require(envimaR) # MANDANTORY: defining the root folder DO NOT change this line rootDIR = “C:/Users/jomue/edu/geoAI” source(file.path(envimaR::alternativeEnvi(root\_folder = rootDIR),“src/geo\_AI\_setup.R”),echo = TRUE) #read data Koralle<-sf::st\_read(“E:/Koralle/images/Coral\_bleaching\_10m\_2022.shp”) Koralle Coral\_ras = raster::stack(“E:/Koralle/images/Coral\_2017\_old.tif”) Coral\_ras names(Coral\_ras)<-c(“red”,“green”,“blue”) Coral\_ras<-subset(Coral\_ras,c(“red”,“green”,“blue”)) Koralle<-Koralle[,c(2:6)] Koralle = sf::st\_transform(Koralle, crs(Coral\_ras)) Coral\_extent <- raster::extent(Coral\_ras) Koralle <- sf::st\_crop(Koralle, Coral\_extent) Koralle # rasterize the coral rasterized\_vector <- raster::rasterize(Koralle, Coral\_ras[[1]]) rasterized\_vector rasterized\_vector[is.na(rasterized\_vector[2:4])] <- 1 rasterized\_vector[is.na(rasterized\_vector[1,3,4])] <- 2 rasterized\_vector[is.na(rasterized\_vector[1,2,4])] <- 3 rasterized\_vector[is.na(rasterized\_vector[1:3])] <- 4 rasterized\_vector raster::writeRaster(rasterized\_vector, (“E:/Koralle/images/Coral\_Mask\_2017\_bleaching.tif”), overwrite = T) # divide to training and testing extent e\_test <- raster::extent(3e+05, 7390240, 320000, 74500000) e\_train <- raster::extent(320000, 74500000, 409800, 7500040)

coral\_mask\_train <- raster::crop(rasterized\_vector, e\_train) coral\_dop\_train <- raster::crop(Coral\_ras, e\_train)

coral\_mask\_test <- raster::crop(rasterized\_vector, e\_test) coral\_dop\_test <- raster::crop(Coral\_ras, e\_test)

raster::writeRaster( coral\_mask\_test, (“E:/Koralle/images/Coral\_Mask\_bleaching\_2017\_test.tif”), overwrite = T )

raster::writeRaster( coral\_dop\_test, (“E:/Koralle/images/Coral\_Dop\_bleaching\_2017\_test.tif”), overwrite = T )

raster::writeRaster( coral\_mask\_train, (“E:/Koralle/images/Coral\_Mask\_bleaching\_2017\_train.tif”), overwrite = T )

raster::writeRaster( coral\_dop\_train, (“E:/Koralle/images/Coral\_Dop\_bleaching\_2017\_train.tif”), overwrite = T )

subset\_ds <- function(input\_raster, model\_input\_shape, path, targetname = ““, mask = FALSE) { # determine next number of quadrats in x and y direction, by simple rounding targetsizeX <- model\_input\_shape[1] targetsizeY <- model\_input\_shape[2] inputX <- ncol(input\_raster) inputY <- nrow(input\_raster) # determine dimensions of raster so that # it can be split by whole number of subsets (by shrinking it) while (inputX %% targetsizeX != 0) { inputX = inputX - 1 } while (inputY %% targetsizeY != 0) { inputY = inputY - 1 } # determine difference diffX <- ncol(input\_raster) - inputX diffY <- nrow(input\_raster) - inputY # determine new dimensions of raster and crop, # cutting evenly on all sides if possible newXmin <- floor(diffX / 2) newXmax <- ncol(input\_raster) - ceiling(diffX / 2) - 1 newYmin <- floor(diffY / 2) newYmax <- nrow(input\_raster) - ceiling(diffY / 2) - 1 rst\_cropped <- suppressMessages(raster::crop( input\_raster, raster::extent(input\_raster, newYmin, newYmax, newXmin, newXmax) )) agg <- suppressMessages(raster::aggregate(rst\_cropped[[1]], c(targetsizeX, targetsizeY))) agg[] <- suppressMessages(1:ncell(agg)) agg\_poly <- suppressMessages(raster::rasterToPolygons(agg)) names(agg\_poly) <-”polis” if (mask) { lapply( seq\_along(agg), FUN = function(i) { subs <- local({ e1 <- raster::extent(agg\_poly[agg\_poly$polis == i,]) subs <- suppressMessages(raster::crop(rst\_cropped, e1)) }) writePNG(as.array(subs), target = paste0(path, targetname, i, ".png")) } ) } else{ lapply( seq\_along(agg), FUN = function(i) { subs <- local({ e1 <- raster::extent(agg\_poly[agg\_poly$polis == i,]) subs <- suppressMessages(raster::crop(rst\_cropped, e1)) # rescale to 0-1, for png export if (mask == FALSE) { subs <- suppressMessages((subs - cellStats(subs, “min”)) / (cellStats(subs, “max”) - cellStats(subs, “min”))) } }) writePNG(as.array(subs), target = paste0(path, targetname, i, “.png”)) } ) } rm(subs, agg, agg\_poly) gc() return(rst\_cropped) } remove\_files <- function(df) { lapply( seq(1, nrow(df)), FUN = function(i) { local({ fil = df$list\_masks[i] png = readPNG(fil) len = length(png) if (AllEqual(png)) { file.remove(df$list\_dops[i]) file.remove(df$list\_masks[i]) } else { } }) } ) }

# read training data

coral\_mask\_train <- raster::stack(“E:/Koralle/images/Coral\_Mask\_bleaching\_2017\_train.tif”) coral\_dop\_train <- raster::stack(“E:/Koralle/images/Coral\_Dop\_bleaching\_2017\_train.tif”) # set the size of each image model\_input\_shape = c(128, 128)

subset\_ds( input\_raster = coral\_mask\_train, path = “E:/Koralle/images/Cor\_bleaching\_2017/”, mask = TRUE, model\_input\_shape = model\_input\_shape )

subset\_ds( input\_raster = coral\_dop\_train, path = “E:/Koralle/images/Dop\_bleaching\_2017/”, mask = FALSE, model\_input\_shape = model\_input\_shape )

# list all created files in both folders

list\_dops <- list.files(“E:/Koralle/images/Dop\_bleaching\_2017/”, full.names = TRUE, pattern = “*.png”) list\_masks <- list.files(”E:/Koralle/images/Cor\_bleaching\_2017/”, full.names = TRUE, pattern = ”*.png”)

# create a data fram

df = data.frame(list\_dops, list\_masks)

remove\_files(df)

# list the files again

files <- data.frame( img = list.files( file.path(“E:/Koralle/images/Dop\_bleaching\_2017/”), full.names = TRUE, pattern = “*.png” ), mask = list.files( file.path(”E:/Koralle/images/Cor\_bleaching\_2017/”), full.names = TRUE, pattern = ”*.png” ) ) # split randomly into training and validation (not testing!!) data sets set.seed(7) data <- initial\_split(files, prop = 0.8)

# function to prepare your data set for all further processes

prepare\_ds <- function(files = NULL, train, predict = FALSE, subsets\_path = NULL, model\_input\_shape = c(256, 256), batch\_size = batch\_size, visual = FALSE) { if (!predict) { # function for random change of saturation,brightness and hue, # will be used as part of the augmentation spectral\_augmentation <- function(img) { img <- tfrandom\_brightness(img, max\_delta = 0.1) img <- tfrandom\_contrast(img, lower = 0.9, upper = 1.1) img <- tfrandom\_saturation(img, lower = 0.9, upper = 1.1) # make sure we still are between 0 and 1 img <- tf$clip\_by\_value(img, 0, 1) } # create a tf\_dataset from the input data.frame # right now still containing only paths to images dataset <- tensor\_slices\_dataset(files) # use dataset\_map to apply function on each record of the dataset # (each record being a list with two items: img and mask), the # function is list\_modify, which modifies the list items # 'img' and 'mask' by using the results of applying decode\_png on the img and the mask # -> i.e. pngs are loaded and placed where the paths to the files were (for each record in dataset) dataset <- dataset\_map(dataset, function(.x) list\_modify( .x, img = tf$imageioimg)), mask = tfdecode\_png(tfread\_file(.x$mask)) )) # convert to float32: # for each record in dataset, both its list items are modified # by the result of applying convert\_image\_dtype to them dataset <- dataset\_map(dataset, function(.x) list\_modify( .x, img = tf$imageimg, dtype = tfimagemask, dtype = tf$float32) )) # data augmentation performed on training set only if (train) { # augmentation 1: flip left right, including random change of # saturation, brightness and contrast # for each record in dataset, only the img item is modified by the result # of applying spectral\_augmentation to it augmentation <- dataset\_map(dataset, function(.x) list\_modify(.x, img = spectral\_augmentation(.x$img))) #…as opposed to this, flipping is applied to img and mask of each record augmentation <- dataset\_map(augmentation, function(.x) list\_modify( .x, img = tfflip\_left\_right(.ximagemask) )) dataset\_augmented <- dataset\_concatenate(augmentation, dataset) # augmentation 2: flip up down, # including random change of saturation, brightness and contrast augmentation <- dataset\_map(dataset, function(.x) list\_modify(.x, img = spectral\_augmentation(.ximageimg), mask = tfflip\_up\_down(.x$mask) )) dataset\_augmented <- dataset\_concatenate(augmentation, dataset\_augmented) # augmentation 3: flip left right AND up down, # including random change of saturation, brightness and contrast augmentation <- dataset\_map(dataset, function(.x) list\_modify(.x, img = spectral\_augmentation(.x$img))) augmentation <- dataset\_map(augmentation, function(.x) list\_modify( .x, img = tfflip\_left\_right(.ximagemask) )) augmentation <- dataset\_map(augmentation, function(.x) list\_modify( .x, img = tfflip\_up\_down(.ximagemask) )) dataset\_augmented <- dataset\_concatenate(augmentation, dataset\_augmented) } # shuffling on training set only # unsauber if (!visual) { if (train) { dataset <- dataset\_shuffle(dataset\_augmented, buffer\_size = batch\_size \* 256) } # train in batches; batch size might need to be adapted depending on # available memory dataset <- dataset\_batch(dataset, batch\_size) } if (visual) { dataset <- dataset\_augmented } # output needs to be unnamed dataset <- dataset\_map(dataset, unname) } else{ # make sure subsets are read in in correct order # so that they can later be reassembled correctly # needs files to be named accordingly (only number) o <- order(as.numeric(tools::file\_path\_sans\_ext(basename( list.files(subsets\_path) )))) subset\_list <- list.files(subsets\_path, full.names = T)[o] dataset <- tensor\_slices\_dataset(subset\_list) dataset <- dataset\_map(dataset, function(.x) tfdecode\_png(tfread\_file(.x))) dataset <- dataset\_map(dataset, function(.x) tfconvert\_image\_dtype(.x, dtype = tf$float32)) dataset <- dataset\_batch(dataset, batch\_size) dataset <- dataset\_map(dataset, unname) } }

# one more parameter

batch\_size = 8

# prepare data for training

training\_dataset <- prepare\_ds( training(data), train = TRUE, predict = FALSE, model\_input\_shape = model\_input\_shape, batch\_size = batch\_size )

# also prepare validation data

validation\_dataset <- prepare\_ds( testing(data), train = FALSE, predict = FALSE, model\_input\_shape = model\_input\_shape, batch\_size = batch\_size )

# we first get a all our training data

it <- as\_iterator(training\_dataset) it <- iterate(it) # head(it)

# we convert our data to an array and also subset our iterator e.g.

# with the 4th batch ([[4]]) of the images ([[1]])

im <-as.array(it[[4]][[1]]) # then we subset just take the first image out of our batch im <- im[1,,,] # and plot it plot(as.raster(im))



# and for the according mask it is almost the same

ma <-as.array(it[[4]][[2]]) ma <- ma[1,,,] plot(as.raster(ma))



#U-Net # function to build a U-Net # of course it is possible to change the input\_shape get\_unet\_128 <- function(input\_shape = c(128, 128, 3), num\_classes = 1) { inputs <- layer\_input(shape = input\_shape) # 128 down1 <- inputs %>% layer\_conv\_2d(filters = 64, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) %>% layer\_conv\_2d(filters = 64, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) down1\_pool <- down1 %>% layer\_max\_pooling\_2d(pool\_size = c(2, 2), strides = c(2, 2)) # 64 down2 <- down1\_pool %>% layer\_conv\_2d(filters = 128, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) %>% layer\_conv\_2d(filters = 128, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) down2\_pool <- down2 %>% layer\_max\_pooling\_2d(pool\_size = c(2, 2), strides = c(2, 2)) # 32 down3 <- down2\_pool %>% layer\_conv\_2d(filters = 256, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) %>% layer\_conv\_2d(filters = 256, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) down3\_pool <- down3 %>% layer\_max\_pooling\_2d(pool\_size = c(2, 2), strides = c(2, 2)) # 16 down4 <- down3\_pool %>% layer\_conv\_2d(filters = 512, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) %>% layer\_conv\_2d(filters = 512, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) down4\_pool <- down4 %>% layer\_max\_pooling\_2d(pool\_size = c(2, 2), strides = c(2, 2)) # # 8 center <- down4\_pool %>% layer\_conv\_2d(filters = 1024, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) %>% layer\_conv\_2d(filters = 1024, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) # center up4 <- center %>% layer\_upsampling\_2d(size = c(2, 2)) %>% { layer\_concatenate(inputs = list(down4, .), axis = 3) } %>% layer\_conv\_2d(filters = 512, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) %>% layer\_conv\_2d(filters = 512, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) %>% layer\_conv\_2d(filters = 512, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) # 16 up3 <- up4 %>% layer\_upsampling\_2d(size = c(2, 2)) %>% { layer\_concatenate(inputs = list(down3, .), axis = 3) } %>% layer\_conv\_2d(filters = 256, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) %>% layer\_conv\_2d(filters = 256, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) %>% layer\_conv\_2d(filters = 256, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) # 32 up2 <- up3 %>% layer\_upsampling\_2d(size = c(2, 2)) %>% { layer\_concatenate(inputs = list(down2, .), axis = 3) } %>% layer\_conv\_2d(filters = 128, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) %>% layer\_conv\_2d(filters = 128, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) %>% layer\_conv\_2d(filters = 128, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) # # 64 up1 <- up2 %>% layer\_upsampling\_2d(size = c(2, 2)) %>% { layer\_concatenate(inputs = list(down1, .), axis = 3) } %>% layer\_conv\_2d(filters = 64, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) %>% layer\_conv\_2d(filters = 64, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) %>% layer\_conv\_2d(filters = 64, kernel\_size = c(3, 3), padding = “same”) %>% layer\_activation(“relu”) # 128 classify <- layer\_conv\_2d( up1, filters = num\_classes, kernel\_size = c(1, 1), activation = “sigmoid” ) model <- keras\_model(inputs = inputs, outputs = classify) return(model) }

unet\_model <- get\_unet\_128() # compile the model unet\_model %>% compile( optimizer = optimizer\_adam(learning\_rate = 0.0001), loss = “binary\_crossentropy”, metrics = “accuracy” )

# train the model

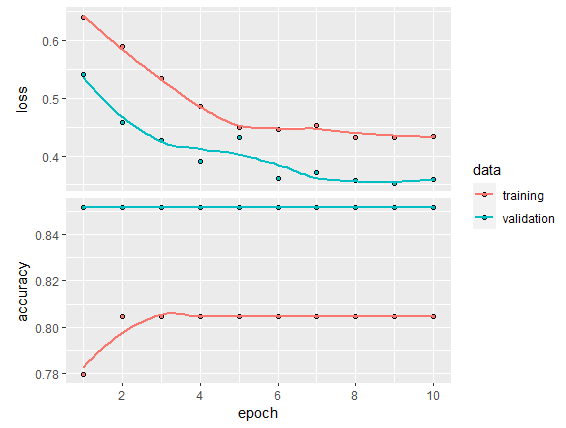
hist <- unet\_model %>% fit( training\_dataset, validation\_data = validation\_dataset, epochs = 10, verbose = 1 )

# 

# save the model

unet\_model %>% save\_model\_hdf5(file.path(“E:/Koralle/images/models/”, “unet\_corals\_2017\_bleaching.hdf5”), overwrite=T)

plot(hist)



# load the test data

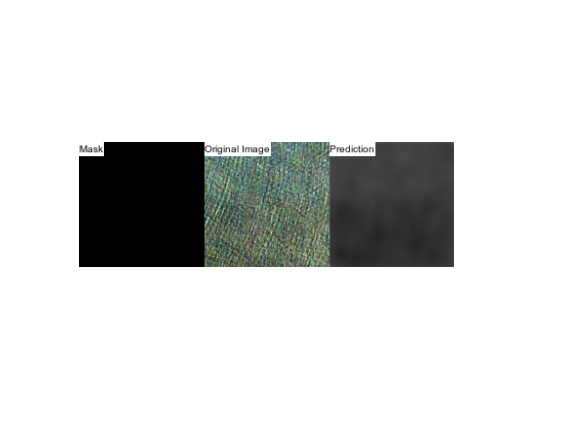
coral\_mask\_test <- stack(“E:/Koralle/images/Coral\_Mask\_bleaching\_2017\_test.tif”) coral\_dop\_test <- stack(“E:/Koralle/images/Coral\_Dop\_bleaching\_2017\_test.tif”) target\_rst <- subset\_ds( input\_raster = coral\_mask\_test, path = “E:/Koralle/images/Cor\_test\_bleaching\_2017/”, mask = TRUE, model\_input\_shape = model\_input\_shape ) subset\_ds( input\_raster = coral\_dop\_test, path = “E:/Koralle/images/Dop\_test\_bleaching\_2017/”, mask = FALSE, model\_input\_shape = model\_input\_shape ) # write the target\_rst to later rebuild your image writeRaster( target\_rst, file.path(“E:/Koralle/images/models/model\_test\_2017\_bleaching/”,“coral\_mask\_bleaching\_2017\_test\_target.tif”), overwrite = T )

#list and prepare files again test\_file <- data.frame( img = list.files( file.path(“E:/Koralle/images/Dop\_test\_bleaching\_2017”), full.names = T, pattern = “*.png” ), mask = list.files( file.path(”E:/Koralle/images/Cor\_test\_bleaching\_2017”), full.names = T, pattern = ”*.png” ) )

testing\_dataset <- prepare\_ds( test\_file, train =FALSE, predict = FALSE, model\_input\_shape = model\_input\_shape, batch\_size = batch\_size ) # load a U-Net unet\_model <- load\_model\_hdf5(file.path(“E:/Koralle/images/models/”, “unet\_corals\_2017\_bleaching.hdf5”), compile = TRUE) # evaluate the model with test set ev <- unet\_model$evaluate(testing\_dataset) # prepare data for prediction prediction\_dataset <- prepare\_ds( predict = TRUE, subsets\_path = paste0(file.path("E:/Koralle/images/Dop\_test\_bleaching\_2017/")), model\_input\_shape = model\_input\_shape, batch\_size = batch\_size ) # get sample of data from testing data t\_sample <- floor(runif(n = 5, min = 1, max = nrow(test\_file))) # simple visual comparison of mask, image and prediction for (i in t\_sample) { png\_path <- test\_file png\_path <- png\_path[i,] img <- image\_read(png\_path[, 1]) mask <- image\_read(png\_path[, 2]) pred <- image\_read(as.raster(predict(object = unet\_model, testing\_dataset)[i, , ,])) out <- image\_append(c( image\_annotate( mask, "Mask", size = 10, color = "black", boxcolor = "white" ), image\_annotate( img, "Original Image", size = 10, color = "black", boxcolor = "white" ), image\_annotate( pred, "Prediction", size = 10, color = "black", boxcolor = "white" ) )) plot(out) }







# function to rebuild your image rebuild\_img <- function(pred\_subsets, out\_path, target\_rst, model\_name) { subset\_pixels\_x <- ncol(pred\_subsets[1, , , ]) subset\_pixels\_y <- nrow(pred\_subsets[1, , , ]) tiles\_rows <- nrow(target\_rst) / subset\_pixels\_y tiles\_cols <- ncol(target\_rst) / subset\_pixels\_x # load target image to determine dimensions target\_stars <- st\_as\_stars(target\_rst, proxy = F) #prepare subfolder for output result\_folder <- paste0(out\_path, model\_name) if (dir.exists(result\_folder)) { unlink(result\_folder, recursive = T) } dir.create(path = result\_folder) # for each tile, create a stars from corresponding predictions, # assign dimensions using original/target image, and save as tif: for (crow in 1:tiles\_rows) { for (ccol in 1:tiles\_cols) { i <- (crow - 1) \* tiles\_cols + (ccol - 1) + 1 dimx <- c(((ccol - 1) \* subset\_pixels\_x + 1), (ccol \* subset\_pixels\_x)) dimy <- c(((crow - 1) \* subset\_pixels\_y + 1), (crow \* subset\_pixels\_y)) cstars <- st\_as\_stars(t(pred\_subsets[i, , , 1])) attr(cstars, "dimensions")[[2]]$delta = -1 #set dimensions using original raster st\_dimensions(cstars) <- st\_dimensions(target\_stars[, dimx[1]:dimx[2], dimy[1]:dimy[2]])[1:2] write\_stars(cstars, dsn = paste0(result\_folder, “/*out*”, i, “.tif”)) } } starstiles <- as.vector(list.files(result\_folder, full.names = T), mode = “character”) sf::gdal\_utils( util = “buildvrt”, source = starstiles, destination = paste0(result\_folder, “/mosaic.vrt”) ) sf::gdal\_utils( util = “warp”, source = paste0(result\_folder, “/mosaic.vrt”), destination = paste0(result\_folder, “/mosaic.tif”) ) } #load target raster target\_rst <- raster(file.path(“E:/Koralle/images/models/model\_test\_2017\_bleaching/”,“coral\_mask\_bleaching\_2017\_test\_target.tif”), overwrite=T) # make the actual prediction pred\_subsets <- predict(object = unet\_model, x = prediction\_dataset) # name your output path model\_name <- “unet\_abc\_bleaching\_2017” # rebuild .tif from each patch rebuild\_img( pred\_subsets = pred\_subsets, out\_path = paste0(file.path(“E:/Koralle/images/prediction/”, “/”)), target\_rst = target\_rst, model\_name = model\_name )

image<-stack(“E:/Koralle/images/prediction/unet\_abc\_bleaching\_2017/mosaic.tif”) plot(image)

