Results check

Generate data

```r
n.sims <- 1
 n.epis <- 10

 fs <- matrix(nrow=n.epis, ncol=n.sims)
 pcts <- matrix(nrow=n.epis, ncol=n.sims)

 K.VC_linear <- fs
 K.VC_rpart <- fs
 K.VC_super <- fs
 K.norm_linear <-fs
 K.norm_rpart <-fs
 K.norm_super <- fs
 K.VC_alone <- fs
 K.norm_alone <- fs
 K.linear_alone <- fs
 K.rpart_alone <- fs
 K.super_alone <- fs

 for (i in 1:n.sims) {

   cat("iteration ", i, "\n")

  pcts[,i] <- runif(n.epis, 0.05,1)

  x <- runif(n.epis, 0, 1)
  beta <- 0.4 * exp(x)

  gamma <- .33
  pop_sz <- rnbinom(n.epis, mu=5000, size=20)

  ecs <- gen.epidemic.curves.SIR(pcts[,i], beta,pop_sz, gamma)


  ## Need to decompose ecs into ecs and true final sizes
  fs[,i] <- ecs$fs
  ecs <- ecs$ecs
 }
```

```
## iteration  1
 fs
```

```
##        [,1]
##  [1,] 6031
##  [2,] 5307
```

```
##  [3,] 3792
##  [4,] 2888
##  [5,] 3787
##  [6,] 5543
##  [7,] 3835
##  [8,] 3064
##  [9,]   13
## [10,] 4934
```

Step 1: initialize K

Set K = 2 times sum of currently observed cases

```r
dat <- data.frame(K=2*sapply(ecs,sum), pop_sz=pop_sz,
                  x=x)
```

Step 2: Fit stat model

```r
stat_fit <- stat.mdl.linear.fit(dat)
```

```
## Loading required package: rpart
```

```r
stat_res <- stat.mdl.linear.pred(stat_fit)
stat_res
```

```
##        1        2        3        4        5        6        7        8
## 7838.839 4953.189 3961.150  648.564 4384.861 4936.682 5975.041 2435.425
##        9       10
## 2810.197 4396.053
```

Step 3: Fit VC model

```r
VC_fit <- epi.mdl.ViboudChowell.fit2(ecs, stat_res, prev.mdl = NULL)
VC_res <- epi.mdl.ViboudChowell.pred2(VC_fit)
VC_res
```

```
##  [1] 7492.64182 5046.48948 3845.09362 1296.00008 1300.00008 4692.88397
##  [7] 5925.94343 2437.91146   11.13454 4275.92773
```

Now iterate: fit VC with linear model

```r
 for (i in 1:n.sims) {
dat <- data.frame(K=2*sapply(ecs,sum), pop_sz=pop_sz,
                  x=x)

  K.VC_linear[,i] <- epiInf.EM(ecs, dat,
                              stat.mdl.linear.fit,
                              epi.mdl.ViboudChowell.fit2,
                              stat.mdl.linear.pred,
                              epi.mdl.ViboudChowell.pred2,
                              threshold = 1)$K
```

```
 }
```

K.VC_linear

```
##                 [,1]
##  [1,] 5255.00022
##  [2,] 1405.00007
##  [3,] 3736.00012
##  [4,] 1296.00008
##  [5,] 2373.26634
##  [6,] 1641.00007
##  [7,] 3495.80900
##  [8,] 1721.00007
##  [9,]   11.21139
## [10,] 2356.36430
```