

DD plots

```
load("DD_model_runs.Rdata")

sds <- list()
sds[[1]] <- DD_rfx_s$BUGSoutput$sims.list[grepl('sd',names(DD_rfx_s$BUGSoutput$sims.list))]
sds[[2]] <- DD_rfx_si$BUGSoutput$sims.list[grepl('sd',names(DD_rfx_si$BUGSoutput$sims.list))]
sds[[3]] <- DD_rfx_u$BUGSoutput$sims.list[grepl('sd',names(DD_rfx_u$BUGSoutput$sims.list))]
sds[[4]] <- DD_rfx_g$BUGSoutput$sims.list[grepl('sd',names(DD_rfx_g$BUGSoutput$sims.list))]
sds[[5]] <- DD_rfx_h$BUGSoutput$sims.list[grepl('sd',names(DD_rfx_h$BUGSoutput$sims.list)) & !grepl('si',names(DD_rfx_h$BUGSoutput$sims.list))]
#sds[[3]] <- JM$BUGSoutput$sims.list[grepl('sd',names(JM$BUGSoutput$sims.list))]

ssd <- plyr::llply(sds,function(x) apply(as.data.frame(x),1,function(z) z/sum(z)))

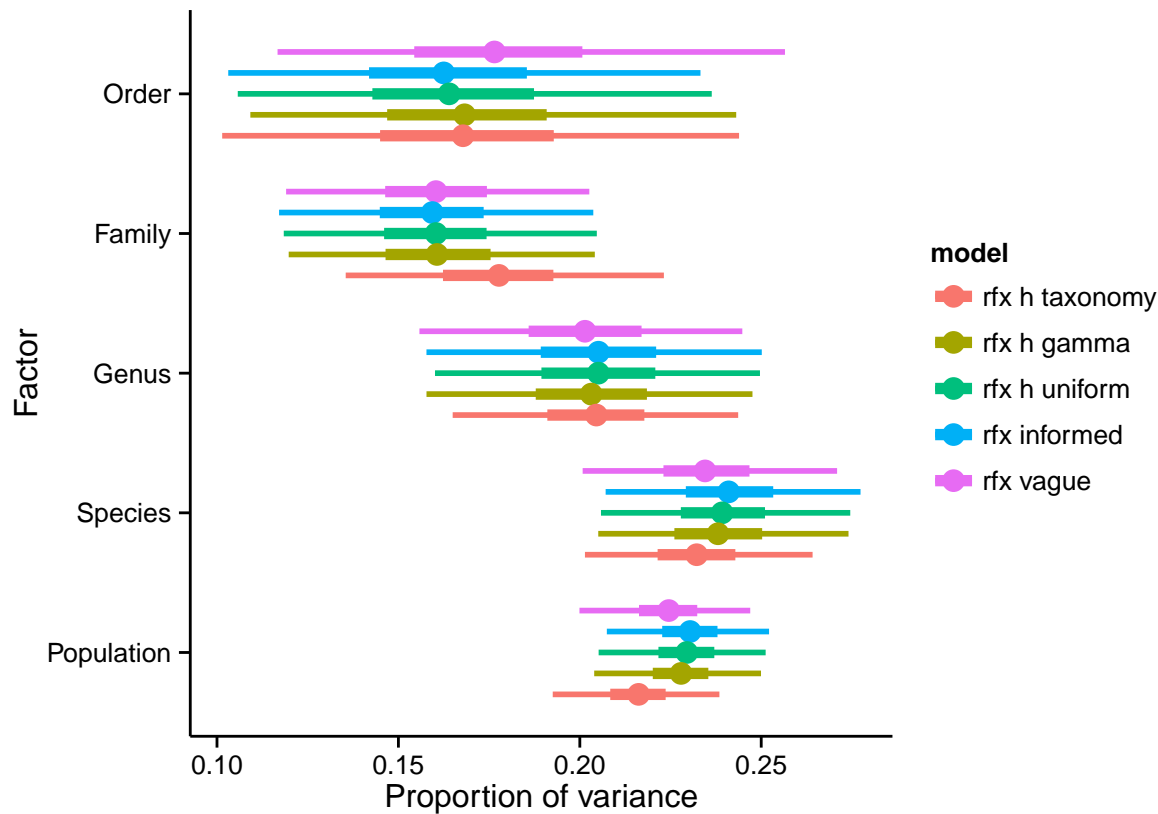
msd <- reshape2::melt(ssd)

msd <- msd %>%
  mutate(Factor = do.call('rbind',strsplit(as.character(Var1),'sd.'))[,2]) %>%
  group_by(L1,Factor) %>%
  summarise(means = median(value),
            q1 = quantile(value,0.025),
            q11 = quantile(value,0.25),
            q33 = quantile(value,0.75),
            q3 = quantile(value,0.975))

msd$Factor <- rep(c('Family','Genus','Order','Population','Species'),5)
msd$L1 <- rep(c('rfx vague','rfx informed','rfx h uniform','rfx h gamma','rfx h taxonomy'),each=5)
colnames(msd)[1] <- 'model'

msd$Factor <- factor(msd$Factor,levels = c('Population','Species','Genus','Family','Order'))
msd$model <- factor(msd$model,levels = rev(c('rfx vague','rfx informed','rfx h uniform','rfx h gamma','rfx h taxonomy')))

dw=0.75
ggplot(msd) +
  geom_point(aes(x=Factor, y=means, col=model), size=4, position=position_dodge(width=dw)) +
  geom_linerange(aes(x=Factor, y=means,ymin=q1,ymax=q3,col=model),size=1,position=position_dodge(width=dw)) +
  geom_linerange(aes(x=Factor, y=means,ymin=q11,ymax=q33,col=model),size=2,position=position_dodge(width=dw)) +
  theme_classic() +
  coord_flip() +
  #ylab(expression(Finite~population~variance~(log[10]~PPMR))) +
  ylab('Proportion of variance')
```



```
sds <- list()
sds[[1]] <- DD_rfx_s$BUGSoutput$sims.list[grepl('pred',names(DD_rfx_s$BUGSoutput$sims.list))]
sds[[2]] <- DD_rfx_si$BUGSoutput$sims.list[grepl('pred',names(DD_rfx_si$BUGSoutput$sims.list))]
sds[[3]] <- DD_rfx_u$BUGSoutput$sims.list[grepl('pred',names(DD_rfx_u$BUGSoutput$sims.list))]
sds[[4]] <- DD_rfx_g$BUGSoutput$sims.list[grepl('pred',names(DD_rfx_g$BUGSoutput$sims.list))]
sds[[5]] <- DD_rfx_h$BUGSoutput$sims.list[grepl('pred',names(DD_rfx_h$BUGSoutput$sims.list))]
#sds[[3]] <- JM$BUGSoutput$sims.list[grepl('sd',names(JM$BUGSoutput$sims.list))]

msd <- reshape2::melt(sds)

msd <- msd %>%
  mutate(Factor = L2) %>%
  group_by(L1,Factor,Var2) %>%
  summarise(means = median(value),
            q1 = quantile(value,0.025),
            q11 = quantile(value,0.25),
            q33 = quantile(value,0.75),
            q3 = quantile(value,0.975))

msd$Factor <- rep(rep(c('Family','Genus','Order','Species'),each=50),5)
msd$L1 <- rep(c('rfx vague','rfx informed','rfx h uniform','rfx h gamma','rfx h taxonomy'),each=200)
colnames(msd)[1] <- 'model'

msd$Factor <- factor(msd$Factor,levels = c('Species','Genus','Family','Order'))
msd$model <- factor(msd$model,levels = rev(c('rfx vague','rfx informed','rfx h uniform','rfx h gamma','rfx h taxonomy')))
msd$DD <- DD$BDT.C[pred]
msd <- msd %>% group_by(model,Factor) %>% arrange(DD) %>% mutate(Var2 = 1:n())
```

```

dw=5
ggplot(msd) +
  facet_wrap(Factor=model)+
  geom_point(aes(x=Var2*10, y=means, col=model), size=4, position=position_dodge(width=dw)) +

  geom_linerange(aes(x=Var2*10, y=means,ymin=q1,ymax=q3,col=model),size=1, position=position_dodge(width=dw)) +
  geom_linerange(aes(x=Var2*10, y=means,ymin=q11,ymax=q33,col=model),size=2, position=position_dodge(width=dw)) +
  theme_classic()+
  geom_point(aes(x=Var2*10, y=DD), size=4, position=position_dodge(width=dw)) +
  #coord_flip() #+
  ylab('Prediction') +
  xlab('Test point')

```

