07 - Age analysis

2019-12-10

This vignette provides an extension of the general method of **phyloflow**. The aim is to understand the transmission flows between one-year increment age groups. The differences between this example with the general pipeline of **phyloflow** is the correlation between flows. To tackle this problem, we impose a Gaussian process prior on transmission flows.

Dataset

We start with simulating transmission counts between seven age groups called "15-19","20-24","25-29","30-34","35-39","40-44","45-49". Note that in practice, it would be good to use this method to investigate transmission dynamics between one-year increment age group, as the squared exponential kernel is for the continuous input space.

```
library(rstan)
library(data.table)
library(ggplot2)
library(viridis)
set.seed(42)
rstan_options(auto_write = TRUE)
options(mc.cores = parallel::detectCores())

set.seed(42)
alpha_true <- c(2.5)
rho_true <- c(12,9)
mu_true <- -1
gp_dim <- 2
xi <- c(0.35, 0.45, 0.5, 0.55, 0.5, 0.55, 0.4)

dobs <- data.table(expand.grid(TR_TRM_CATEGORY = c("15-19","20-24","25-29","30-34","35-39","40-44","45-4
                               REC_TRM_CATEGORY = c("15-19","20-24","25-29","30-34","35-39","40-44","45-

ds <- data.table(CATEGORY = c("15-19","20-24","25-29","30-34","35-39","40-44","45-49"),
                 P = xi,ID = 1:7)
setnames(ds,colnames(ds),paste0('TR_TRM_',colnames(ds)))
dobs <- merge(dobs,ds,by='TR_TRM_CATEGORY')
setnames(ds,colnames(ds),gsub('TR_','REC_',colnames(ds)))
dobs <- merge(dobs,ds,by='REC_TRM_CATEGORY')
setnames(ds,colnames(ds),gsub('REC_TRM_','',colnames(ds)))
dobs[,P:= TR_TRM_P * REC_TRM_P]
dobs[,TR_SMOOTH_CATEGORY:=as.numeric(substr(TR_TRM_CATEGORY,1,2))+2]
dobs[,REC_SMOOTH_CATEGORY:=as.numeric(substr(REC_TRM_CATEGORY,1,2))+2]
dobs[, TR_SAMPLING_CATEGORY:= TR_TRM_CATEGORY]
dobs[, REC_SAMPLING_CATEGORY:= REC_TRM_CATEGORY]

simu_pars <- list(  N=nrow(dobs), D=gp_dim, x=cbind(dobs$TR_SMOOTH_CATEGORY,dobs$REC_SMOOTH_CATEGORY),
```

```r
                   alpha=alpha_true, rho=rho_true,
                   mu=mu_true,xi=dobs$P)
#   simulate data set
simu_fit <- stan(   file="simu_poiss.stan",
                  data=simu_pars, iter=1,
                  chains=1, seed=424838, algorithm="Fixed_param")
```

```
##
## SAMPLING FOR MODEL 'simu_poiss' NOW (CHAIN 1).
## Chain 1: Iteration: 1 / 1 [100%]  (Sampling)
## Chain 1:
## Chain 1:  Elapsed Time: 0 seconds (Warm-up)
## Chain 1:                4.8e-05 seconds (Sampling)
## Chain 1:                4.8e-05 seconds (Total)
## Chain 1:
```

```r
dobs$TRM_OBS <- extract(simu_fit)$y[1,]
```

Input data: observed transmission flows

Input data of the similar format of **phyloflow** are expected.

```r
dobs <- subset(dobs, select = c('TR_TRM_CATEGORY', 'REC_TRM_CATEGORY','TR_SAMPLING_CATEGORY',
                                'REC_SAMPLING_CATEGORY', 'TR_SMOOTH_CATEGORY','REC_SMOOTH_CATEGORY',
                                'TRM_OBS'))
head(dobs)
```

```
##    TR_TRM_CATEGORY REC_TRM_CATEGORY TR_SAMPLING_CATEGORY REC_SAMPLING_CATEGORY TR_SMOOTH_CATEGORY REC
## 1:           15-19            15-19                15-19                 15-19                 17
## 2:           20-24            15-19                20-24                 15-19                 22
## 3:           25-29            15-19                25-29                 15-19                 27
## 4:           30-34            15-19                30-34                 15-19                 32
## 5:           35-39            15-19                35-39                 15-19                 37
## 6:           40-44            15-19                40-44                 15-19                 42
##    TRM_OBS
## 1:       0
## 2:       1
## 3:       0
## 4:       1
## 5:       0
## 6:       0
```

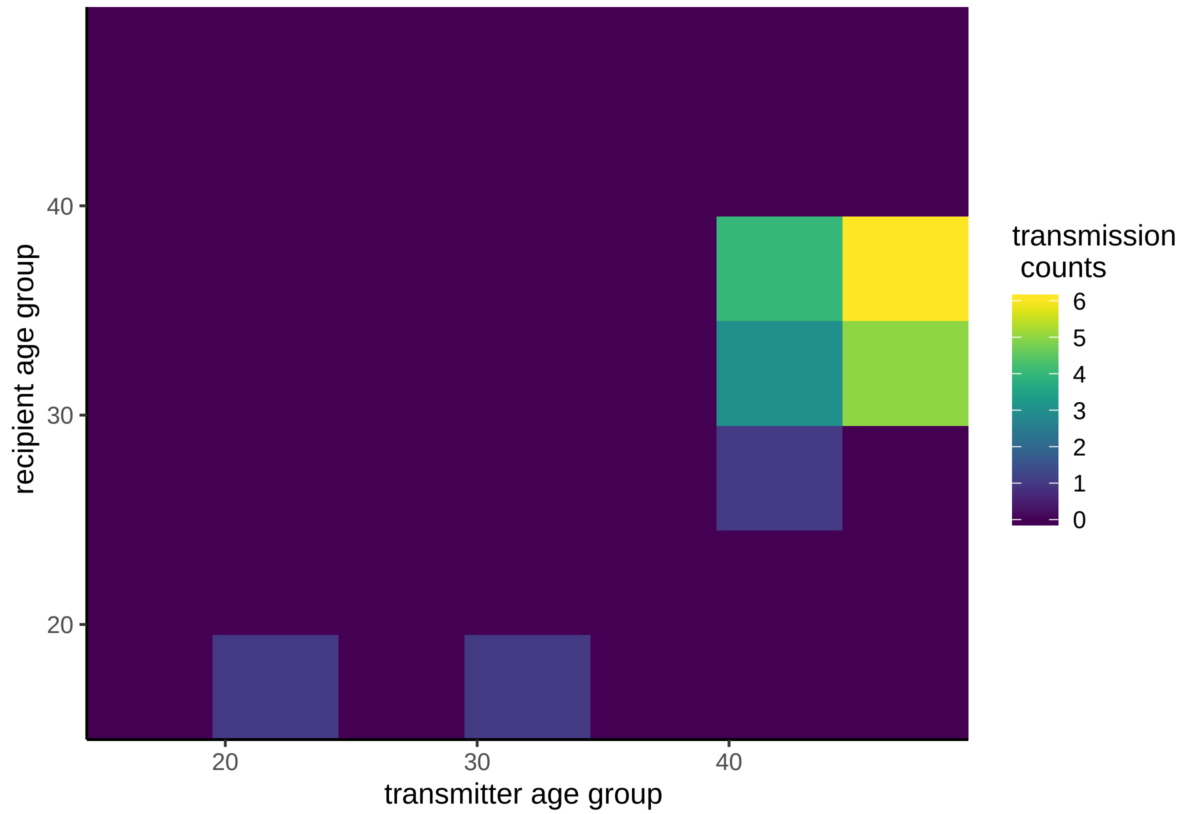
`dobs` specifies observed counts of transmissions from a transmitter age group to a recipient age group. It must contain the following columns:

- *TR_TRM_CATEGORY* name of transmitter group.
- *REC_TRM_CATEGORY* name of recipient group.
- *TR_SMOOTH_CATEGORY* midpoint of transmitter age group.
- *REC_SMOOTH_CATEGORY* midpoint of recipient age group.
- *TRM_CAT_PAIR_ID* identifier of transmitter-recipient pair
- *TRM_OBS* observed transmission counts

Let us look at the data. The first row shows zero counts of transmission flows from age group "15-19" to age group "15-19".

Here is a heatmap of our input data:

```
ggplot(dobs, aes(TR_SMOOTH_CATEGORY, REC_SMOOTH_CATEGORY))+
  geom_tile(aes(fill = TRM_OBS)) +
  scale_fill_viridis() +
  scale_x_continuous(expand = c(0,0), limits = c(14.5,49.5))+
  scale_y_continuous(expand = c(0,0), limits = c(14.5,49.5))+
  theme_classic()+
  labs(x='transmitter age group \n', y='\n recipient age group',fill='transmission \n counts')
```



Input data: sampling information

** dobs also must contain information about how each group was sampled. This is stored in the following columns:

- *TR_SAMPLING_CATEGORY* sampling strata of transmitter group
- *REC_SAMPLING_CATEGORY* sampling strata of recipient group

dprior.fit specifies the distribution of probability of sampling an individual from each sampling group. This is either given by or approximated by beta distribution in SARWS model or GLM model. This information is stored in the following columns:

- *SAMPLING_CATEGORY* name of sampling strata
- *ALPHA, BETA* shape parameters of the distribution of sampling probability.

Let us look at the sampling information:

```
ds$TRIAL <- c(4000, 3700, 3300, 2500, 1700, 1000, 500)
ds[,SUC := round(TRIAL * P)]
dprior.fit <- copy(ds)
```

```
dprior.fit[,ALPHA := SUC+1]
dprior.fit[,BETA := TRIAL-SUC+1]
dprior.fit
```

```
##    CATEGORY    P ID TRIAL  SUC ALPHA BETA
## 1:    15-19 0.35  1  4000 1400  1401 2601
## 2:    20-24 0.45  2  3700 1665  1666 2036
## 3:    25-29 0.50  3  3300 1650  1651 1651
## 4:    30-34 0.55  4  2500 1375  1376 1126
## 5:    35-39 0.50  5  1700  850   851  851
## 6:    40-44 0.55  6  1000  550   551  451
## 7:    45-49 0.40  7   500  200   201  301
```

Method

We use **rstan** to sample from the posterior distribution

$$p(\lambda, s|n) \propto \prod_{i=1,\cdots,7;j=1,\cdots,7} Poisson(n_{ij}; \lambda_{ij} * s_i * s_j) p(\lambda_{ij}) p(s_i) p(s_j).$$

Then, we calculate the main quantity of interest, π, via

$$\pi_{ij} = \lambda_{ij} / \sum_{k=1,2;l=1,2} \lambda_{kl}.$$

for $i = 1, , \cdots, 7$ and $j = 1, , \cdots, 7$.

Independent Gamma prior

```
tmp <- subset(ds,select = c('CATEGORY','ID'))
setnames(tmp, colnames(tmp), paste0('TR_TRM_',colnames(tmp)))
dobs <- merge(dobs,tmp,by='TR_TRM_CATEGORY')
setnames(tmp, colnames(tmp), gsub('TR_TRM_','REC_TRM_',colnames(tmp)))
dobs <- merge(dobs,tmp,by='REC_TRM_CATEGORY')
setnames(tmp, colnames(tmp), gsub('REC_TRM_','',colnames(tmp)))


data.gamma <- list(N=nrow(dobs),
                   Y=dobs$TRM_OBS,
                   N_xi = nrow(dprior.fit),
                   shape = cbind(dprior.fit$ALPHA,dprior.fit$BETA),
                   xi_id = cbind(dobs$TR_TRM_ID,dobs$REC_TRM_ID),
                   alpha = 0.8/nrow(dobs))
```

After preparing data, we could estimate flows under independent Gamma prior.

```
 fit.gamma <- stan(file = 'gamma.stan',
             data = data.gamma,
             iter = 3000,  warmup = 500, chains=1, thin=1, seed = 42,
             algorithm = "NUTS", verbose = FALSE,
             control = list(adapt_delta = 0.8, max_treedepth=10))
```

```
##
## SAMPLING FOR MODEL 'gamma' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 8e-05 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.8 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Iteration:    1 / 3000 [  0%]  (Warmup)
## Chain 1: Iteration:  300 / 3000 [ 10%]  (Warmup)
## Chain 1: Iteration:  501 / 3000 [ 16%]  (Sampling)
## Chain 1: Iteration:  800 / 3000 [ 26%]  (Sampling)
## Chain 1: Iteration: 1100 / 3000 [ 36%]  (Sampling)
## Chain 1: Iteration: 1400 / 3000 [ 46%]  (Sampling)
## Chain 1: Iteration: 1700 / 3000 [ 56%]  (Sampling)
## Chain 1: Iteration: 2000 / 3000 [ 66%]  (Sampling)
## Chain 1: Iteration: 2300 / 3000 [ 76%]  (Sampling)
## Chain 1: Iteration: 2600 / 3000 [ 86%]  (Sampling)
## Chain 1: Iteration: 2900 / 3000 [ 96%]  (Sampling)
## Chain 1: Iteration: 3000 / 3000 [100%]  (Sampling)
## Chain 1:
## Chain 1:  Elapsed Time: 6.34811 seconds (Warm-up)
## Chain 1:                16.9041 seconds (Sampling)
## Chain 1:                23.2522 seconds (Total)
## Chain 1:
```

```
M <- 30
D <- 2
indices <- matrix(NA, M^D, D)
mm=0;
for (m1 in 1:M){
  for (m2 in 1:M){
    mm = mm+1
    indices[mm,] = c(m1, m2)
  }
}



data.gp <- list( M= M, M_nD= M^D,
                       L= c(3/2*max(dobs$TR_SMOOTH_CATEGORY),3/2*max(dobs$REC_SMOOTH_CATEGORY)),
                       N = nrow(dobs),
                       x = cbind(dobs$TR_SMOOTH_CATEGORY,dobs$REC_SMOOTH_CATEGORY),
                       D = D,
                       y = dobs$TRM_OBS,
                       indices= indices,
                       N_xi = nrow(ds),
                       shape = cbind(dprior.fit$ALPHA,dprior.fit$BETA),
                       xi_id = cbind(dobs$TR_TRM_ID,dobs$REC_TRM_ID))
```

After preparing data, we could estimate flows under independent Gaussian process prior.

```
fit.gp <- stan(file = 'gp.stan',
           data = data.gp,
           iter = 3000,  warmup = 500, chains=1, thin=1, seed = 42,
```

```r
            algorithm = "NUTS", verbose = FALSE,
            control = list(adapt_delta = 0.8, max_treedepth=10))
```

```
##
## SAMPLING FOR MODEL 'gp' NOW (CHAIN 1).
## Chain 1:
## Chain 1: Gradient evaluation took 0.001967 seconds
## Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 19.67 seconds.
## Chain 1: Adjust your expectations accordingly!
## Chain 1:
## Chain 1:
## Chain 1: Iteration:    1 / 3000 [  0%]  (Warmup)
## Chain 1: Iteration:  300 / 3000 [ 10%]  (Warmup)
## Chain 1: Iteration:  501 / 3000 [ 16%]  (Sampling)
## Chain 1: Iteration:  800 / 3000 [ 26%]  (Sampling)
## Chain 1: Iteration: 1100 / 3000 [ 36%]  (Sampling)
## Chain 1: Iteration: 1400 / 3000 [ 46%]  (Sampling)
## Chain 1: Iteration: 1700 / 3000 [ 56%]  (Sampling)
## Chain 1: Iteration: 2000 / 3000 [ 66%]  (Sampling)
## Chain 1: Iteration: 2300 / 3000 [ 76%]  (Sampling)
## Chain 1: Iteration: 2600 / 3000 [ 86%]  (Sampling)
## Chain 1: Iteration: 2900 / 3000 [ 96%]  (Sampling)
## Chain 1: Iteration: 3000 / 3000 [100%]  (Sampling)
## Chain 1:
## Chain 1:  Elapsed Time: 81.5593 seconds (Warm-up)
## Chain 1:                200.284 seconds (Sampling)
## Chain 1:                281.844 seconds (Total)
## Chain 1:
```

Finally, we checked the effective sample size and Rhat for the Gamma fit.

```r
range(summary(fit.gamma)$summary[, "n_eff"])
```

```
## [1]  528.7714 3199.4158
```

```r
range(summary(fit.gamma)$summary[, "Rhat"])
```

```
## [1] 0.9995999 1.0017399
```

```r
params_gamma <- extract(fit.gamma)
```

Finally, we checked the effective sample size and Rhat for the GP fit.

```r
range(summary(fit.gp)$summary[, "n_eff"])
```

```
## [1]  276.4037 4002.5037
```

```r
range(summary(fit.gp)$summary[, "Rhat"])
```

```
## [1] 0.9995999 1.0135090
```

```r
params_gp <- extract(fit.gp)
```

The histograms of hyperparameters are plotted in order to compare with true hyperparameter values under GP prior.

```r
c_light <- c("#DCBCBC")
c_dark <- c("#8F2727")
c_dark_highlight <- c("#7C0000")
```

```
par(mfrow=c(2, 2))
hist(params_gp$alpha, main="", xlab="alpha", col=c_dark, border=c_dark_highlight, yaxt='n')
abline(v=2.5, col=c_light, lty=1, lwd=3)
hist(params_gp$rho[,1], main="", xlab="rho1", col=c_dark, border=c_dark_highlight, yaxt='n')
abline(v=12, col=c_light, lty=1, lwd=3)
hist(params_gp$rho[,2], main="", xlab="rho2", col=c_dark, border=c_dark_highlight, yaxt='n')
abline(v=9, col=c_light, lty=1, lwd=3)
hist(params_gp$mu, main="", xlab="mu", col=c_dark, border=c_dark_highlight, yaxt='n')
abline(v=-1, col=c_light, lty=1, lwd=3)
```