```
if(Sys.info()["user"]!="fraser"){setwd("~/Desktop/streamcontourplot/plots/");
} else {setwd("/Users/fraser/myrepos/sdegrowth/R");}

rm(list=ls());
library("data.table")
library("ggplot2")
library("gridExtra")

# ------------------------------------------------------------------------
# ----------------------- FIGURE 1 ---------------------------------------
# ------------------------------------------------------------------------
if(Sys.info()["user"]!="fraser"){setwd("~/Desktop/streamcontourplot/plots/");
} else {setwd("/Users/fraser/myrepos/sdegrowth/R");}


load("TZtraj.RData");# provides TZtraj list
load("TZchild24.RData");# provides TZchild24.df
load("SAtraj.RData");# provides SAtraj list
load("SAchild24.RData");# provides SAchild24.df

if(Sys.info()["user"]!="fraser"){setwd("~/Desktop/streamcontourplot/plots");
} else {setwd("/Users/fraser/myrepos/sdegrowth/SASUniversityEdition/myfolders");}


fittedSDE.df<-read.csv("predcondSDE.csv",header=TRUE); # fitted values with 95% CI SDE
preds <- as.data.table(fittedSDE.df)
preds[, resid:= zwfl1 - Pred]
preds[, error:= sum(resid^2), by=subjidN]


fig1<-ggplot(data=preds, aes(x=agemnth1, y=zwfl1))+
  geom_line( aes(group=subjid), size=0.2, alpha=0.1)+
  geom_smooth(colour="black",size=0.9) +
  coord_cartesian(ylim = c(-2, 3)) +
  #
  geom_line(data=preds[preds$subjid==unique(preds$subjid[preds$country=="TZ"])[9]], size=0.7, colour="gold1")+
  geom_line(data=preds[preds$subjid==unique(preds$subjid[preds$country=="TZ"])[103]], size=0.7,
colour="darkorchid2")+
  geom_line(data=preds[preds$subjid==unique(preds$subjid[preds$country=="TZ"])[1]], size=0.7,
colour="springgreen4")+
  #
  geom_line(data=preds[preds$subjid==unique(preds$subjid[preds$country=="SA"])[103]], size=0.7,
colour="royalblue1")+
  geom_line(data=preds[preds$subjid==unique(preds$subjid[preds$country=="SA"])[102]], size=0.7, colour="tan1")+
  geom_line(data=preds[preds$subjid==unique(preds$subjid[preds$country=="SA"])[10]], size=0.7,
colour="deeppink3")+
  #
  scale_x_continuous(breaks=seq(0,24,by=6))+
  facet_wrap(~country, labeller=as_labeller(c("SA"=paste0("Venda, South Africa"," (n=",length(SAtraj),")"),
                                              "TZ"=paste0("Haydom, Tanzania"," (n=",length(TZtraj),")")))) +
  theme_classic() +
  labs(x="Age (Months)", y="Weight-for-Length z-score (ZWfL)")

print(fig1)

ggsave("Figure1ggplot.png", fig1, height=4, width = 6)


fig1bw<-ggplot(data=preds, aes(x=agemnth1, y=zwfl1))+
  geom_line( aes(group=subjid), size=0.2, alpha=0.1)+
  geom_smooth(colour="black",size=0.3,se=F) +
  #
  geom_line(data=preds[preds$subjid==unique(preds$subjid[preds$country=="TZ"])[9]], size=0.7, colour="grey60")+
  geom_line(data=preds[preds$subjid==unique(preds$subjid[preds$country=="TZ"])[103]], size=0.7, colour="grey45")+
  geom_line(data=preds[preds$subjid==unique(preds$subjid[preds$country=="TZ"])[1]], size=0.7, colour="grey30")+
  #
  geom_line(data=preds[preds$subjid==unique(preds$subjid[preds$country=="SA"])[103]], size=0.7, colour="grey60")+
  geom_line(data=preds[preds$subjid==unique(preds$subjid[preds$country=="SA"])[102]], size=0.7, colour="grey45")+
  geom_line(data=preds[preds$subjid==unique(preds$subjid[preds$country=="SA"])[10]], size=0.7, colour="grey30")+
  #
  scale_x_continuous(breaks=seq(0,24,by=6))+
  facet_wrap(~country, labeller=as_labeller(c("SA"=paste0("Venda, South Africa"," (n=",length(SAtraj),")"),
                                              "TZ"=paste0("Haydom, Tanzania"," (n=",length(TZtraj),")")))) +
  theme_classic() +
  labs(x="Age (Months)", y="Weight-for-Length z-score (ZWfL)")
print(fig1bw)

ggsave("Figure1ggplot_BW.png", fig1bw, height=4, width = 6)

# ------------------------------------------------------------------------
# ----------------------- FIGURE 2 ---------------------------------------
# ------------------------------------------------------------------------
ou.c9<-read.csv("OUfitschild9.csv",header=TRUE);
ou.c103<-read.csv("OUfitschild103.csv",header=TRUE);
ou.c2<-read.csv("OUfitschild2.csv",header=TRUE);
ou.c100<-read.csv("OUfitschild100.csv",header=TRUE);
```

```
lm.c9<-read.csv("LMfitschild9.csv",header=TRUE);
lm.c103<-read.csv("LMfitschild103.csv",header=TRUE);
lm.c2<-read.csv("LMfitschild2.csv",header=TRUE);
lm.c100<-read.csv("LMfitschild100.csv",header=TRUE);

dat.df<-read.csv("combined.csv",header=TRUE);## observed data - as used to fit models
dat <- as.data.table(dat.df)


fits <- merge(
  subset(rbind(ou.c9,ou.c103,ou.c100), select=c("subjid","agects1","Pred")),
  subset(rbind(lm.c9,lm.c103,lm.c100), select=c("subjid","agects1","Pred")),
  by=c("subjid","agects1"),suffixes = c(".ou",".lm"))
dat.fit <- merge(dat.df, fits, by=c("subjid","agects1"), all.y=T)
dat.melt <- melt(dat.fit, id.vars=c("subjid","country","agects1"),
                 measure.vars = c("Pred.ou","Pred.lm","zwfl0"))


## different patients
idx <- unique(dat$subjid)[c(47, 106, 174, 233, 369, 305)]

fig2<-ggplot(data=dat.melt, aes(x=agects1*24, y=value,
                                colour=variable, size=variable))+
  geom_line()+
  geom_text(data=data.frame(subjid=unique(dat.melt$subjid),
                            label=c("(i)","(ii)","(iii)")),
            inherit.aes = F,
            aes(x=3,y=3.1,label=label))+
  facet_wrap(~subjid) +
  theme_classic()+
  scale_x_continuous(breaks=seq(0,24,by=6))+
  theme(legend.position = c(0.9,0.88),
        strip.background = element_blank(),
        strip.text.x = element_blank())+
  guides(size="none")+
  scale_size_manual(values=c("zwfl0"=0.2,
                             "Pred.ou"=0.7,
                             "Pred.lm"=0.7))+
  scale_colour_manual(name="Model",
                      values=c("zwfl0"="grey20",
                               "Pred.ou"="dodgerblue3",
                               "Pred.lm"="firebrick3"),
                      labels=c("zwfl0"="Observed",
                               "Pred.ou"="Ornstein-\nUhlenbeck",
                               "Pred.lm"="Linear\nregression"))+
  labs(x="Age (Months)", y="Weight-for-Length z-score (ZWfL)")
print(fig2);
ggsave("Figure2ggplot.png", fig2, height=4, width = 6)

fig2bw <- fig2+scale_colour_grey()
ggsave("Figure2ggplot_BW.png", fig2bw, height=4, width = 6)

# ------------------------------------------------------------------------
# ---------------------- FIGURE 3  ---------------------------------------
# ------------------------------------------------------------------------
if(Sys.info()["user"]!="fraser"){setwd("~/Desktop/streamcontourplot/plots/");
} else {setwd("/Users/fraser/myrepos/sdegrowth/SASUniversityEdition/myfolders");}

## Read data
curve <- fread('curvepredcond.csv')
sde <- fread('predcondSDE.csv')

D <- merge(
  subset(curve, select=c("subjid","agemnth0","zwfl0","zwfl1","Pred","Lower","Upper")),
  subset(sde, select=c("subjid","agemnth0","zwfl0","zwfl1","Pred","Lower","Upper")),
  by=c("subjid","agemnth0","zwfl0","zwfl1"),
  suffixes=c(".c",".s"))
D[, country:= substr(subjid,1,2)]

## Calculate residuals from each model
D[, Resid.c:= zwfl1 - Pred.c]
D[, Resid.s:= zwfl1 - Pred.s]


D[, change:= zwfl0 - zwfl1]

Z <- D[, lapply(.SD, mean), by=c("country", "agemnth0"),
       .SDcols=c("zwfl1", "Pred.c", "Pred.s")]
Z <- melt(Z, id.vars=c("country","agemnth0"),
          measure.vars = c("zwfl1", "Pred.c", "Pred.s"))
Z$variable <- factor(Z$variable, levels=c("zwfl1", "Pred.c", "Pred.s"),
                     labels=c("Observed","LMM", "SDE"))
Z$size <- ifelse(Z$variable=="Observed",0.2,0.7)


W <- D[, lapply(.SD, mean), by=c("country", "agemnth0"),
       .SDcols=c("zwfl1", "Pred.c", "Lower.c", "Upper.c",
                 "Pred.s","Lower.s","Upper.s")]
```

```
Wb <- W
W <- melt(W, id.vars=c("country","agemnth0"),
          measure.vars = c("zwfl1", "Pred.c", "Lower.c", "Upper.c",
                           "Pred.s","Lower.s","Upper.s"))
W$variable <- factor(W$variable,
                     levels=c("zwfl1", "Pred.c", "Pred.s", "Lower.c", "Upper.c", "Lower.s","Upper.s"),
                     labels=c("Observed","LMM", "SDE", "Lower.c", "Upper.c", "Lower.s","Upper.s"))
W$size <- ifelse(W$variable=="Observed",0.2,0.7)

fig3<-ggplot(data=W[variable%in%c("Observed","LMM", "SDE")],
             aes(x=agemnth0, y=value, colour=variable, linetype=variable))+
  geom_ribbon(data=Wb, inherit.aes=F, aes(x=agemnth0, ymin=Lower.c, ymax=Upper.c), alpha=0.3, fill="firebrick3")+
  geom_ribbon(data=Wb, inherit.aes=F, aes(x=agemnth0, ymin=Lower.s, ymax=Upper.s), alpha=0.4,
fill="dodgerblue3")+
  geom_line(aes(size=size))+
  scale_size(range=c(0.4,1))+
  scale_x_continuous(breaks=seq(0,24,by=6))+
  scale_colour_manual(values=c("Observed"="grey20","SDE"="dodgerblue3", "LMM"="firebrick3"))+
  facet_wrap(~country, labeller=as_labeller(c("SA"="Venda, South Africa",
                                              "TZ"="Haydom, Tanzania")))+
  theme_classic()+theme(legend.position = c(0.85,0.65))+guides(size="none")+
  labs(x="Age (months)", y="Weight-for-Length z-score (ZWfL)", colour="Model", linetype="Model")
print(fig3);
ggsave("Figure3ggplot.png", fig3, height=4, width = 6)

fig3bw<-ggplot(data=W[variable%in%c("Observed","LMM", "SDE")],
               aes(x=agemnth0, y=value, colour=variable, linetype=variable))+
  geom_ribbon(data=Wb, inherit.aes=F, aes(x=agemnth0, ymin=Lower.c, ymax=Upper.c), alpha=0.3, fill="grey70")+
  geom_ribbon(data=Wb, inherit.aes=F, aes(x=agemnth0, ymin=Lower.s, ymax=Upper.s), alpha=0.4, fill="grey50")+
  geom_line(aes(size=size))+
  scale_size(range=c(0.4,1))+
  scale_x_continuous(breaks=seq(0,24,by=6))+
  scale_colour_manual(values=c("Observed"="grey20","SDE"="grey50", "LMM"="grey90"))+
  facet_wrap(~country, labeller=as_labeller(c("SA"="Venda, South Africa",
                                              "TZ"="Haydom, Tanzania")))+
  theme_classic()+theme(legend.position = c(0.85,0.65))+guides(size="none")+
  labs(x="Age (months)", y="Weight-for-Length z-score (ZWfL)", colour="Model", linetype="Model")
print(fig3bw);
ggsave("Figure3ggplot_BW.png", fig3bw, height=4, width = 6)

# ------------------------------------------------------------------------
# ---------------------- FIGURE 4 ----------------------------------------
# ------------------------------------------------------------------------
save.image("allplot.RData");
if(Sys.info()["user"]!="fraser"){setwd("~/Desktop/streamcontourplot/plots/");
} else {setwd("/Users/fraser/myrepos/sdegrowth/SASUniversityEdition/myfolders");}

rv<-read.csv("rvsSDE.csv",header=TRUE);## random effects per child SDE model
fixedPar<-read.csv("paramsSDE.csv",header=TRUE);## fixed effects params SDE model
## create a data.frame with format {subjidN=,b1=,b2,b3,b4,b5}
rv.wide <- dcast(rv, subjidN ~ Effect, value.var="Estimate")

### global fixed parameters
a1a<-fixedPar$Estimate[fixedPar$Parameter=="a1a_ind"];
a1b<-fixedPar$Estimate[fixedPar$Parameter=="a1b_ind"];
a2<-fixedPar$Estimate[fixedPar$Parameter=="a2_ind"];
a3<-fixedPar$Estimate[fixedPar$Parameter=="a3_ind"];
a4a<-fixedPar$Estimate[fixedPar$Parameter=="a4a_ind"];
a4b<-fixedPar$Estimate[fixedPar$Parameter=="a4b_ind"];
a5<-fixedPar$Estimate[fixedPar$Parameter=="a5_ind"];
sigma2a<-fixedPar$Estimate[fixedPar$Parameter=="sigma2a_ind"];
sigma2b<-fixedPar$Estimate[fixedPar$Parameter=="sigma2b_ind"];


#---------------------------------
a<-split(dat$agects0,list(dat$subjidN));
initt0=unlist(lapply(a,min));
a<-split(dat$zwfl0,list(dat$subjidN));
initY0=unlist(lapply(a,min));
allinits<-data.frame(subijdN=as.numeric(names(a)),t0=initt0,Y0=initY0);
head(allinits);
dim(allinits); dim(rv.wide);
SA.subjidN<-unique(dat$subjidN[which(dat$country=="SA")]);
TZ.subjidN<-unique(dat$subjidN[which(dat$country=="TZ")]);


#---------------------------------

## for each of the 236 SDEs compute the prediction Y1 at t=0.2 given child is at Y0=-0.5,t0=0.1
## first part - compute the density value for Y1=-0.5 at t=0.1 given observed starting conditions at t=0.035
## only work with TZ data
SAinits<-allinits[SA.subjidN,];## id is same as row number
SArv<-rv.wide[SA.subjidN,];

TZinits<-allinits[TZ.subjidN,];## id is same as row number
TZrv<-rv.wide[TZ.subjidN,];

#---------------------------------
```

```
sdeMoments<-function(time0,# start time
                     Y0,# start value
                     country2,# country = 0=SA, 1=TZ
                     timevec,# time points to evaluate at after time0
                     a1a.fx,a1b.fx,a2.fx,a3.fx,a4a.fx,a4b.fx,a5.fx, #fixed effect parameters
                     sigma2a.fx,sigma2b.fx, # fixed effect parameters
                     b1,b2,b3,b4, # random effect parameters
                     Yt=NULL# compute the density value under the current model for Y(timevec|Y0,t0)
){

  if(!is.null(Yt)){## want to compute density to check only single future time point passed
    if(length(timevec)!=1){stop("for density value estimation timevec must be single time point")}

  }
  a1=a1a.fx+a1b.fx*country2+b1;
  a2=a2.fx+b2;
  a3=a3.fx+b3;
  a4=a4a.fx+a4b.fx*country2;
  a5=a5.fx;
  sigma2=sigma2a.fx+sigma2b.fx*country2+b4;


  loc.mean<-(1/(a1**4))*exp(-a1*time0)*(6*a5*(exp(a1*timevec) - exp(a1*time0)) +
                                          2*a1*(a4*exp(a1*timevec) - a4*exp(a1*time0) -
3*a5*exp(a1*time0)*timevec +
                                                  3*a5*exp(a1*timevec)*time0) +
                                          a1**2*(a3*(exp(a1*timevec) - exp(a1*time0)) -
2*a4*exp(a1*time0)*timevec -
                                                   3*a5*exp(a1*time0)*timevec**2 + 2*a4*exp(a1*timevec)*time0 +
3*a5*exp(a1*timevec)*time0**2) +
                                          a1**3*(a2*(exp(a1*timevec) - exp(a1*time0)) - a3*exp(a1*time0)*timevec
-
                                                   a4*exp(a1*time0)*timevec**2 - a5*exp(a1*time0)*timevec**3 +
a3*exp(a1*timevec)*time0 +
                                                   a4*exp(a1*timevec)*time0**2 + a5*exp(a1*timevec)*time0**3) +
a1**4*exp(a1*timevec)*Y0);

  #cat(a1," ",sigma2," ",exp(2*a1*(timevec-time0)),"\n");
  loc.sd<-sqrt(((-1.0+exp(2*a1*(timevec-time0)))*sigma2)/(2*a1));

  if(is.null(Yt)){## if Yt is null then compute mean trajectory
    return(list(Y0=Y0,t0=time0,mean=loc.mean,sd=loc.sd,times=timevec))
  } else {
    # Yt is valid so compute single density value at Y(timevec|Y0,t0)
    return(list(Y0=Y0,t0=time0,t1=timevec,
                density=dnorm(Yt,mean=loc.mean,sd=loc.sd)));
  }

}

### - MAIN manuscript version - weights are based on likelihood condition on starting point at the earliest
possible age of the each child
##SA
Y0=-0.5
t0=0.1
use.these.traj<-sort(which(SAinits$t0<0.1));
timestep=0.01
nfolds <- 10
Z <- NULL
for(start in seq(-4, 2, by=0.5)){
  Q <- NULL
  for(startT in c(0.1,0.2,0.35, 0.5, 0.7, 0.9)){
    P <- NULL
    t0=startT
    P <- data.frame(Y=start,Y1=start,Y2=start,Y3=start,Y4=start,
                    Y5=start,Y6=start,Y7=start,Y8=start,
                    Y9=start,Y10=start,t=t0, startT=startT, start=start)
    for(k in seq(1,(1-startT)/timestep)){
      ## need to discard small number of trajectories whose start AFTER t1=0.1
      weights <- pred <-NULL;
      for(i in use.these.traj){## for each trajectory - small number dumped as not available before t=0.1
        # if(k==1){
        t0i<-SAinits$t0[i];
        Y0i<-SAinits$Y0[i];
        t0 <- P$t[k]
        Y1 <- P$Y[k]
        t1 <- P$t[k]+timestep
        # t1i <- P$t[k]
        # } else{
        # t0i <- P$t[k-1]
        # Y0i <- P$Y[k-1]
        #  t0i<-SAinits$t0[i];
        #  Y0i<-SAinits$Y0[i];
        #  t0 <- P$t[k]
        #  Y1 <- P$Y[k]
        #  t1 <- P$t[k]+timestep
        #}
```

```
        b<-sdeMoments(time0=t0i,Y0=Y0i,country2=0,timevec=t0,
                      a1a.fx=a1a,a1b.fx=a1b,a2.fx=a2,a3.fx=a3,a4a.fx=a4a,a4b.fx=a4b,a5.fx=a5,
                      sigma2a.fx=sigma2a,sigma2b.fx=sigma2b,
                      b1=SArv$b1[i],b2=SArv$b2[i],b3=SArv$b3[i],b4=SArv$b4[i],
                      Yt=Y1)$density;#
        weights<-c(weights,b);


        ## need to discard small number of trajectories whose start AFTER t1=0.1 - see above
        b<-sdeMoments(time0=t0,Y0=Y1,country2=0,timevec=t1,
                      a1a.fx=a1a,a1b.fx=a1b,a2.fx=a2,a3.fx=a3,a4a.fx=a4a,a4b.fx=a4b,a5.fx=a5,
                      sigma2a.fx=sigma2a,sigma2b.fx=sigma2b,
                      b1=SArv$b1[i],b2=SArv$b2[i],b3=SArv$b3[i],b4=SArv$b4[i],
                      Yt=NULL)$mean;#
        pred<-c(pred,b);
      }


      ## N folds validation
      foldsW <- foldsP <- cut( sample(1:length(weights),length(weights),replace=F),
                               breaks=nfolds,labels=FALSE)

      Ybest <- rep(NA,nfolds+1)
      for(j in 1:nfolds){
        predj <- pred[foldsP==j]
        weightsj <- weights[foldsW==j]
        Ybest[j]<-predj[which(weightsj==max(weightsj))];
      }
      Ybest[nfolds+1] <-pred[which(weights==max(weights))]
      P<-rbind( P, data.frame(Y= Ybest[11],
                              Y1=Ybest[1],Y2=Ybest[2],Y3=Ybest[3],Y4=Ybest[4],
                              Y5=Ybest[5],Y6=Ybest[6],Y7=Ybest[7],Y8=Ybest[8],
                              Y9=Ybest[9],Y10=Ybest[10],
                              t=t1, startT=startT, start=start) )

    }
    Q <- rbind(Q,P)
  }
  Z <- rbind(Z,Q)
}
SA <- Z

##TZ
Y0=-0.5
t0=0.1
use.these.traj<-sort(which(TZinits$t0<0.1));
timestep=0.01
nfolds <- 10
Z <- NULL
for(start in seq(-4, 2, by=0.5)){
  Q <- NULL
  for(startT in c(0.1,0.2,0.35, 0.5, 0.7, 0.9)){
    P <- NULL
    t0=startT
    P <- data.frame(Y=start,Y1=start,Y2=start,Y3=start,Y4=start,
                    Y5=start,Y6=start,Y7=start,Y8=start,
                    Y9=start,Y10=start,t=t0, startT=startT, start=start)
    for(k in seq(1,(1-startT)/timestep)){
      ## need to discard small number of trajectories whose start AFTER t1=0.1
      weights <- pred <-NULL;
      for(i in use.these.traj){## for each trajectory - small number dumped as not available before t=0.1
        #if(k==1){
        t0i<-TZinits$t0[i];
        Y0i<-TZinits$Y0[i];
        t0 <- P$t[k]
        Y1 <- P$Y[k]
        t1 <- P$t[k]+timestep
        # t1i <- P$t[k]
        # } else{
        # t0i <- P$t[k-1]
        # Y0i <- P$Y[k-1]
        #t0i<-TZinits$t0[i];
        #Y0i<-TZinits$Y0[i];
        #t0 <- P$t[k]
        #Y1 <- P$Y[k]
        #t1 <- P$t[k]+timestep
        #}

        b<-sdeMoments(time0=t0i,Y0=Y0i,country2=0,timevec=t0,
                      a1a.fx=a1a,a1b.fx=a1b,a2.fx=a2,a3.fx=a3,a4a.fx=a4a,a4b.fx=a4b,a5.fx=a5,
                      sigma2a.fx=sigma2a,sigma2b.fx=sigma2b,
                      b1=TZrv$b1[i],b2=TZrv$b2[i],b3=TZrv$b3[i],b4=TZrv$b4[i],
                      Yt=Y1)$density;#
        weights<-c(weights,b);


        ## need to discard small number of trajectories whose start AFTER t1=0.1 - see above
        b<-sdeMoments(time0=t0,Y0=Y1,country2=0,timevec=t1,
```

```
                      a1a.fx=a1a,a1b.fx=a1b,a2.fx=a2,a3.fx=a3,a4a.fx=a4a,a4b.fx=a4b,a5.fx=a5,
                      sigma2a.fx=sigma2a,sigma2b.fx=sigma2b,
                      b1=SArv$b1[i],b2=TZrv$b2[i],b3=TZrv$b3[i],b4=TZrv$b4[i],
                      Yt=NULL)$mean;#
        pred<-c(pred,b);
      }


      ## N folds validation
      foldsW <- foldsP <- cut( sample(1:length(weights),length(weights),replace=F),
                               breaks=nfolds,labels=FALSE)

      Ybest <- rep(NA,nfolds+1)
      for(j in 1:nfolds){
        predj <- pred[foldsP==j]
        weightsj <- weights[foldsW==j]
        Ybest[j]<-predj[which(weightsj==max(weightsj))];
      }
      Ybest[nfolds+1] <-pred[which(weights==max(weights))]
      P<-rbind( P, data.frame(Y= Ybest[11],
                              Y1=Ybest[1],Y2=Ybest[2],Y3=Ybest[3],Y4=Ybest[4],
                              Y5=Ybest[5],Y6=Ybest[6],Y7=Ybest[7],Y8=Ybest[8],
                              Y9=Ybest[9],Y10=Ybest[10],
                              t=t1, startT=startT, start=start) )

    }
    Q <- rbind(Q,P)
  }
  Z <- rbind(Z,Q)
}
TZ <- Z

Z <- rbind( cbind(SA,site="SA"), cbind(TZ, site="TZ"))

Z$idx <- interaction(Z$startT,Z$start)
fig4 <- ggplot(data=Z, aes(x=t*24, y=Y, colour=start, by=idx))+
  geom_line(alpha=0.8, size=0.3)+
  geom_line(aes(y=Y1), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y2), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y3), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y4), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y5), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y6), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y7), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y8), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y9), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y10), alpha=0.2,size=0.1)+
  #geom_path(arrow = arrow(length = unit(0.05, "cm")),alpha=0.1)+
  facet_wrap(~site, labeller=as_labeller(c("SA"="Venda, South Africa",
                                           "TZ"="Haydom, Tanzania")))+
  theme_classic()+
  guides(colour="none")+
  labs(x="Age", y="Weight-for-Length z-score (ZWfL)",colour="Starting\nZWfL")
print(fig4);
ggsave("Figure4ggplot_old.png", fig4, height=4, width = 6)

fig4bw <- fig4+scale_colour_gradient(low="grey90",high="grey10")
ggsave("Figure4ggplot_BW_old.png", fig4bw, height=4, width = 6)



# save.image("plots.Rdata")


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X <- dat[, list(zwfl.0=zwfl0[which.min(agedys0)],zwfl.1=zwfl1[which.max(agedys1)]),by=subjid]
X <- melt(X, id.vars = "subjid"); X$site=substr(X$subjid,1,2)
sa.density <- ggplot(data=X[site=="SA",],
                     aes(x=value, fill=variable, linetype=variable))+
  geom_density(data=X[site=="SA" & variable=="zwfl.0",], alpha=0.3, size=0.2)+
  geom_line(data=X[site=="SA" & variable=="zwfl.1",], aes(y=..density..), stat="density",
            alpha=0.8, size=0.3, colour="darkorchid3")+
  #
geom_text(data=X[site=="SA",list(value=mean(value),label=ifelse(variable[1]=="zwfl.0","0mo","24mo")),by="variable"

  #           aes(x=value, y=c(0.1,0.3), label=label, colour=variable),alpha=0.8, size=1.2)+
  # geom_vline(xintercept=seq(-4,2,by=2),colour="white") +
  scale_fill_manual("Age (mo)",values=c("zwfl.0"="darkorange3","zwfl.1"=NA),
                    labels=c("zwfl.0"="0","zwfl.1"="24"))+
  scale_colour_manual("Age (mo)",values=c("zwfl.0"="darkorange3","zwfl.1"="darkorchid3"),
                      labels=c("zwfl.0"="0","zwfl.1"="24"))+
  scale_linetype_manual("Age (mo)",values=c("zwfl.0"="blank","zwfl.1"="solid"),
                        labels=c("zwfl.0"="0","zwfl.1"="24"))+
```

```
  coord_flip() +  theme_void() +
  theme(legend.position = c(0.1,0.1),
        legend.title = element_text(size=rel(0.7)),
        legend.text = element_text(size=rel(0.7)),
        legend.key.size = unit(0.5,"line"))


tz.density <- ggplot(data=X[site=="TZ",],
                     aes(x=value, fill=variable, linetype=variable))+
  geom_density(data=X[site=="TZ" & variable=="zwfl.0",], alpha=0.3, size=0.2)+
  geom_line(data=X[site=="TZ" & variable=="zwfl.1",], aes(y=..density..), stat="density",
            alpha=0.8, size=0.3, colour="darkorchid3")+
  #
geom_text(data=X[site=="SA",list(value=mean(value),label=ifelse(variable[1]=="zwfl.0","0mo","24mo")),by="variable"

  #           aes(x=value, y=c(0.1,0.3), label=label, colour=variable),alpha=0.8, size=1.2)+
  # geom_vline(xintercept=seq(-4,2,by=2),colour="white") +
  scale_fill_manual("Age (mo)",values=c("zwfl.0"="darkorange3","zwfl.1"=NA),
                    labels=c("zwfl.0"="0","zwfl.1"="24"))+
  scale_colour_manual("Age (mo)",values=c("zwfl.0"="darkorange3","zwfl.1"="darkorchid3"),
                      labels=c("zwfl.0"="0","zwfl.1"="24"))+
  scale_linetype_manual("Age (mo)",values=c("zwfl.0"="blank","zwfl.1"="solid"),
                        labels=c("zwfl.0"="0","zwfl.1"="24"))+
  coord_flip() +  theme_void() +
  theme(legend.position = "none")
fig4a <- ggplot(data=Z[Z$site=="SA",], aes(x=t*24, y=Y, by=idx))+
  geom_line(aes(y=Y1), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y2), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y3), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y4), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y5), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y6), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y7), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y8), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y9), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y10), alpha=0.2,size=0.1)+
  geom_line(alpha=0.8, size=0.3, colour="tomato3")+
  scale_x_continuous(limits=c(1,24), expand=c(0,0), breaks=seq(0,24,by=6))+
  theme_classic()+
  labs(x="Age", y="Weight-for-Length z-score (ZWfL)")
fig4b <- ggplot(data=Z[Z$site=="TZ",], aes(x=t*24, y=Y, by=idx))+
  geom_line(aes(y=Y1), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y2), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y3), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y4), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y5), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y6), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y7), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y8), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y9), alpha=0.2, size=0.1)+
  geom_line(aes(y=Y10), alpha=0.2,size=0.1)+
  geom_line(alpha=0.8, size=0.3, colour="tomato3")+
  scale_x_continuous(limits=c(1,24), expand=c(0,0), breaks=seq(0,24,by=6))+
  theme_classic()+
  labs(x="Age", y="Weight-for-Length z-score (ZWfL)")
library("cowplot")
x_min=-4.1; x_max=2.4

fig4alt <- plot_grid(fig4a   + scale_y_continuous(breaks = seq(-4,2,by=2),limits=c(x_min, x_max), expand =
c(0,0)),
                     sa.density + scale_x_continuous(breaks = seq(-4,2,by=2),limits=c(x_min, x_max), expand =
c(0,0)),
                     #
                     ggplot(data=SAchild24.df) + theme_void(),
                     #
                     fig4b   + scale_y_continuous(breaks = seq(-4,2,by=2),limits=c(x_min, x_max), expand =
c(0,0)) +
                       theme(axis.text.y = element_blank(), axis.title.y = element_blank()),
                     tz.density + scale_x_continuous(breaks = seq(-4,2,by=2),limits=c(x_min, x_max), expand =
c(0,0)),
                     #
                     nrow = 1, axis="l", align="h",
                     rel_widths = c(0.9,0.1,0.125,0.9,0.1),
                     labels=c("Venda, South Africa","",
                              "",
                              "Haydom, Tanzania",""),
                     label_size = 10,label_fontface="plain", label_x=0,hjust=-0.5)
ggsave("Figure4ggplot.png", fig4alt, height=4, width = 6)
```