax[[i]][,age:=age+1]
    peopleNoVax[[i]] <- rbind(peopleNoVax[[i]],newPeople)
    peopleNoVax[[i]][,year:=2000+i]

    N <- nrow(peopleNoVax[[i]])
    peopleNoVax[[i]][sample(1:N,size=round(N*0.050)),ltbi:=1]
    peopleNoVax[[i]][,timeNotVax:=timeNotVax+1]

    Nltbi <- sum(peopleNoVax[[i]]$ltbi)
    peopleNoVax[[i]][sample(which(peopleNoVax[[i]]$ltbi==1),size=round(Nltbi*0.05)),atbi:=1]
  }
  peopleNoVax
}) -> peopleNoVax

pomp::bake("data/peopleWithVax.RDS",{
  set.seed(4)
  peopleWithVax <- vector("list",length=17)
  peopleWithVax[[1]] <- newPeople[1,][-1,]
  for(i in 1:17){
    # WITH VACCINATIONS, BUT STOPPING THEM AFTERWARDS
    if(i!=1) peopleWithVax[[i]] <- copy(peopleWithVax[[i-1]])
    peopleWithVax[[i]][,age:=age+1]
    peopleWithVax[[i]] <- rbind(peopleWithVax[[i]],newPeople)
    peopleWithVax[[i]][,year:=2000+i]
    N <- nrow(peopleWithVax[[i]])
    if(i>=10){
      peopleWithVax[[i]][sample(1:N,size=round(N*0.050)),ltbi:=1]
      peopleWithVax[[i]][,timeNotVax:=timeNotVax+1]
    } else {
      peopleWithVax[[i]][sample(1:N,size=round(N*0.050)),ltbi:=1]
```

```

    peopleWithVax[[i]][,timeWithVax:=timeWithVax+1]
  }

  Nltbi <- sum(peopleWithVax[[i]]$ltbi)
  peopleWithVax[[i]][sample(which(peopleWithVax[[i]]$ltbi==1),size=round(Nltbi*0.05)),atbi:=1]
}
peopleWithVax
}) -> peopleWithVax

```

Lets try an easy model, detecting LTBI in unvaccinated people.

```

stanData=peopleNoVax[[17]]
data = list(N=nrow(stanData),
            y=stanData$ltbi,
            timeNotVax=stanData$timeNotVax)

stan_code = "
data {
  int<lower=0> N;
  vector[N] timeNotVax;
  int y[N];
}
parameters {
  real<lower=0,upper=0.5> thetaNotVax;
}
model {
  thetaNotVax ~ beta(0.05, 1);

  for (n in 1:N)
    y[n] ~ bernoulli(1-((1-thetaNotVax)^timeNotVax[n]));
}
"
pomp::bake("results/noVax.RDS",{
stan(model_code=stan_code,
      model_name="noVax",
      data=data,
      iter=2000, chains=1, init=0)
}) -> fit

```

```

##
## SAMPLING FOR MODEL 'noVax' NOW (CHAIN 1).
##
## Gradient evaluation took 0.000289 seconds
## 1000 transitions using 10 leapfrog steps per transition would take 2.89 seconds.
## Adjust your expectations accordingly!
##
##
## Iteration:    1 / 2000 [  0%] (Warmup)
## Iteration:   200 / 2000 [ 10%] (Warmup)
## Iteration:   400 / 2000 [ 20%] (Warmup)
## Iteration:   600 / 2000 [ 30%] (Warmup)
## Iteration:   800 / 2000 [ 40%] (Warmup)
## Iteration:  1000 / 2000 [ 50%] (Warmup)
## Iteration:  1001 / 2000 [ 50%] (Sampling)

```

```
## Iteration: 1200 / 2000 [ 60%] (Sampling)
## Iteration: 1400 / 2000 [ 70%] (Sampling)
## Iteration: 1600 / 2000 [ 80%] (Sampling)
## Iteration: 1800 / 2000 [ 90%] (Sampling)
## Iteration: 2000 / 2000 [100%] (Sampling)
##
## Elapsed Time: 0.776254 seconds (Warm-up)
##               0.919816 seconds (Sampling)
##               1.69607 seconds (Total)
```

```
summary(fit)$summary
```

```
##               mean      se_mean      sd      2.5%
## thetaNotVax  0.05049601 0.0001064867 0.002089335  0.0463865
## lp__        -981.84337461 0.0367368723 0.744695137 -984.3416927
##               25%      50%      75%      97.5%
## thetaNotVax  0.04916255  0.05057602  0.05188691  0.05479823
## lp__        -981.99694446 -981.53906294 -981.37179339 -981.32075617
##               n_eff      Rhat
## thetaNotVax 384.9685 0.9992804
## lp__        410.9156 1.0003625
```

Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Cmd+Option+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Cmd+Shift+K* to preview the HTML file).