# function for the likelihood of the data given that the logit(probability of maturity) is a linear function of size

# ‘mat’ is 0,1 for juvenile,adult

# ‘mean’ and ‘slope’ are the regression parameters

s\_mat <- function(size,mat,mean,slope){

logit\_p <- (size-mean)\*slope

p <- exp(logit\_p)/(exp(logit\_p)+1)

minusll <- -sum(dbinom(mat,1,p,log=T))

return(minusll)

}

# can fit this to the data without clinal variation – so, overall size vs maturity relationship – here using BBMLE

theta.init <- list(mean=5,slope=5)

mle.s\_mat <- mle2(s\_mat,theta.init,data=list(size=log(snail$length\_mm),mat=snail$mature))

summary(mle.s\_mat)

AIC(mle.s\_mat)

# build that into a cline fit (cline for mean size at maturity first, constant slope of the maturity – size relationship across the cline)

# ‘c\_mean’ and ‘w\_mean’ are the size at maturity in crab and wave

# ‘c’ and ‘w’ are the centre and width of the cline in size at maturity (this is an old script – better to make log(w) the fitted parameter)

s\_mat\_cline <- function(position,size,mat,c\_mean,w\_mean,slope, c, w){

d <- position-c

p\_x <- 1/(1+exp(0-4\*(d)/w))

mean <- c\_mean+(w\_mean-c\_mean)\*p\_x

logit\_p <- (size-mean)\*slope

p <- exp(logit\_p)/(exp(logit\_p)+1)

minusll <- -sum(dbinom(mat,1,p,log=T))

return(minusll)

}

theta.init <- list(c\_mean=1,w\_mean=1,slope=2,c=80,w=20)

mle.s\_mat\_cline <- mle2(s\_mat\_cline,theta.init,data=list(position=snail$line\_dist,size=log(snail$length\_mm),mat=snail$mature))

summary(mle.s\_mat\_cline)

AIC(mle.s\_mat\_cline)