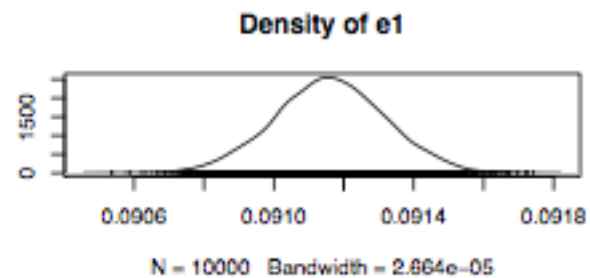
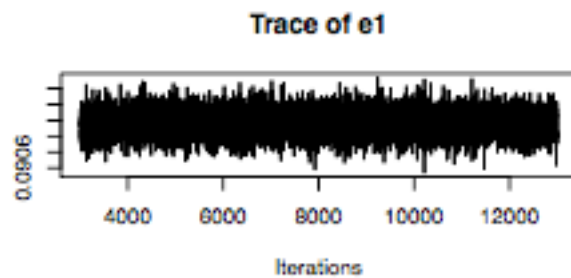


what if we get rid of the intrinsic scatter?

```
## broad priors:
# e1 <- 0.0912
# e1 ~ dunif(0.01, 1.0)
# ex <- 0.0912
# gi <- 2.93
# gf <- 0.0794
# gi ~ dunif(0.01, 100)
# gf ~ dunif(0.01, 100)
# ri <- 6.0
# rf <- 5.0
# ue <- 0.0
```

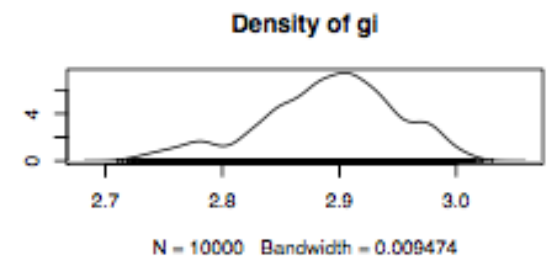
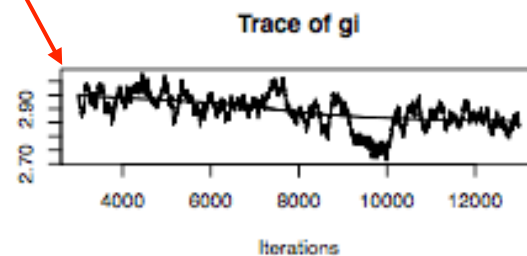
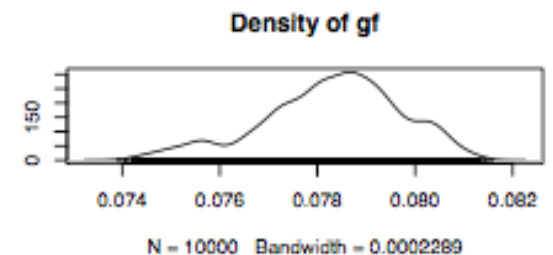
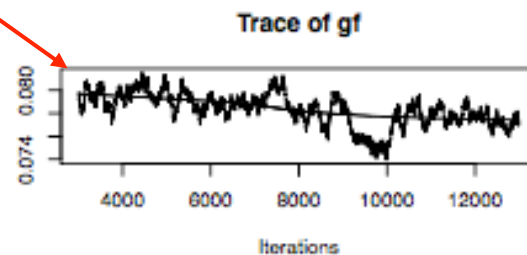
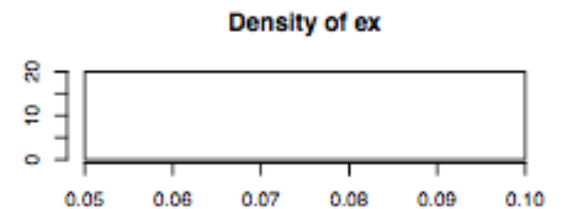
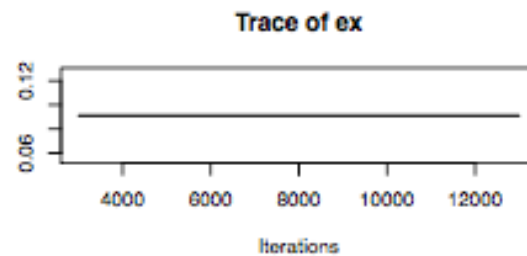
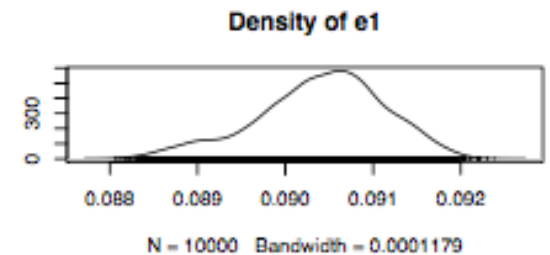
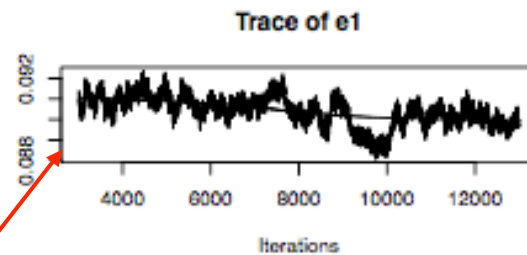
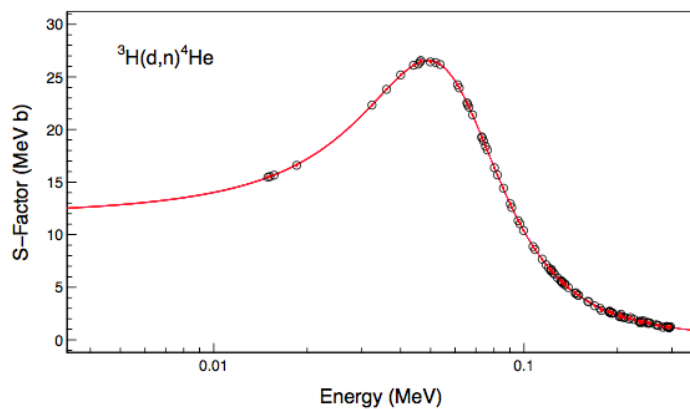
sample only energy



```
## broad priors:
# e1 <- 0.0912
e1 ~ dunif(0.01, 0.2)
ex <- 0.0912
# gi <- 2.93
# gf <- 0.0794
gi ~ dunif(0.0, 10)
gf ~ dunif(0.0, 10)
ri <- 6.0
rf <- 5.0
ue <- 0.0
```

why strong  
correlation??

sample energy and  
reduced widths



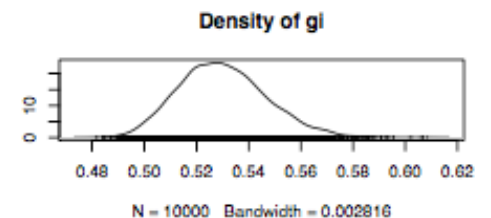
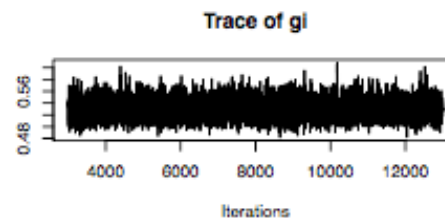
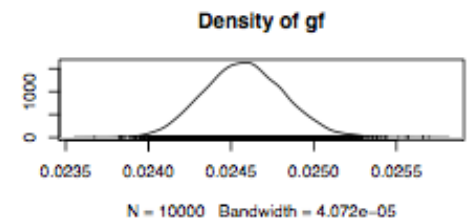
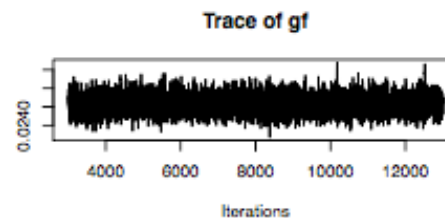
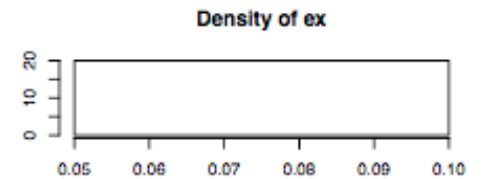
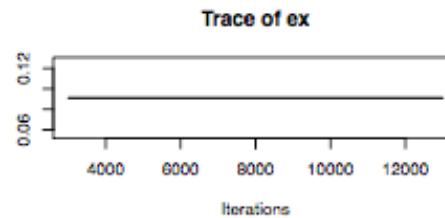
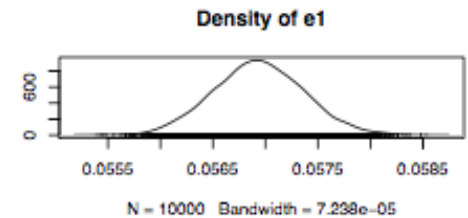
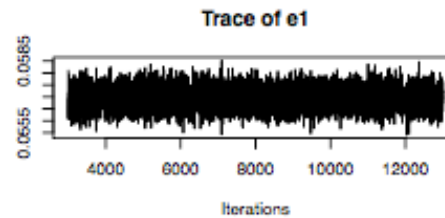
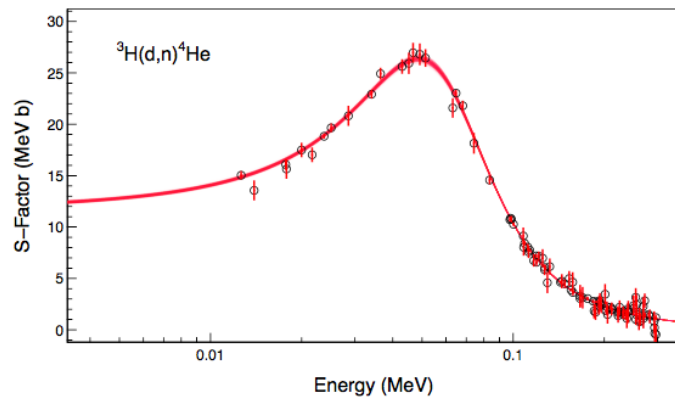
question:

how does the chain look like for a PREDICTED S-factor at a given energy?

```
## broad priors:
# e1 <- 0.0912
e1 ~ dunif(0.01, 1.0)
ex <- 0.0912
# gi <- 2.93
# gf <- 0.0794
gi ~ dunif(0.0, 100)
gf ~ dunif(0.0, 100)
ri <- 6.0
rf <- 5.0
ue <- 0.0

bar[1] <- 0.0912 # eigenenergy
bar[2] <- 0.0912 # Er for Bc=Sc(Er)
bar[3] <- 2.93   # reduced width incoming
bar[4] <- 0.0794 # reduced width outgoing
bar[5] <- 6.0
bar[6] <- 5.0
bar[7] <- 0.0
```

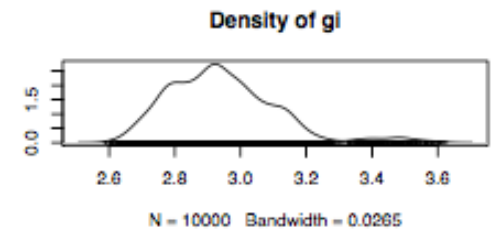
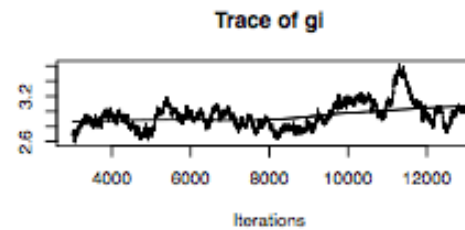
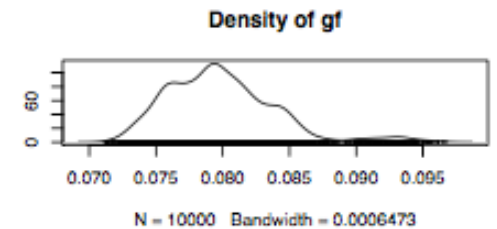
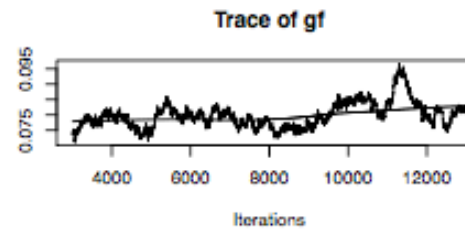
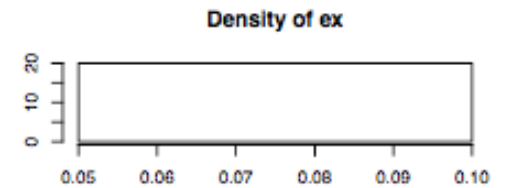
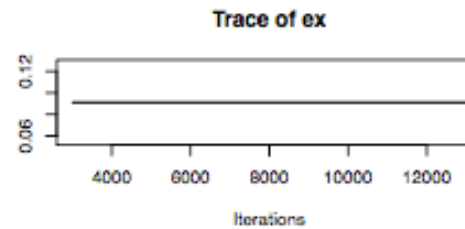
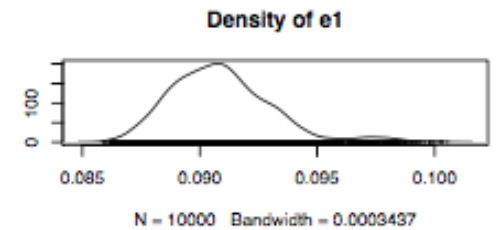
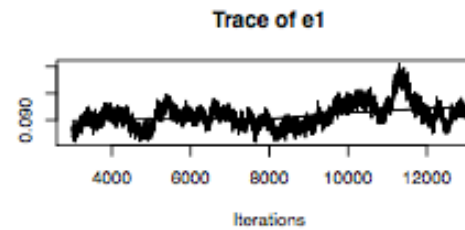
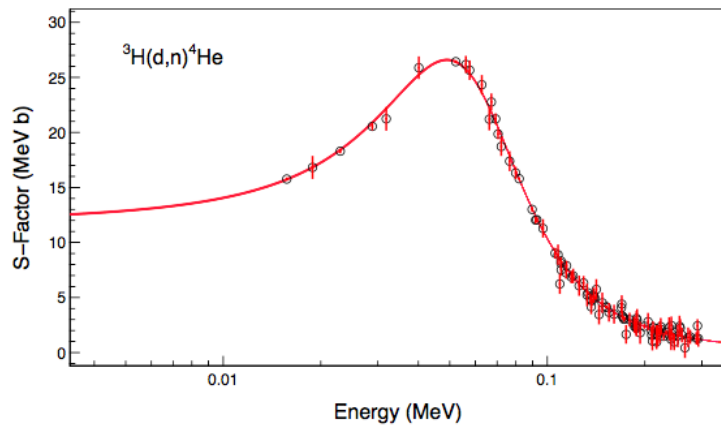
mixing looks good, but the  
artificial data have been  
generated with vastly different  
parameter values



```
## broad priors:
# e1 <- 0.0912
e1 ~ dunif(0.01, 1.0)
ex <- 0.0912
# gi <- 2.93
# gf <- 0.0794
gi ~ dunif(0.0, 100)
gf ~ dunif(0.0, 100)
ri <- 6.0
rf <- 5.0
ue <- 0.0
```

```
inits = list(e1 = 0.091, gi = 2.9, gf = 0.079),
```

with initial starting values...

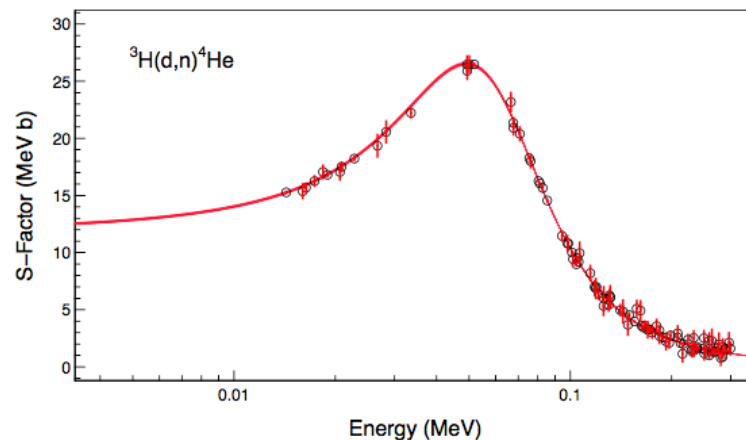
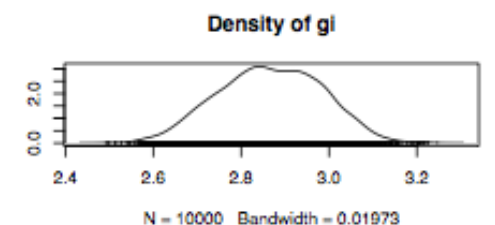
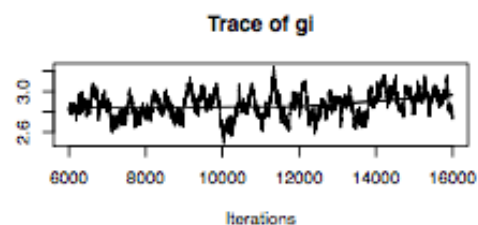
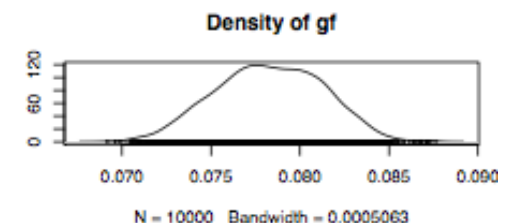
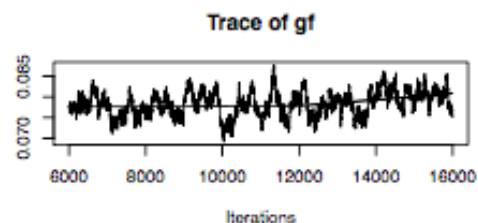
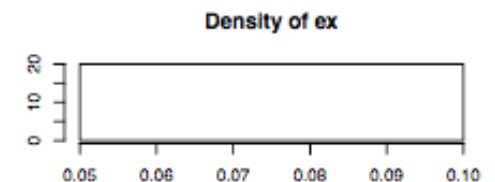
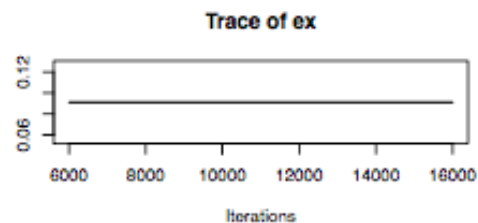
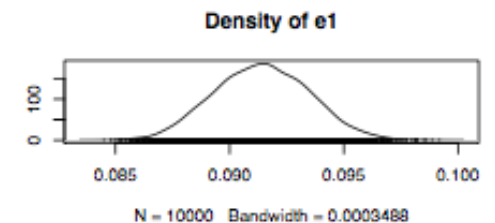
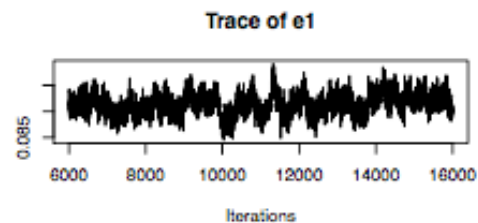


```
## broad priors:
# e1 <- 0.0912
  e1 ~ dunif(0.01, 1.0)
ex <- 0.0912
# gi <- 2.93
# gf <- 0.0794
  gi ~ dunif(0.0, 100)
  gf ~ dunif(0.0, 100)
ri <- 6.0
rf <- 5.0
ue <- 0.0
```

```
n.adapt <- 1000
#n.burnin <- 5000
n.update <- 5000
n.iter <- 10000
n.chains <- 1
n.thin <- 1
```

results are not stable; repeated runs yield garbage

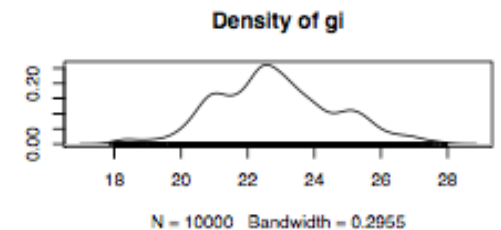
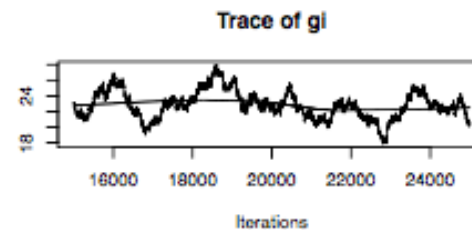
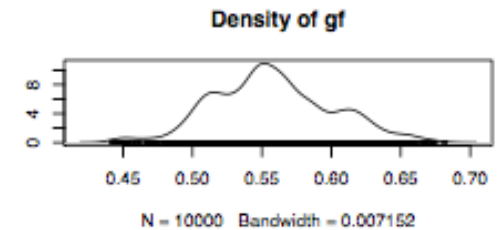
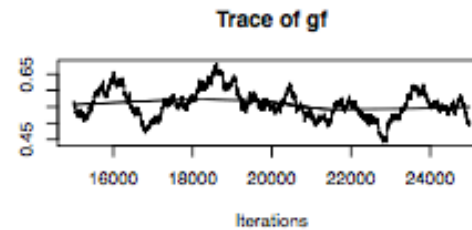
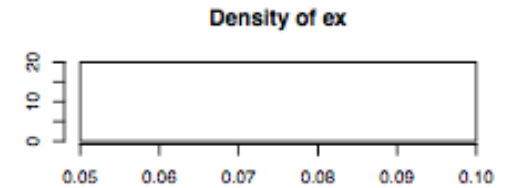
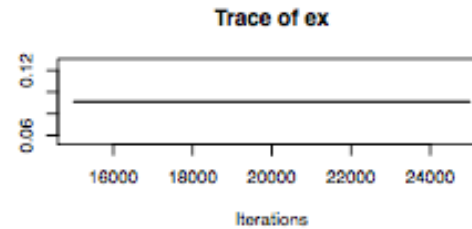
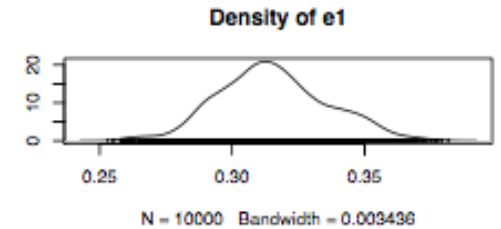
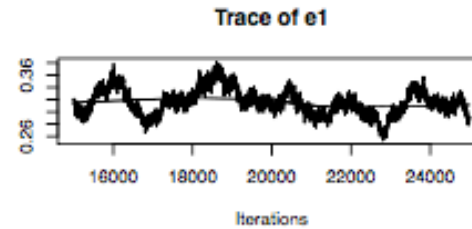
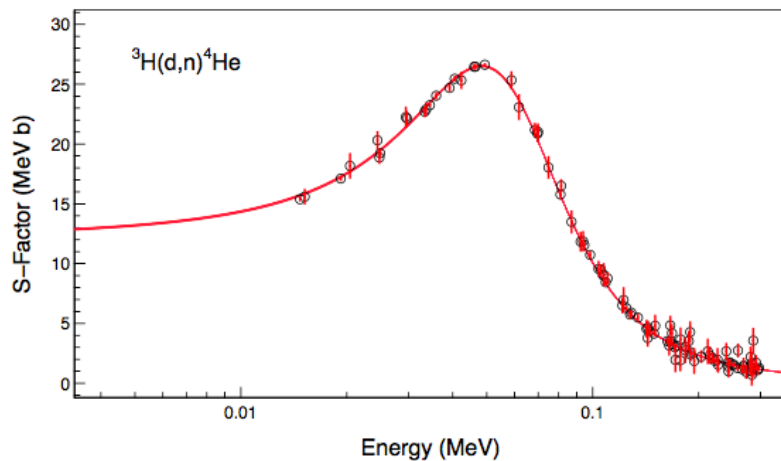
no starting values, but used longer burnin



```
## broad priors:
# e1 <- 0.0912
e1 ~ dunif(0.01, 1.0)
ex <- 0.0912
# gi <- 2.93
# gf <- 0.0794
gi ~ dunif(0.0, 100)
gf ~ dunif(0.0, 100)
ri <- 6.0
rf <- 5.0
ue <- 0.0
```

```
n.adapt <- 5000
#n.burnin <- 5000
n.update <- 10000
n.iter <- 10000
n.chains <- 1
n.thin <- 1
```

parameters are way off,  
but fit looks good...





results so far:

we get essentially identical fits with vastly different sets of parameters, with most of these solutions vastly different compared to the set used to generate the artificial data

- (1) I cannot see how any sampler in the world could pull out the original parameter set
- (2) I do not understand how previous chi-square fitting [Argo et al.; Jarmie et al.] could find any solutions for the resonance parameters
- (3) use different sampler [Stan] to see if the fits can be improved

```
## broad priors:
# e1 <- 0.0912
# n.burnin <- 5000
e1 ~ dunif(0.01, 1.0)
ex <- 0.0912
n.update <- 20000
# gi <- 2.93
n.iter <- 50000
# gf <- 0.0794
n.chains <- 1
gi ~ dunif(0.0, 100)
gf ~ dunif(0.0, 100)
n.thin <- 1
ri <- 6.0
rf <- 5.0
ue <- 0.0
```

