Setpember W2

Awais Choudhry

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## R Shiny App

#  
# This is the server logic of a Shiny web application. You can run the   
# application by clicking 'Run App' above.  
#  
# Find out more about building applications with Shiny here:  
#   
# http://shiny.rstudio.com/  
#  
  
library(shiny)  
library(gridExtra)  
library(Gviz)  
library(coMET)  
library(GenomicInteractions)  
library(rtracklayer)  
library(magrittr)  
library(parallel)  
library(TxDb.Hsapiens.UCSC.hg19.knownGene)  
library(TxDb.Mmusculus.UCSC.mm9.knownGene)  
library(org.Hs.eg.db)  
library(org.Mm.eg.db)  
  
  
  
shinyServer(function(input, output) {  
   
  
  
 ##############################################  
 #Render Human GVIZ plot 1  
 #############################################33  
 output$HumangvizPlot <- renderPlot({  
  
if(!exists("chrM")){  
   
 chrM<-input$chrM  
 assign("chrM", chrM, .GlobalEnv)  
   
 humanIdeogramTrack<-IdeogramTrack(chromosome = input$chrM, genome="hg19",name= "Ideogram")  
 gHumanTrack<-GenomeAxisTrack(name= "Axis")  
   
 assign("humanIdeogramTrack", humanIdeogramTrack, .GlobalEnv)  
 assign("gHumanTrack", gHumanTrack, .GlobalEnv)  
 ########################################  
 ###HumanInputs  
 #######################################  
   
 ## Human ChormHMM Tracks  
 PancreasHMM="~/DataFiles/ChromHMM/human/coMET/E098\_15\_coreMarks\_mnemonics.bed.gz"%>%import()  
 PancreasIsletsHMM="~/DataFiles/ChromHMM/human/coMET/E093\_15\_coreMarks\_mnemonics.bed.gz"%>%import()  
 fetalBrainFemaleHMM="~/DataFiles/ChromHMM/human/coMET/E082\_15\_coreMarks\_mnemonics.bed.gz"%>%import()  
 fetalBrainMaleHMM="~/DataFiles/ChromHMM/human/coMET/E081\_15\_coreMarks\_mnemonics.bed.gz"%>%import()  
 H9NeuronCellsHMM="~/DataFiles/ChromHMM/human/coMET/E010\_15\_coreMarks\_mnemonics.bed.gz"%>%import()  
 H9NeuronProgenitorCellsHMM="~/DataFiles/ChromHMM/human/coMET/E009\_15\_coreMarks\_mnemonics.bed.gz"%>%import()  
   
   
 assign("PancreasHMM", PancreasHMM, .GlobalEnv)  
 assign("PancreasIsletsHMM", PancreasIsletsHMM, .GlobalEnv)  
 assign("fetalBrainFemaleHMM", fetalBrainFemaleHMM, .GlobalEnv)  
 assign("fetalBrainMaleHMM", fetalBrainMaleHMM, .GlobalEnv)  
 assign("H9NeuronCellsHMM", H9NeuronCellsHMM, .GlobalEnv)  
 assign("H9NeuronProgenitorCellsHMM", H9NeuronProgenitorCellsHMM, .GlobalEnv)  
   
   
 #Enhancers  
 EnhancersHuman<-import("~/DataFiles/Enhancer Tracks/Human/human\_permissive\_enhancers\_phase\_1\_and\_2.bed")  
   
 #Motifs In Enhancers  
 ARXHuman6Mer<-readRDS("~/DataFiles/ChIPseq/Human/ARX6merHg19Sites")  
 mcols(ARXHuman6Mer)<-cbind.data.frame("Model"="6Mer")  
 ARXTandem2<-readRDS("~/DataFiles/ChIPseq/Human/ARXTande2SpacedSites")  
 mcols(ARXTandem2)<-cbind.data.frame("Model"="ARXTandem2")  
 ARXHumanJolma<-readRDS("~/DataFiles/ChIPseq/Human/JolmaTFBS")  
 mcols(ARXHumanJolma)<-cbind.data.frame("Model"="Jolma")  
 Plaindromic4SpacedTFBS<-readRDS("~/DataFiles/ChIPseq/Human/Plaindromic4SpacedTFBS")  
 mcols(Plaindromic4SpacedTFBS)<-cbind.data.frame("Model"="ARXPlaindromic4Spaced")  
 ARXMotifModels<-c(ARXHuman6Mer, ARXTandem2, ARXHumanJolma, Plaindromic4SpacedTFBS)%>%unlist()  
 HumanEnhancerMotifs<-subsetByOverlaps(ARXMotifModels,EnhancersHuman)  
   
 ARXEnhancerMotifs<-HumanEnhancerMotifs%>%AnnotationTrack(genome = "hg19", stacking = "dense", strand= "\*",  
 col.line="black", feature= (mcols(HumanEnhancerMotifs))$Model,  
 name="ARX Motifs In Enhancers")  
 #ColoringTrack  
 displayPars(ARXEnhancerMotifs) <- list(`6Mer` = "#FF0000", `ARXTandem2` = "#FF6E00",   
 `Jolma` = "#32CD32", `ARXPlaindromic4Spaced` = "#99CD32")  
   
   
 assign("ARXEnhancerMotifs", ARXEnhancerMotifs, .GlobalEnv)  
 assign("EnhancersHuman", EnhancersHuman, .GlobalEnv)  
   
   
   
 geneTracks<-import("~/DataFiles/Gene Tracks/Human/hg.bed")  
 promoterTracks<-geneTracks%>%promoters()%>%GRanges()  
 arx6MerTFBSHg19<-readRDS("~/DataFiles/ChIPseq/Human/ARX6merHg19Sites")  
   
 #Human HiC Data  
 interactionsHumanBrain<-readRDS(file= "~/DataFiles/HiC/Human/SignificantInteractionsBetweenEnhancersContainingARX")%>%InteractionTrack(  
 name= "ARX Significant Interactions")  
 contactProbabilities<- readRDS(file="~/DataFiles/HiC/Human/contactProbabilitiesHuman")%>%InteractionTrack(  
 name= "Contact Probabilities"  
 )  
   
   
 #Coloring the HiC data  
 displayPars(contactProbabilities) = list(col.interactions="red",  
 col.anchors.line = "black",  
 interaction.dimension="height",   
 interaction.measure ="counts",  
 plot.trans=FALSE,  
 plot.outside = TRUE,   
 col.outside="lightblue",   
 anchor.height = 0.1)  
   
 displayPars(interactionsHumanBrain) = list(col.interactions="red",  
 col.anchors.line = "black",  
 interaction.dimension="height",   
 interaction.measure ="counts",  
 plot.trans=FALSE,  
 plot.outside = TRUE,   
 col.outside="lightblue",   
 anchor.height = 0.1)  
   
 assign("promoterTracks", promoterTracks, .GlobalEnv)  
 assign("arx6MerTFBSHg19", arx6MerTFBSHg19, .GlobalEnv)  
 assign("interactionsHumanBrain", interactionsHumanBrain, .GlobalEnv)  
 assign("contactProbabilities", contactProbabilities, .GlobalEnv)  
  
   
   
   
   
 ##ChromHMM Track Generator specifically for humans  
 chromHMMTrackGenerator<-function (gen = "hg19", chr, from, to, bedFile, featureDisplay = featureDisplay,   
 colorcase = "roadmap15")   
 {  
 desiredRegion <- subset(get(bedFile), end > from &   
 start < to & seqnames == chr)  
 track <- AnnotationTrack(desiredRegion,   
 stacking = "dense",  
 col.line="black",  
 feature =   
 (mcols(desiredRegion))$name,  
 genome = "hg19",  
 strand= "\*",  
 name = paste(bedFile))  
   
 displayPars(track) <- list(`1\_TssA` = "#FF0000", `2\_TssAFlnk` = "#FF6E00",   
 `3\_TxFlnk` = "#32CD32", `4\_Tx` = "#008000", `5\_TxWk` = "#006400",   
 `6\_EnhG` = "#C2E105", `7\_Enh` = "#FFFF00", `8\_ZNF/Rpts` = "#66CDAA",   
 `9\_Het` = "#8A91D0", `10\_TssBiv` = "#CD5C5C", `11\_BivFlnk` = "#E9967A",   
 `12\_EnhBiv` = "#BDB76B", `13\_ReprPC` = "#3A3838",   
 `14\_ReprPCWk` = "#808080", `15\_Quies` = "#DCDCDC",   
 Empty = "#ffffff")  
 return(track)  
 }  
   
 chromHMM\_RoadMapAll<-lapply(c("PancreasHMM",  
 "PancreasIsletsHMM",  
 "fetalBrainFemaleHMM",  
 "fetalBrainMaleHMM",  
 "H9NeuronCellsHMM",  
 "H9NeuronProgenitorCellsHMM"), function(x){chromHMMTrackGenerator(gen="hg19",  
 chr= input$chrM,  
 from = input$fromM,  
 to = input$toM,  
 bedFile = x,  
 featureDisplay = "all",   
 colorcase='roadmap15' )})  
   
 # Gene Track with symbols :D  
 knownGenes <- GeneRegionTrack(TxDb.Hsapiens.UCSC.hg19.knownGene,   
 genome="hg19",   
 chromosome="chrX",   
 showId=TRUE,  
 geneSymbol=TRUE,   
 name="UCSC")  
   
 symbols <- unlist(mapIds(org.Hs.eg.db, gene(knownGenes),  
 "SYMBOL", "ENTREZID",   
 multiVals = "first"))  
 symbol(knownGenes) <- symbols[gene(knownGenes)]  
   
 #Promoter and Motif Track  
 promotertrackChromosomeSpecific<-promoterTracks%>%subset(. ,   
 seqnames==input$chrM)%>%AnnotationTrack(., name= "PromoterTrack",   
 genome="hg19")  
 geneTrackChromosomeSpecific<-knownGenes  
 EnhancersHumanChromosomeSpecific<-EnhancersHuman%>%subset(. ,  
 seqnames==input$chrM)%>%AnnotationTrack(., name = "Enhancers",  
 genome = "hg19")  
   
 Arx6merHumanTrack<-subset(arx6MerTFBSHg19,   
 seqnames==input$chrM & start > input$fromM & end< input$toM)%>%AnnotationTrack(name= "ARX Motifs",  
 stacking= "dense",  
 col.line= "black",  
 genome= "hg19")  
 assign("chromHMM\_RoadMapAll", chromHMM\_RoadMapAll, .GlobalEnv)  
 assign("Arx6merHumanTrack", Arx6merHumanTrack, .GlobalEnv)  
 assign("EnhancersHumanChromosomeSpecific", EnhancersHumanChromosomeSpecific, .GlobalEnv)  
 assign("promotertrackChromosomeSpecific", promotertrackChromosomeSpecific, .GlobalEnv)  
 assign("geneTrackChromosomeSpecific", geneTrackChromosomeSpecific, .GlobalEnv)  
 assign("knownGenes", knownGenes, .GlobalEnv)  
 assign("chromHMMTrackGenerator", chromHMMTrackGenerator, .GlobalEnv)  
   
   
   
   
   
 if(input$contactProbabilities==TRUE){  
 plotTracks(trackList = c(humanIdeogramTrack,  
 gHumanTrack,  
 contactProbabilities,   
 EnhancersHumanChromosomeSpecific,  
 ARXEnhancerMotifs,  
 Arx6merHumanTrack,   
 promotertrackChromosomeSpecific,   
 geneTrackChromosomeSpecific,  
 chromHMM\_RoadMapAll),   
 sizes= c(1,1,2,1,1,1,1,3,rep(1,6)),  
 from =input$fromM,   
 to= input$toM,  
 chromosome= input$chrM,  
 cex.title = 0.72,   
 rotation.title = 0,   
 showAxis = FALSE,   
 background.title = "white",  
 lwd.title = 2,   
 title.width = 2,   
 cex.main = 5,   
 col = NULL,   
 fontcolor.title = "black")  
 } else{  
   
 plotTracks(trackList =c(humanIdeogramTrack,  
 gHumanTrack,  
 interactionsHumanBrain,   
 EnhancersHumanChromosomeSpecific,  
 ARXEnhancerMotifs,  
 Arx6merHumanTrack,   
 promotertrackChromosomeSpecific,   
 geneTrackChromosomeSpecific,  
 chromHMM\_RoadMapAll),   
 sizes= c(1,1,2,1,1,1,1,3,rep(1,6)),  
 from =input$fromM,   
 to= input$toM,  
 chromosome= input$chrM,  
 cex.title = 0.72,   
 rotation.title = 0,   
 showAxis = FALSE,   
 background.title = "white",  
 lwd.title = 2,   
 title.width = 2,   
 cex.main = 5,   
 col = NULL,   
 fontcolor.title = "black")  
   
}}else if(!chrM==input$chrM){   
 chrM<-input$chrM  
 assign("chrM", chrM, .GlobalEnv)  
 humanIdeogramTrack<-IdeogramTrack(chromosome = input$chrM, genome="hg19",name= "Ideogram")  
 chromHMM\_RoadMapAll<-lapply(c("PancreasHMM",  
 "PancreasIsletsHMM",  
 "fetalBrainFemaleHMM",  
 "fetalBrainMaleHMM",  
 "H9NeuronCellsHMM",  
 "H9NeuronProgenitorCellsHMM"), function(x){chromHMMTrackGenerator(gen="hg19",  
 chr=input$chrM,  
 from = input$fromM,  
 to = input$toM,  
 bedFile = x,  
 featureDisplay = "all",   
 colorcase='roadmap15' )})  
   
 # Gene Track with symbols :D  
 knownGenes <- GeneRegionTrack(TxDb.Hsapiens.UCSC.hg19.knownGene,   
 genome="hg19",   
 chromosome=input$chrM,   
 showId=TRUE,  
 geneSymbol=TRUE,   
 name="UCSC")  
 symbols <- unlist(mapIds(org.Hs.eg.db, gene(knownGenes),  
 "SYMBOL", "ENTREZID",   
 multiVals = "first"))  
 symbol(knownGenes) <- symbols[gene(knownGenes)]  
   
 #Promoter and Motif Track  
 promotertrackChromosomeSpecific<-promoterTracks%>%subset(. ,   
 seqnames==input$chrM)%>%AnnotationTrack(., name= "PromoterTrack",   
 genome="hg19")  
 geneTrackChromosomeSpecific<-knownGenes  
 EnhancersHumanChromosomeSpecific<-EnhancersHuman%>%subset(. ,  
 seqnames==input$chrM)%>%AnnotationTrack(., name = "Enhancers",  
 genome = "hg19")  
   
 Arx6merHumanTrack<-subset(arx6MerTFBSHg19,   
 seqnames==input$chrM & start > input$fromM & end< input$toM)%>%AnnotationTrack(name= "ARX Motifs",  
 stacking= "dense",  
 col.line= "black",  
 genome= "hg19")  
   
   
 assign("humanIdeogramTrack", humanIdeogramTrack, .GlobalEnv)  
 assign("chromHMM\_RoadMapAll", chromHMM\_RoadMapAll, .GlobalEnv)  
 assign("Arx6merHumanTrack", Arx6merHumanTrack, .GlobalEnv)  
 assign("EnhancersHumanChromosomeSpecific", EnhancersHumanChromosomeSpecific, .GlobalEnv)  
 assign("promotertrackChromosomeSpecific", promotertrackChromosomeSpecific, .GlobalEnv)  
 assign("geneTrackChromosomeSpecific", geneTrackChromosomeSpecific, .GlobalEnv)  
 assign("knownGenes", knownGenes, .GlobalEnv)  
   
   
   
   
 if(input$contactProbabilities==TRUE){  
 plotTracks(trackList = c(humanIdeogramTrack,  
 gHumanTrack,  
 contactProbabilities,   
 EnhancersHumanChromosomeSpecific,  
 ARXEnhancerMotifs,  
 Arx6merHumanTrack,   
 promotertrackChromosomeSpecific,   
 geneTrackChromosomeSpecific,  
 chromHMM\_RoadMapAll),   
 sizes= c(1,1,2,1,1,1,1,3,rep(1,6)),  
 from =input$fromM,   
 to= input$toM,  
 chromosome= input$chrM,  
 cex.title = 0.72,   
 rotation.title = 0,   
 showAxis = FALSE,   
 background.title = "white",  
 lwd.title = 2,   
 title.width = 2,   
 cex.main = 5,   
 col = NULL,   
 fontcolor.title = "black")  
 } else{  
   
 plotTracks(trackList =c(humanIdeogramTrack,  
 gHumanTrack,  
 interactionsHumanBrain,   
 EnhancersHumanChromosomeSpecific,  
 ARXEnhancerMotifs,  
 Arx6merHumanTrack,   
 promotertrackChromosomeSpecific,   
 geneTrackChromosomeSpecific,  
 chromHMM\_RoadMapAll),   
 sizes= c(1,1,2,1,1,1,1,3,rep(1,6)),  
 from =input$fromM,   
 to= input$toM,  
 chromosome= input$chrM,  
 cex.title = 0.72,   
 rotation.title = 0,   
 showAxis = FALSE,   
 background.title = "white",  
 lwd.title = 2,   
 title.width = 2,   
 cex.main = 5,   
 col = NULL,   
 fontcolor.title = "black")  
 }} else if(input$contactProbabilities==TRUE) {  
   
   
 chromHMM\_RoadMapAll<-lapply(c("PancreasHMM",  
 "PancreasIsletsHMM",  
 "fetalBrainFemaleHMM",  
 "fetalBrainMaleHMM",  
 "H9NeuronCellsHMM",  
 "H9NeuronProgenitorCellsHMM"), function(x){chromHMMTrackGenerator(gen="hg19",  
 chr=input$chrM,  
 from = input$fromM,  
 to = input$toM,  
 bedFile = x,  
 featureDisplay = "all",   
 colorcase='roadmap15' )})  
 Arx6merHumanTrack<-subset(arx6MerTFBSHg19,   
 seqnames==input$chrM & start > input$fromM & end< input$toM)%>%AnnotationTrack(name= "ARX Motifs",  
 stacking= "dense",  
 col.line= "black",  
 genome="hg19")  
   
 assign("chromHMM\_RoadMapAll", chromHMM\_RoadMapAll, .GlobalEnv)  
 assign("Arx6merHumanTrack", Arx6merHumanTrack, .GlobalEnv)  
 assign("EnhancersHumanChromosomeSpecific", EnhancersHumanChromosomeSpecific, .GlobalEnv)  
 assign("promotertrackChromosomeSpecific", promotertrackChromosomeSpecific, .GlobalEnv)  
 assign("knownGenes", knownGenes, .GlobalEnv)  
   
   
   
 plotTracks(trackList = c(humanIdeogramTrack,  
 gHumanTrack,  
 contactProbabilities,   
 EnhancersHumanChromosomeSpecific,  
 ARXEnhancerMotifs,  
 Arx6merHumanTrack,   
 promotertrackChromosomeSpecific,   
 geneTrackChromosomeSpecific,  
 chromHMM\_RoadMapAll),   
 sizes= c(1,1,2,1,1,1,1,3,rep(1,6)),  
 from =input$fromM,   
 to= input$toM,  
 chromosome= input$chrM,  
 cex.title = 0.72,   
 rotation.title = 0,   
 showAxis = FALSE,   
 background.title = "white",  
 lwd.title = 2,   
 title.width = 2,   
 cex.main = 5,   
 col = NULL,   
 fontcolor.title = "black")  
   
}else {  
   
 chromHMM\_RoadMapAll<-lapply(c("PancreasHMM",  
 "PancreasIsletsHMM",  
 "fetalBrainFemaleHMM",  
 "fetalBrainMaleHMM",  
 "H9NeuronCellsHMM",  
 "H9NeuronProgenitorCellsHMM"), function(x){chromHMMTrackGenerator(gen="hg19",  
 chr=input$chrM,  
 from = input$fromM,  
 to = input$toM,  
 bedFile = x,  
 featureDisplay = "all",   
 colorcase='roadmap15' )})  
 Arx6merHumanTrack<-subset(arx6MerTFBSHg19,   
 seqnames=="chrX" & start > input$fromM & end< input$toM)%>%AnnotationTrack(name= "ARX Motifs",  
 stacking= "dense",  
 col.line= "black",  
 genome="hg19")  
   
   
 plotTracks(trackList = c(humanIdeogramTrack,  
 gHumanTrack,  
 interactionsHumanBrain,   
 EnhancersHumanChromosomeSpecific,  
 ARXEnhancerMotifs,  
 Arx6merHumanTrack,   
 promotertrackChromosomeSpecific,   
 geneTrackChromosomeSpecific,  
 chromHMM\_RoadMapAll),   
 sizes= c(1,1,2,1,1,1,1,3,rep(1,6)),  
 from =input$fromM,   
 to= input$toM,  
 chromosome= input$chrM,  
 cex.title = 0.72,   
 rotation.title = 0,   
 showAxis = FALSE,   
 background.title = "white",  
 lwd.title = 2,   
 title.width = 2,   
 cex.main = 5,   
 col = NULL,   
 fontcolor.title = "black")  
 }  
 },height = 850,width = 1600)  
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
   
 ######################################################  
 ############MOuse GVIZ PLot 1  
 ######################################################  
  
 output$MousegvizPlot <- renderPlot({  
 if(!exists("testesMouseHMM")){  
   
   
 mouseIdeogramTrack<-IdeogramTrack(chromosome = input$chrM, genome="mm9",name= "Ideogram")  
 gmouseTrack<-GenomeAxisTrack(name= "Axis")  
   
 assign("mouseIdeogramTrack", mouseIdeogramTrack, .GlobalEnv)  
 assign("gmouseTrack", gmouseTrack, .GlobalEnv)  
 ####################################################  
 #####MOUSE DATA  
 ###########################################################3  
 #Mouse ChromHMM inputs  
 testesMouseHMM="~/DataFiles/ChromHMM/mouse/testes\_cStates\_HMM.bed"%>%import()  
 brainMouseHMM= "~/DataFiles/ChromHMM/mouse/brain\_cStates\_HMM.bed"%>%import()  
 thymusMouseHMM="~/DataFiles/ChromHMM/mouse/thymus\_cStates\_HMM.bed"%>%import()  
 heartMouseHMM="~/DataFiles/ChromHMM/mouse/heart\_cStates\_HMM.bed"%>%import()  
 mESCMouseHMM="~/DataFiles/ChromHMM/mouse/mESC\_cStates\_HMM.bed"%>%import()  
 intestineMouseHMM="~/DataFiles/ChromHMM/mouse/intestine\_cStates\_HMM.bed"%>%import()  
   
 assign("testesMouseHMM", testesMouseHMM, .GlobalEnv)  
 assign("brainMouseHMM", brainMouseHMM, .GlobalEnv)  
 assign("thymusMouseHMM", thymusMouseHMM, .GlobalEnv)  
 assign("heartMouseHMM", heartMouseHMM, .GlobalEnv)  
 assign("mESCMouseHMM", mESCMouseHMM, .GlobalEnv)  
 assign("intestineMouseHMM", intestineMouseHMM, .GlobalEnv)  
   
 #Mouse Inputs  
 Arx6merMouse<-readRDS("~/DataFiles/ChIPseq/Mouse/ARX6mermm9Sites")  
 EnhancersMouse<-import("~/DataFiles/Enhancer Tracks/Mouse/mouse\_permissive\_enhancers\_phase\_1\_and\_2.bed")  
 geneTracksMouse<-import("~/DataFiles/Gene Tracks/Mouse/mm9.bed")  
 promoterTracksMouse<-promoters(geneTracksMouse)%>%GRanges()  
   
 assign("promoterTracksMouse", promoterTracksMouse, .GlobalEnv)  
 assign("EnhancersMouse", EnhancersMouse, .GlobalEnv)  
   
   
   
 #Hic Data  
 contactProbabilitiesMouse<-readRDS("~/DataFiles/HiC/Mouse/contactProbabilitiesMouse")%>%InteractionTrack(name= "Contact Probabilities")  
 interactionBrainMouse<-readRDS("~/DataFiles/HiC/Mouse/mm9StasticallySignificantInteractions")%>%InteractionTrack(name = "Significant Interactions")  
   
 #Coloring the tracks  
 displayPars(contactProbabilitiesMouse) = list(col.interactions="red",  
 col.anchors.line = "black",  
 interaction.dimension="height",   
 interaction.measure ="counts",  
 plot.trans=FALSE,  
 plot.outside = TRUE,   
 col.outside="lightblue",   
 anchor.height = 0.1)  
 displayPars(interactionBrainMouse) = list(col.interactions="red",  
 col.anchors.line = "black",  
 interaction.dimension="height",   
 interaction.measure ="counts",  
 plot.trans=FALSE,  
 plot.outside = TRUE,   
 col.outside="lightblue",   
 anchor.height = 0.1)  
   
   
   
 assign("contactProbabilitiesMouse", contactProbabilitiesMouse, .GlobalEnv)  
 assign("interactionBrainMouse", interactionBrainMouse, .GlobalEnv)  
 assign("promoterTracksMouse", promoterTracksMouse, .GlobalEnv)  
 assign("Arx6merMouse", Arx6merMouse, .GlobalEnv)  
  
   
 #Mouse Enhancer Motifs  
 ARXMouse6Mer<-readRDS("~/DataFiles/ChIPseq/Mouse/ARX6mermm9Sites")  
 mcols(ARXMouse6Mer)<-cbind.data.frame("Model"="6Mer")  
 ARXTandem2Mouse<-readRDS("~/DataFiles/ChIPseq/Mouse/ARXTande2SpacedSites")  
 mcols(ARXTandem2Mouse)<-cbind.data.frame("Model"="ARXTandem2")  
 ARXJolmaMouse<-readRDS("~/DataFiles/ChIPseq/Mouse/Jolmamm9Sites")  
 mcols(ARXJolmaMouse)<-cbind.data.frame("Model"="Jolma")  
 Plaindromic4SpacedTFBSMouse<-readRDS("~/DataFiles/ChIPseq/Mouse/Plaindromic4Spacedmm9")  
 mcols(Plaindromic4SpacedTFBSMouse)<-cbind.data.frame("Model"="ARXPlaindromic4Spaced")  
   
   
 ARXMotifModelsMouse<-c(ARXMouse6Mer, ARXTandem2Mouse, ARXJolmaMouse, Plaindromic4SpacedTFBSMouse)%>%unlist()  
 MouseEnhancerMotifs<-subsetByOverlaps(ARXMotifModelsMouse,EnhancersMouse)  
 ARXEnhancerMotifsMouse<-MouseEnhancerMotifs%>%AnnotationTrack(genome = "mm9", stacking = "dense", strand= "\*",  
 col.line="black", feature= (mcols(MouseEnhancerMotifs))$Model,  
 name= "Motifs In Enhancers")  
 displayPars(ARXEnhancerMotifsMouse) <- list(`6Mer` = "#FF0000", `ARXTandem2` = "#FF6E00",   
 `Jolma` = "#32CD32", `ARXPlaindromic4Spaced` = "#99CD32")  
   
   
   
   
 assign("ARXEnhancerMotifsMouse", ARXEnhancerMotifsMouse, .GlobalEnv)  
 assign("interactionBrainMouse", interactionBrainMouse, .GlobalEnv)  
   
   
 chromHMMTrackGeneratorMouse<-function (gen = "mm9", chr, from, to, bedFile, featureDisplay = featureDisplay,   
 colorcase = "roadmap15")   
 {  
 desiredRegion <- subset(get(bedFile), end > from &   
 start < to & seqnames == chr)  
 mcols(desiredRegion)<-cbind.data.frame("name"=(mcols(desiredRegion))$name)  
 track<-AnnotationTrack(desiredRegion, stacking = "dense", col.line="black", feature =   
 (mcols(desiredRegion))$name, genome = "mm9", strand= "\*",  
 name = paste(bedFile))  
 if (colorcase == "roadmap15") {  
 displayPars(track) <- list(`1\_Txn\_Elongation` = "#FF0000", `2\_Weak\_Txn` = "#FF6E00",   
 `9\_Strong\_Enhancer` = "#32CD32", `4\_Poised\_Enhancer` = "#008000", `5\_Active\_Promoter` = "#006400",   
 `6\_Strong\_Enhancer` = "#C2E105", `7\_Active\_Promoter` = "#FFFF00", `8\_Strong\_Enhancer` = "#66CDAA",   
 `9\_Txn\_Transition` = "#8A91D0", `10\_Poised\_Promoter` = "#CD5C5C", `11\_Repressed` = "#E9967A",   
 `15\_Insulator` = "#BDB76B", `12\_Heterochrom` = "#3A3838",   
 `14\_Heterochrom` = "#808080", `13\_Heterochrom` = "#DCDCDC",   
 Empty = "#ffffff")  
 } else {  
 stop("Invalid in function RoadMap :color choice invalid :\n")  
 }  
 track  
 }  
   
   
  
   
 #Gene Symbol Track   
 knownGenesMouse <- GeneRegionTrack(TxDb.Mmusculus.UCSC.mm9.knownGene,  
 genome="mm9",  
 chromosome=input$chrM,  
 showId=TRUE,  
 geneSymbol=TRUE,   
 name="UCSC")  
 symbolsMouse <- unlist(mapIds(org.Mm.eg.db,   
 gene(knownGenesMouse),  
 "SYMBOL",   
 "ENTREZID",  
 multiVals = "first"))  
 symbol(knownGenesMouse) <- symbolsMouse[gene(knownGenesMouse)]  
   
   
 promotertrackChromosomeSpecificMouse<-promoterTracksMouse%>%subset(. ,   
 seqnames==input$chrM)%>%AnnotationTrack(., name= "PromoterTrack",  
 genome= "mm9",   
 stacking= "dense")  
 geneTrackChromosomeSpecificMouse<-knownGenesMouse  
   
 EnhancersMouseChromosomeSpecificMouse<-subset(EnhancersMouse, seqnames==input$chrM)%>%AnnotationTrack(name= "Enhancer Track",   
 stacking= "dense",  
 genome= "mm9")  
   
 assign("promotertrackChromosomeSpecificMouse", promotertrackChromosomeSpecificMouse , .GlobalEnv)  
 assign("geneTrackChromosomeSpecificMouse", geneTrackChromosomeSpecificMouse, .GlobalEnv)  
 assign("EnhancersMouseChromosomeSpecificMouse", EnhancersMouseChromosomeSpecificMouse, .GlobalEnv)  
 assign("chromHMMTrackGeneratorMouse", chromHMMTrackGeneratorMouse, .GlobalEnv)  
 assign("knownGenesMouse", knownGenesMouse, .GlobalEnv)  
   
   
 #Base pair and Chormosome specific Tracks  
 chromHMM\_RoadMapAllMouse<-lapply(c("testesMouseHMM",  
 "brainMouseHMM",  
 "thymusMouseHMM",  
 "heartMouseHMM",  
 "mESCMouseHMM",  
 "intestineMouseHMM"), function(x){chromHMMTrackGeneratorMouse(gen="mm9",  
 chr=input$chrM,  
 from = input$fromM,  
 to = input$toM,  
 bedFile = x,  
 featureDisplay = "all",   
 colorcase='roadmap15' )})  
   
 Arx6merMouseTrack<-subset(Arx6merMouse, seqnames==input$chrM & start > input$fromM & end< input$toM)%>%AnnotationTrack(name= "ARX Motifs",  
 stacking= "dense",  
 col.line= "black",  
 genome="mm9")  
 assign( "chromHMM\_RoadMapAllMouse",chromHMM\_RoadMapAllMouse, .GlobalEnv)  
 assign( "Arx6merMouseTrack",Arx6merMouseTrack, .GlobalEnv)  
   
   
 if(input$contactProbabilities==TRUE){  
   
 plotTracks(trackList = c(mouseIdeogramTrack,  
 gmouseTrack,  
 contactProbabilitiesMouse,   
 EnhancersMouseChromosomeSpecificMouse,  
 ARXEnhancerMotifsMouse,  
 Arx6merMouseTrack,  
 promotertrackChromosomeSpecificMouse,   
 geneTrackChromosomeSpecificMouse,  
 chromHMM\_RoadMapAllMouse),   
 sizes= c(1,1,2,1,1,1,1,3,rep(1,6)),  
 from =input$fromM,   
 to= input$toM,  
 chromosome= input$chrM,  
 cex.title = 0.72,   
 rotation.title = 0,   
 showAxis = FALSE,   
 background.title = "white",  
 lwd.title = 2,   
 title.width = 2,   
 cex.main = 5,   
 col = NULL,   
 fontcolor.title = "black")  
 } else{  
 plotTracks(trackList = c(mouseIdeogramTrack,  
 gmouseTrack,  
 interactionBrainMouse,   
 EnhancersMouseChromosomeSpecificMouse,  
 ARXEnhancerMotifsMouse,  
 Arx6merMouseTrack,  
 promotertrackChromosomeSpecificMouse,   
 geneTrackChromosomeSpecificMouse,  
 chromHMM\_RoadMapAllMouse),   
 sizes= c(1,1,2,1,1,1,1,3,rep(1,6)),  
 from =input$fromM,   
 to= input$toM,  
 chromosome= input$chrM,  
 cex.title = 0.72,   
 rotation.title = 0,   
 showAxis = FALSE,   
 background.title = "white",  
 lwd.title = 2,   
 title.width = 2,   
 cex.main = 5,   
 col = NULL,   
 fontcolor.title = "black")  
   
   
   
 }  
 }else if(!chrM==input$chrM ){   
 chrM<- input$chrM  
 assign("chrM", chrM, .GlobalEnv)  
   
 #Gene Symbol Track   
 knownGenesMouse <- GeneRegionTrack(TxDb.Mmusculus.UCSC.mm9.knownGene,  
 genome="mm9",  
 chromosome=input$chrM,  
 showId=TRUE,  
 geneSymbol=TRUE,   
 name="UCSC")  
 symbolsMouse <- unlist(mapIds(org.Mm.eg.db,   
 gene(knownGenesMouse),  
 "SYMBOL",   
 "ENTREZID",  
 multiVals = "first"))  
 symbol(knownGenesMouse) <- symbolsMouse[gene(knownGenesMouse)]  
   
   
 promotertrackChromosomeSpecificMouse<-promoterTracksMouse%>%subset(. ,   
 seqnames==input$chrM)%>%AnnotationTrack(., name= "PromoterTrack",  
 genome= "mm9",   
 stacking= "dense")  
 geneTrackChromosomeSpecificMouse<-knownGenesMouse  
   
 EnhancersMouseChromosomeSpecificMouse<-subset(EnhancersMouse, seqnames==input$chrM)%>%AnnotationTrack(name= "Enhancer Track",   
 stacking= "dense",  
 genome= "mm9")  
   
   
 #Base pair and Chormosome specific Tracks  
 chromHMM\_RoadMapAllMouse<-lapply(c("testesMouseHMM",  
 "brainMouseHMM",  
 "thymusMouseHMM",  
 "heartMouseHMM",  
 "mESCMouseHMM",  
 "intestineMouseHMM"), function(x){chromHMMTrackGeneratorMouse(gen="mm9",  
 chr=input$chrM,  
 from = input$fromM,  
 to = input$toM,  
 bedFile = x,  
 featureDisplay = "all",   
 colorcase='roadmap15' )})  
   
 Arx6merMouseTrack<-subset(Arx6merMouse, seqnames==input$chrM & start > input$fromM & end< input$toM)%>%AnnotationTrack(name= "ARX Motifs",  
 stacking= "dense",  
 col.line= "black",  
 genome="mm9")  
 assign( "chromHMM\_RoadMapAllMouse",chromHMM\_RoadMapAllMouse, .GlobalEnv)  
 assign( "Arx6merMouseTrack",Arx6merMouseTrack, .GlobalEnv)  
 assign("promotertrackChromosomeSpecificMouse", promotertrackChromosomeSpecificMouse , .GlobalEnv)  
 assign("geneTrackChromosomeSpecificMouse", geneTrackChromosomeSpecificMouse, .GlobalEnv)  
 assign("EnhancersMouseChromosomeSpecificMouse", EnhancersMouseChromosomeSpecificMouse, .GlobalEnv)  
 assign("knownGenesMouse", knownGenesMouse, .GlobalEnv)  
   
 if(input$contactProbabilities==TRUE){  
   
 plotTracks(trackList = c(mouseIdeogramTrack,  
 gmouseTrack,  
 contactProbabilitiesMouse,   
 EnhancersMouseChromosomeSpecificMouse,  
 ARXEnhancerMotifsMouse,  
 Arx6merMouseTrack,  
 promotertrackChromosomeSpecificMouse,   
 geneTrackChromosomeSpecificMouse,  
 chromHMM\_RoadMapAllMouse),   
 sizes= c(1,1,2,1,1,1,1,3,rep(1,6)),  
 from =input$fromM,   
 to= input$toM,  
 chromosome= input$chrM,  
 cex.title = 0.72,   
 rotation.title = 0,   
 showAxis = FALSE,   
 background.title = "white",  
 lwd.title = 2,   
 title.width = 2,   
 cex.main = 5,   
 col = NULL,   
 fontcolor.title = "black")  
 } else{  
 plotTracks(trackList = c(mouseIdeogramTrack,  
 gmouseTrack,  
 contactProbabilitiesMouse,   
 EnhancersMouseChromosomeSpecificMouse,  
 ARXEnhancerMotifsMouse,  
 Arx6merMouseTrack,  
 promotertrackChromosomeSpecificMouse,   
 geneTrackChromosomeSpecificMouse,  
 chromHMM\_RoadMapAllMouse),   
 sizes= c(1,1,2,1,1,1,1,3,rep(1,6)),  
 from =input$fromM,   
 to= input$toM,  
 chromosome= input$chrM,  
 cex.title = 0.72,   
 rotation.title = 0,   
 showAxis = FALSE,   
 background.title = "white",  
 lwd.title = 2,   
 title.width = 2,   
 cex.main = 5,   
 col = NULL,   
 fontcolor.title = "black")  
   
   
   
   
   
   
 }} else if(input$contactProbabilities==TRUE) {  
 #If there is just a base pair change  
   
   
   
 chromHMM\_RoadMapAllMouse<-lapply(c("testesMouseHMM",  
 "brainMouseHMM",  
 "thymusMouseHMM",  
 "heartMouseHMM",  
 "mESCMouseHMM",  
 "intestineMouseHMM"), function(x){chromHMMTrackGeneratorMouse(gen="mm9",  
 chr=input$chrM,  
 from = input$fromM,  
 to = input$toM,  
 bedFile = x,  
 featureDisplay = "all",   
 colorcase='roadmap15' )})  
   
 Arx6merMouseTrack<-subset(Arx6merMouse, seqnames==input$chrM & start > input$fromM & end< input$toM)%>%AnnotationTrack(name= "ARX Motifs",  
 stacking= "dense",  
 col.line= "black",  
 genome="mm9")  
 assign( "chromHMM\_RoadMapAllMouse",chromHMM\_RoadMapAllMouse, .GlobalEnv)  
 assign( "Arx6merMouseTrack",Arx6merMouseTrack, .GlobalEnv)  
 assign("promotertrackChromosomeSpecificMouse", promotertrackChromosomeSpecificMouse , .GlobalEnv)  
 assign("geneTrackChromosomeSpecificMouse", geneTrackChromosomeSpecificMouse, .GlobalEnv)  
 assign("EnhancersMouseChromosomeSpecificMouse", EnhancersMouseChromosomeSpecificMouse, .GlobalEnv)  
 assign("knownGenesMouse", knownGenesMouse, .GlobalEnv)  
   
  
 plotTracks(trackList = c(mouseIdeogramTrack,  
 gmouseTrack,  
 contactProbabilitiesMouse,   
 EnhancersMouseChromosomeSpecificMouse,  
 ARXEnhancerMotifsMouse,  
 Arx6merMouseTrack,  
 promotertrackChromosomeSpecificMouse,   
 geneTrackChromosomeSpecificMouse,  
 chromHMM\_RoadMapAllMouse),   
 sizes= c(1,1,2,1,1,1,1,3,rep(1,6)),  
 from =input$fromM,   
 to= input$toM,  
 chromosome= input$chrM,  
 cex.title = 0.72,   
 rotation.title = 0,   
 showAxis = FALSE,   
 background.title = "white",  
 lwd.title = 2,   
 title.width = 2,   
 cex.main = 5,   
 col = NULL,   
 fontcolor.title = "black")  
   
 }else {  
 chromHMM\_RoadMapAllMouse<-lapply(c("testesMouseHMM",  
 "brainMouseHMM",  
 "thymusMouseHMM",  
 "heartMouseHMM",  
 "mESCMouseHMM",  
 "intestineMouseHMM"), function(x){chromHMMTrackGeneratorMouse(gen="mm9",  
 chr=input$chrM,  
 from = input$fromM,  
 to = input$toM,  
 bedFile = x,  
 featureDisplay = "all",   
 colorcase='roadmap15' )})  
   
   
 Arx6merMouseTrack<-subset(Arx6merMouse, seqnames==input$chrM & start > input$fromM & end< input$toM)%>%AnnotationTrack(name= "ARX Motifs",  
 stacking= "dense",  
 col.line= "black",   
 genome="mm9")  
 assign( "chromHMM\_RoadMapAllMouse",chromHMM\_RoadMapAllMouse, .GlobalEnv)  
 assign( "Arx6merMouseTrack",Arx6merMouseTrack, .GlobalEnv)  
   
   
   
   
   
 plotTracks(trackList =c(mouseIdeogramTrack,  
 gmouseTrack,  
 interactionBrainMouse,   
 EnhancersMouseChromosomeSpecificMouse,  
 ARXEnhancerMotifsMouse,  
 Arx6merMouseTrack,  
 promotertrackChromosomeSpecificMouse,   
 geneTrackChromosomeSpecificMouse,  
 chromHMM\_RoadMapAllMouse),   
 sizes= c(1,1,2,1,1,1,1,3,rep(1,6)),  
 from =input$fromM,   
 to= input$toM,  
 chromosome= input$chrM,  
 cex.title = 0.72,   
 rotation.title = 0,   
 showAxis = FALSE,   
 background.title = "white",  
 lwd.title = 2,   
 title.width = 2,   
 cex.main = 5,   
 col = NULL,   
 fontcolor.title = "black")  
 }  
 },height = 850,width = 1600)  
   
   
 output$LegendsPlot<- renderImage({  
   
 list(  
 src = "www/EpigenomicsRoadMapLegendHMM.jpeg",  
 contentType = "image/jpeg",  
 alt = "Human/Epigenomics Road Map Legend"  
 )  
   
 }, deleteFile = FALSE)  
   
   
 output$LegendsPlotMouse<- renderImage({  
   
 list(  
 src = "www/mm9ChromHMMStates.jpeg",  
 contentType = "image/jpeg",  
 alt = "Human/Epigenomics Road Map Legend"  
 )  
   
 }, deleteFile = FALSE)  
   
   
})

## Ui SScript

library(shiny)  
library(shinycssloaders)  
library(shinydashboard)  
library(gridExtra)  
  
  
dashboardPage(  
 dashboardHeader(title = "ARX Genome Browser"),  
 dashboardSidebar(  
 numericInput("fromM", "Starting Base",value = 25016813),  
 numericInput("toM", "Finishing Base", value = 25038065),  
 numericInput("counts", "Contact Probability", value = 1),  
 selectInput("chrM", label = h3("Select box"),   
 choices = list("Chromosome 1" = "chr1",  
 "Chromosome 2" = "chr2",   
 "Chromosome 3" = "chr3",  
 "Chromosome 4" = "chr4",  
 "Chromosome 5" = "chr5",  
 "Chromosome 6" = "chr6",  
 "Chromosome 7" = "chr7",  
 "Chromosome 8" = "chr8",  
 "Chromosome 9" = "chr9",  
 "Chromosome 10" = "chr10",  
 "Chromosome 11" = "chr11",  
 "Chromosome 12" = "chr12",  
 "Chromosome 13" = "chr13",  
 "Chromosome 14" = "chr14",  
 "Chromosome 15" = "chr15",  
 "Chromosome 16" = "chr16",  
 "Chromosome 17" = "chr17",  
 "Chromosome 18" = "chr18",  
 "Chromosome 19" = "chr19",  
 "Chromosome 20" = "chr20",  
 "Chromosome 21" = "chr21",  
 "Chromosome 22" = "chr22",  
 "Chromosome X" = "chrX",  
 "Chromosome Y" = "chrY"), selected = "chrX"),  
 hr(),  
 fluidRow(column(3, verbatimTextOutput("value"))  
 ),  
   
 # Copy the line below to make a checkbox  
 checkboxInput("contactProbabilities", label = "Raw Interactions", value = TRUE)  
   
 ),  
 dashboardBody(tabsetPanel(  
 tabPanel("Human (hg19) Genome Browser",   
 withSpinner(plotOutput("HumangvizPlot"),  
 type = getOption("spinner.type", default = 3),  
 color = getOption("spinner.color", default = "#0275D8"),  
 color.background = getOption("spinner.color.background", default = "#FFFFFF"))),  
 tabPanel("Mouse (mm9) Genome Browser",   
 withSpinner(plotOutput("MousegvizPlot"),  
 type = getOption("spinner.type", default = 3),  
 color = getOption("spinner.color", default = "#0275D8"),  
 color.background = getOption("spinner.color.background", default = "#FFFFFF"))),  
 tabPanel("Legends",   
 fluidRow(  
 column(6,plotOutput(outputId="LegendsPlot", width="300px",height="700px")),   
 column(6,plotOutput(outputId="LegendsPlotMouse", width="300px",height="700px"))  
   
 # withSpinner(plotOutput(c("LegendsPlot")),  
 # type = getOption("spinner.type", default = 3),  
 # color = getOption("spinner.color", default = "#0275D8"),  
 # color.background = getOption("spinner.color.background", default = "#FFFFFF")),  
 # withSpinner(plotOutput(c("LegendsPlotMouse")),  
 # type = getOption("spinner.type", default = 3),  
 # color = getOption("spinner.color", default = "#0275D8"),  
 # color.background = getOption("spinner.color.background", default = "#FFFFFF"))  
 ))  
 )  
 )  
 )