Emergence (E ) and Germination (G) analysis of pigeonpea genotype (GTP) in R-Studio

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2020-02-20

library(here)

## here() starts at D:/Consulting/Germination-analysis

library(tidyverse)

## -- Attaching packages --------------------------------- tidyverse 1.3.0 --

## v ggplot2 3.2.1 v purrr 0.3.3  
## v tibble 2.1.3 v dplyr 0.8.4  
## v tidyr 1.0.2 v stringr 1.4.0  
## v readr 1.3.1 v forcats 0.4.0

## -- Conflicts ------------------------------------ tidyverse\_conflicts() --  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag() masks stats::lag()

library(nls.multstart)  
library(nlstools)

##   
## 'nlstools' has been loaded.

## IMPORTANT NOTICE: Most nonlinear regression models and data set examples

## related to predictive microbiolgy have been moved to the package 'nlsMicrobio'

library(broom)  
# To change fonts read this: https://stackoverflow.com/questions/34522732/changing-fonts-in-ggplot2  
# The natural fonts are pretty good still.  
  
E\_G <- read.csv(here("E\_G.csv"))  
#E\_G <- subset(E\_G,!(E\_R == 0 & TEM < 30))  
E\_G$GTP2 <- substr(E\_G$GTP,1,1)  
Germ <- subset(E\_G,EXP=="G")  
Emer <- subset(E\_G,EXP=="E")  
  
#Emergence  
fit\_many <- Emer %>% group\_by(GTP) %>% nest() %>%  
 mutate(fit = purrr::map(data, ~nls\_multstart(E\_R ~ (b1 + b2 \* TEM)\*(TEM<d) +  
 (b1 - b3\*d + (b2+b3)\*TEM)\* (TEM>=d), data = .x,  
 iter = 10^5,  
 start\_lower = c(b1=-2,b2=0,b3=-2,d=20),  
 start\_upper = c(b1=0,b2=0.6,b3=0,d=50),  
 supp\_errors = 'Y')))  
  
select(fit\_many, GTP, data, fit)

# get summary  
info <- fit\_many %>%  
 mutate(summary = map(fit, glance)) %>%  
 unnest(summary)

params <- fit\_many %>%  
 mutate(., p = map(fit, tidy)) %>%  
 unnest(p)  
Emercard <- with(params,data.frame(GTP=unique(GTP),  
 baseTemp = -estimate[term=="b1"]/estimate[term=="b2"],  
 maxTemp = -(estimate[term=="b1"]-estimate[term=="b3"]\*estimate[term=="d"])/(estimate[term=="b2"]+estimate[term=="b3"]),  
 optimumTemp = estimate[term=="d"],  
 ttsub = 1/estimate[term=="b2"],  
 ttsup = -1/(estimate[term=="b2"]+estimate[term=="b3"]),  
 oneSeed = ((1/23)-estimate[term=="b1"])/estimate[term=="b2"],  
 maxOne = ((1/23)-estimate[term=="b1"]+estimate[term=="b3"]\*estimate[term=="d"])/(estimate[term=="b2"]+estimate[term=="b3"]))  
)

preds <- fit\_many %>% mutate (., p = map(fit,augment)) %>% unnest(p)  
preds

ggplot(preds,aes(x=TEM,y=E\_R, colour=GTP)) + geom\_point() +  
 geom\_path(aes(y=.fitted))

# get confidence intervals  
CI <- fit\_many %>%  
 mutate(., cis = map (fit, confint2),  
 cis = map(cis, data.frame)) %>%  
 unnest(cis) %>%  
 rename(., conf.low = X2.5.., conf.high = X97.5..) %>%  
 group\_by(., GTP) %>%  
 mutate(., term = c('b1', 'b2', 'd', 'b3')) %>%  
 ungroup() %>%  
 select(., -data, -fit)

# merge parameters and CI estimates  
params <- inner\_join(params,CI, by = c("GTP","term"))  
  
select(info, GTP, logLik, AIC, BIC, deviance, df.residual)

new\_preds <- Emer %>%  
 #do(., data.frame(TEM = seq(min(.$TEM),max(.$TEM),length.out = 500),stringsAsFactors = FALSE))  
 do(., data.frame(TEM = seq(0,50,length.out = 500),stringsAsFactors = FALSE))  
  
max\_min <- group\_by(Emer,GTP) %>%  
 summarise(.,min\_TEM = min(TEM),max\_TEM = max(TEM)) %>% ungroup()  
  
pred2 <- fit\_many %>% mutate(., p = map(fit, augment, newdata = new\_preds)) %>%  
 unnest(p) %>% merge(.,max\_min, by = "GTP") %>% group\_by(.,GTP) %>%  
 #filter(., TEM > unique(min\_TEM) & TEM < unique(max\_TEM)) %>%  
 filter(.,.fitted >= 0) %>%  
 rename(., E\_R = .fitted) %>% ungroup()  
  
png(filename = here("Figures","EmgTemp.png"))  
ggplot(pred2,aes(x=TEM,y=E\_R, linetype=GTP)) + geom\_path(size=1) + theme\_linedraw() +  
 theme(panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x= expression('Temperature '(degree\*C)), y= expression("Emergence Rate "(1/t^50))) + scale\_linetype\_discrete(name="Genotype")  
dev.off()

png(filename = here("Figures","EmgTemp2.png"))  
ggplot() + geom\_point(aes(TEM,E\_R), size = 2, Emer) +  
 geom\_line(aes(TEM,E\_R,group = GTP), alpha = 0.5, pred2) +  
 facet\_wrap(~ GTP) + ylim(0,0.3) + theme\_linedraw(base\_size = 12)+  
 theme(panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x=expression('Temperature '(degree\*C)),y=expression("Emergence Rate "(1/t^50)))  
dev.off()

png(filename = here("Figures","EmgParams.png"))  
ggplot(params) + geom\_point(aes(GTP,estimate)) +  
 facet\_wrap(~ term, scale = "free\_x", ncol = 4, labeller=as\_labeller(c(b1="b1",b2="b2",b3="b3",d="Break Point"))) +  
 geom\_linerange(aes(GTP,ymin=conf.low,ymax=conf.high)) +  
 coord\_flip() + theme\_linedraw(base\_size = 12) +  
 theme(axis.text.x = element\_text(angle = 90, vjust = 0.5, hjust=1),panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x="Genotype",y="Estimate")  
dev.off()

## png   
## 2

paramsE <- params  
paramsE$flux <- "Emergence"  
  
#Germination  
fit\_many <- Germ %>% group\_by(GTP) %>% nest() %>%  
 mutate(fit = purrr::map(data, ~nls\_multstart(E\_R ~ (b1 + b2 \* TEM)\*(TEM<d) +  
 (b1 - b3\*d + (b2+b3)\*TEM)\* (TEM>=d), data = .x,  
 iter = 10^5,  
 start\_lower = c(b1=-2,b2=0,b3=-2,d=20),  
 start\_upper = c(b1=0,b2=0.6,b3=0,d=50),  
 supp\_errors = 'Y')))  
  
select(fit\_many, GTP, data, fit)

# get summary  
info <- fit\_many %>%  
 mutate(summary = map(fit, glance)) %>%  
 unnest(summary)

params <- fit\_many %>%  
 mutate(., p = map(fit, tidy)) %>%  
 unnest(p)

Germcard <- with(params,data.frame(GTP=unique(GTP),  
 baseTemp = -estimate[term=="b1"]/estimate[term=="b2"],  
 maxTemp = -(estimate[term=="b1"]-estimate[term=="b3"]\*estimate[term=="d"])/(estimate[term=="b2"]+estimate[term=="b3"]),  
 optimumTemp = estimate[term=="d"],  
 ttsub = 1/estimate[term=="b2"],  
 ttsup = -1/(estimate[term=="b2"]+estimate[term=="b3"]),  
 oneSeed = ((1/23)-estimate[term=="b1"])/estimate[term=="b2"],  
 maxOne = ((1/23)-estimate[term=="b1"]+estimate[term=="b3"]\*estimate[term=="d"])/(estimate[term=="b2"]+estimate[term=="b3"]))  
)  
preds <- fit\_many %>% mutate(., p = map(fit,augment)) %>% unnest(p)  
preds

ggplot(preds,aes(x=TEM,y=E\_R, colour=GTP)) + geom\_point() +  
 geom\_path(aes(y=.fitted))

# get confidence intervals  
CI <- fit\_many %>%  
 mutate(., cis = map(fit, confint2),  
 cis = map(cis, data.frame)) %>%  
 unnest(cis) %>%  
 rename(., conf.low = X2.5.., conf.high = X97.5..) %>%  
 group\_by(., GTP) %>%  
 mutate(., term = c('b1', 'b2', 'd', 'b3')) %>%  
 ungroup() %>%  
 select(., -data, -fit)  
# merge parameters and CI estimates  
params <- inner\_join(params,CI, by = c("GTP","term"))  
  
select(info, GTP, logLik, AIC, BIC, deviance, df.residual)

new\_preds <- Germ %>%  
 #do(., data.frame(TEM = seq(min(.$TEM),max(.$TEM),length.out = 500),stringsAsFactors = FALSE))  
 do(., data.frame(TEM = seq(0,50,length.out = 500),stringsAsFactors = FALSE))  
  
max\_min <- group\_by(Germ,GTP) %>%  
 summarise(.,min\_TEM = min(TEM),max\_TEM = max(TEM)) %>% ungroup()  
  
pred2 <- fit\_many %>% mutate(., p = map(fit, augment, newdata = new\_preds)) %>%  
 unnest(p) %>% merge(.,max\_min, by = "GTP") %>% group\_by(.,GTP) %>%  
 #filter(., TEM > unique(min\_TEM) & TEM < unique(max\_TEM)) %>%  
 filter(.,.fitted >= 0) %>%  
 rename(., E\_R = .fitted) %>% ungroup()  
  
png(filename = here("Figures","GerTemp.png"))  
ggplot(pred2,aes(x=TEM,y=E\_R, linetype=GTP)) + geom\_path(size=1) + theme\_linedraw() +  
 labs(x= expression('Temperature '(degree\*C)), y= expression("Germination Rate "(1/t^50))) + scale\_linetype\_discrete(name="Genotype")  
dev.off()

png(filename = here("Figures","GerTemp2.png"))  
ggplot() + geom\_point(aes(TEM,E\_R), size = 2, Germ) +  
 geom\_line(aes(TEM,E\_R,group = GTP), alpha = 0.5, pred2) +  
 facet\_wrap(~ GTP) + ylim(0,1.3) + theme\_linedraw(base\_size = 12) +  
 theme(panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x=expression('Temperature '(degree\*C)),y=expression("Germination Rate "(1/t^50)))  
dev.off()

png(filename = here("Figures","GerParams.png"))  
ggplot(params) + geom\_point(aes(GTP,estimate)) +  
 facet\_wrap(~ term, scale = "free\_x", ncol = 4, labeller=as\_labeller(c(b1="b1",b2="b2",b3="b3",d="Break Point"))) +  
 geom\_linerange(aes(GTP,ymin=conf.low,ymax=conf.high)) +  
 coord\_flip() + theme\_linedraw(base\_size = 12) +  
 theme(axis.text.x = element\_text(angle = 90, vjust = 0.5, hjust=1),panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x="Genotype",y="Estimate")  
dev.off()

params$flux <- "Germination"  
params <- rbind(paramsE,params)  
  
png(filename = here("Figures","Params.png"))  
ggplot(params,aes(shape=flux)) + geom\_point(aes(GTP,estimate)) +  
 facet\_wrap(~ term, scale = "free\_x", ncol = 4, labeller=as\_labeller(c(b1="b1",b2="b2",b3="b3",d="Break Point"))) +  
 geom\_linerange(aes(GTP,ymin=conf.low,ymax=conf.high)) +  
 #scale\_color\_manual(values=c("green4", "black")) +  
 scale\_shape\_discrete(name="Phase") +  
 coord\_flip() + theme\_linedraw(base\_size = 12) +  
 theme(axis.text.x = element\_text(angle = 90, vjust = 0.5, hjust=1),panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x="Genotype",y="Estimate")  
dev.off()

library(reshape2)

##   
## Attaching package: 'reshape2'

## The following object is masked from 'package:tidyr':  
##   
## smiths

Germcard <- melt(Germcard,id.vars="GTP",variable.name = "Parameter",value.name = "Value")  
Germcard$flux <- "Germination"  
Emercard <- melt(Emercard,id.vars="GTP",variable.name = "Parameter",value.name = "Value")  
Emercard$flux <- "Emergence"  
cards <- rbind(Emercard,Germcard)  
  
levels(cards$Parameter)

## [1] "baseTemp" "maxTemp" "optimumTemp" "ttsub" "ttsup"   
## [6] "oneSeed" "maxOne"

labels <- as\_labeller(c(baseTemp="Tb",maxTemp="Tm",optimumTemp="To",ttsub="Ttsub",ttsup="Ttsup"))  
  
png(filename = here("Figures","Cards.png"))  
ggplot(cards,aes(shape=flux)) + geom\_point(aes(GTP,Value)) +  
 facet\_wrap(~ Parameter, scale="free\_x", ncol= 5,labeller=labels) +  
 scale\_shape\_discrete(name="Phase") +  
 coord\_flip() + theme\_linedraw(base\_size = 12) +  
 theme(panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x="Genotype",y="Estimate")  
dev.off()

EG2 <- cbind(Emer,Germ%>%rename(.,G\_R=E\_R,TEMy=TEM,GTPy=GTP,EXPy=EXP,GTP2y=GTP2))  
png(filename = here("Figures","Cards2.png"))  
ggplot(EG2,aes(x=E\_R,y=G\_R,linetype=GTP)) + geom\_point() + geom\_smooth(method="lm",se=FALSE,colour = "black") +  
 theme\_linedraw() +  
 theme(axis.text.x = element\_text(angle = 90, vjust = 0.5, hjust=1),panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x="Emergence Rate (1/days)",y="Germination Rate (1/days)") +scale\_linetype\_discrete(name="Genotype")  
dev.off()

png(filename = here("Figures","GRvsER.png"))  
ggplot(,aes(x=Emer$E\_R,y=Germ$E\_R,linetype=Emer$GTP)) + geom\_point() + geom\_smooth(method="lm",se=FALSE,colour = "black") +  
 theme\_linedraw() +  
 theme(panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x="Emergence Rate (1/days)",y="Germination Rate (1/days)") +scale\_linetype\_discrete(name="Genotype")  
dev.off()

modelFirst <- lm(Germ$E\_R~Emer$E\_R)  
summary(modelFirst)

png(filename = here("Figures","GrVErdiagnostics.png"))  
par(mfrow=c(2,2))  
plot(modelFirst)  
dev.off()

par(mfrow=c(1,1))  
  
# Clustered  
#Emergence  
fit\_many <- Emer %>% group\_by(GTP2) %>% nest() %>%  
 mutate(fit = purrr::map(data, ~nls\_multstart(E\_R ~ (b1 + b2 \* TEM)\*(TEM<d) +  
 (b1 - b3\*d + (b2+b3)\*TEM)\* (TEM>=d), data = .x,  
 iter = 10^5,  
 start\_lower = c(b1=-2,b2=0,b3=-2,d=20),  
 start\_upper = c(b1=0,b2=0.6,b3=0,d=50),  
 supp\_errors = 'Y')))  
  
select(fit\_many, GTP2, data, fit)

# get summary  
info <- fit\_many %>%  
 mutate(summary = map(fit, glance)) %>%  
 unnest(summary)

params <- fit\_many %>%  
 mutate(., p = map(fit, tidy)) %>%  
 unnest(p)  
Emercard <- with(params,data.frame(GTP2=unique(GTP2),  
 baseTemp = -estimate[term=="b1"]/estimate[term=="b2"],  
 maxTemp = -(estimate[term=="b1"]-estimate[term=="b3"]\*estimate[term=="d"])/(estimate[term=="b2"]+estimate[term=="b3"]),  
 optimumTemp = estimate[term=="d"],  
 ttsub = 1/estimate[term=="b2"],  
 ttsup = -1/(estimate[term=="b2"]+estimate[term=="b3"]),  
 oneSeed = ((1/23)-estimate[term=="b1"])/estimate[term=="b2"],  
 maxOne = ((1/23)-estimate[term=="b1"]+estimate[term=="b3"]\*estimate[term=="d"])/(estimate[term=="b2"]+estimate[term=="b3"]))  
)  
preds <- fit\_many %>% mutate(., p = map(fit,augment)) %>% unnest(p)  
preds

ggplot(preds[order(preds$TEM),],aes(x=TEM,y=E\_R, colour=GTP2)) + geom\_point() +  
 geom\_path(aes(y=.fitted))

# get confidence intervals  
CI <- fit\_many %>%  
 mutate(., cis = map(fit, confint2),  
 cis = map(cis, data.frame)) %>%  
 unnest(cis) %>%  
 rename(., conf.low = X2.5.., conf.high = X97.5..) %>%  
 group\_by(., GTP2) %>%  
 mutate(., term = c('b1', 'b2', 'd', 'b3')) %>%  
 ungroup() %>%  
 select(., -data, -fit)  
# merge parameters and CI estimates  
params <- inner\_join(params,CI, by = c("GTP2","term"))  
  
select(info, GTP2, logLik, AIC, BIC, deviance, df.residual)

new\_preds <- Emer %>%  
 #do(., data.frame(TEM = seq(min(.$TEM),max(.$TEM),length.out = 500),stringsAsFactors = FALSE))  
 do(., data.frame(TEM = seq(0,50,length.out = 500),stringsAsFactors = FALSE))  
  
max\_min <- group\_by(Emer,GTP2) %>%  
 summarise(.,min\_TEM = min(TEM),max\_TEM = max(TEM)) %>% ungroup()  
  
pred2 <- fit\_many %>% mutate(., p = map(fit, augment, newdata = new\_preds)) %>%  
 unnest(p) %>% merge(.,max\_min, by = "GTP2") %>% group\_by(.,GTP2) %>%  
 #filter(., TEM > unique(min\_TEM) & TEM < unique(max\_TEM)) %>%  
 filter(.,.fitted >= 0) %>%  
 rename(., E\_R = .fitted) %>% ungroup()  
  
ggplot(pred2,aes(x=TEM,y=E\_R, linetype=GTP2)) + geom\_path(size=1) + theme\_linedraw() +  
 theme(panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x= expression('Temperature '(degree\*C)), y= expression("Emergence Rate "(1/t^50))) + scale\_linetype\_discrete(name="Genotype")

ggplot() + geom\_point(aes(TEM,E\_R), size = 2.5, Emer) +  
 geom\_line(aes(TEM,E\_R,group = GTP2), alpha = 0.5, pred2) +  
 facet\_wrap(~ GTP2) + ylim(0,0.3) + theme\_linedraw(base\_size = 12) +  
 theme(panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x=expression("Emergence Rate "(1/t^50)),y=expression('Temperature '(degree\*C)))

ggplot(params) + geom\_point(aes(GTP2,estimate),size=2.5) +  
 facet\_wrap(~ term, scale = "free\_x", ncol = 4, labeller=as\_labeller(c(b1="b1",b2="b2",b3="b3",d="Break Point"))) +  
 geom\_linerange(aes(GTP2,ymin=conf.low,ymax=conf.high)) +  
 coord\_flip() + theme\_linedraw(base\_size = 12) +  
 theme(panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x="Genotype",y="Estimate")

paramsE <- params  
paramsE$flux <- "Emergence"  
  
#Germination  
fit\_many <- Germ %>% group\_by(GTP2) %>% nest() %>%  
 mutate(fit = purrr::map(data, ~nls\_multstart(E\_R ~ (b1 + b2 \* TEM)\*(TEM<d) +  
 (b1 - b3\*d + (b2+b3)\*TEM)\* (TEM>=d), data = .x,  
 iter = 10^5,  
 start\_lower = c(b1=-2,b2=0,b3=-2,d=20),  
 start\_upper = c(b1=0,b2=0.6,b3=0,d=50),  
 supp\_errors = 'Y')))  
  
select(fit\_many, GTP2, data, fit)

# get summary  
info <- fit\_many %>%  
 mutate(summary = map(fit, glance)) %>%  
 unnest(summary)

params <- fit\_many %>%  
 mutate(., p = map(fit, tidy)) %>%  
 unnest(p)  
Germcard <- with(params,data.frame(GTP2=unique(GTP2),  
 baseTemp = -estimate[term=="b1"]/estimate[term=="b2"],  
 maxTemp = -(estimate[term=="b1"]-estimate[term=="b3"]\*estimate[term=="d"])/(estimate[term=="b2"]+estimate[term=="b3"]),  
 optimumTemp = estimate[term=="d"],  
 ttsub = 1/estimate[term=="b2"],  
 ttsup = -1/(estimate[term=="b2"]+estimate[term=="b3"]),  
 oneSeed = ((1/23)-estimate[term=="b1"])/estimate[term=="b2"],  
 maxOne = ((1/23)-estimate[term=="b1"]+estimate[term=="b3"]\*estimate[term=="d"])/(estimate[term=="b2"]+estimate[term=="b3"]))  
)  
Germcard

preds <- fit\_many %>% mutate(., p = map(fit,augment)) %>% unnest(p)  
preds

ggplot(preds[order(preds$TEM),],aes(x=TEM,y=E\_R, colour=GTP2)) + geom\_point() +  
 geom\_path(aes(y=.fitted))

# get confidence intervals  
CI <- fit\_many %>%  
 mutate(., cis = map(fit, confint2),  
 cis = map(cis, data.frame)) %>%  
 unnest(cis) %>%  
 rename(., conf.low = X2.5.., conf.high = X97.5..) %>%  
 group\_by(., GTP2) %>%  
 mutate(., term = c('b1', 'b2', 'd', 'b3')) %>%  
 ungroup() %>%  
 select(., -data, -fit)  
# merge parameters and CI estimates  
params <- inner\_join(params,CI, by = c("GTP2","term"))  
  
select(info, GTP2, logLik, AIC, BIC, deviance, df.residual)

new\_preds <- Germ %>%  
 #do(., data.frame(TEM = seq(min(.$TEM),max(.$TEM),length.out = 500),stringsAsFactors = FALSE))  
 do(., data.frame(TEM = seq(0,50,length.out = 500),stringsAsFactors = FALSE))  
  
max\_min <- group\_by(Germ,GTP2) %>%  
 summarise(.,min\_TEM = min(TEM),max\_TEM = max(TEM)) %>% ungroup()  
  
pred2 <- fit\_many %>% mutate(., p = map(fit, augment, newdata = new\_preds)) %>%  
 unnest(p) %>% merge(.,max\_min, by = "GTP2") %>% group\_by(.,GTP2) %>%  
 #filter(., TEM > unique(min\_TEM) & TEM < unique(max\_TEM)) %>%  
 filter(.,.fitted >= 0) %>%  
 rename(., E\_R = .fitted) %>% ungroup()  
  
ggplot(pred2,aes(x=TEM,y=E\_R, linetype=GTP2)) + geom\_path(size=1) + theme\_linedraw() +  
 theme(panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x= expression('Temperature '(degree\*C)), y= expression("Germination Rate "(1/t^50))) + scale\_linetype\_discrete(name="Genotype")

ggplot() + geom\_point(aes(TEM,E\_R), size = 2, Germ) +  
 geom\_line(aes(TEM,E\_R,group = GTP2), alpha = 0.5, pred2) +  
 facet\_wrap(~ GTP2) + ylim(0,1.3) + theme\_linedraw(base\_size = 12) +  
 theme(panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x=expression('Temperature '(degree\*C)),y=expression("Germination Rate "(1/t^50)))

ggplot(params) + geom\_point(aes(GTP2,estimate),size=2.5) +  
 facet\_wrap(~ term, scale = "free\_x", ncol = 4,labeller = as\_labeller(c(b1="b1",b2="b2",b3="b3",d="Break Point"))) +  
 geom\_linerange(aes(GTP2,ymin=conf.low,ymax=conf.high)) +  
 coord\_flip() + theme\_linedraw(base\_size = 12) +  
 theme(panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x="Genotype",y="Estimate")

params$flux <- "Germination"  
params <- rbind(paramsE,params)  
  
ggplot(params,aes(shape=flux)) + geom\_point(aes(GTP2,estimate),size=2.5) +  
 facet\_wrap(~ term, scale = "free\_x", ncol = 4,labeller = as\_labeller(c(b1="b1",b2="b2",b3="b3",d="Break Point"))) +  
 geom\_linerange(aes(GTP2,ymin=conf.low,ymax=conf.high)) +  
 scale\_shape\_discrete(name="Phase") +  
 coord\_flip() + theme\_linedraw(base\_size = 12) +  
 theme(panel.grid.major = element\_blank(), panel.grid.minor = element\_blank()) +  
 labs(x="Genotype",y="Estimate")