As we found for natural language processing, R is a little bit limited when it comes to deep neural networks. Unfortunately, these networks are the current gold-standard methods for medical image analysis. The ML/DL R packages that do exist provide interfaces (APIs) to libraries built in other languages like C/C++ and Java. This means there are a few “non-reproducible” installation and data gathering steps to run first. It also means there are a few “compromises” to get a practical that will A) be runnable B) actually complete within the allotted time and C) even vaguely works. Doing this on a full real dataset would likely follow a similar process (admittedly with more intensive training and more expressive architectures). Google colab running an R kernel hasn’t proven a very effective alternative thus far either.

Install packages

In this practical, we will be performing image classification on real medical images using the Torch deep learning library and several packages to manage and preprocess the images. We will utilize the following packages for our task:

`gridExtra` : This package provides functions for arranging multiple plots in a grid layout, allowing us to visualize and compare our results effectively.

`jpeg` : This package enables us to read and write JPEG images, which is a commonly used image format.

`imager` : This package offers a range of image processing functionalities, such as loading, saving, resizing, and transforming images.

`magick` : This package provides an interface to the ImageMagick library, allowing us to manipulate and process images using a wide variety of operations.

To ensure that the required packages are available, we can install them using the `install.packages()` function. Additionally, some packages may require additional dependencies to be installed. In such cases, we can use the `BiocManager::install()` function from the Bioconductor project to install the necessary dependencies.

Here is an example code snippet to install the required packages: you can uncomment the following code to install required packages

```
#utils::chooseCRANmirror(ind = 1, graphics = FALSE, "https://cran.rstudio.com/")
#install.packages("gridExtra")
#install.packages("jpeg")
#install.packages("imager")
#install.packages("magick")

# Install Bioconductor package (if not already installed)
#if (!require("BiocManager", quietly = TRUE))
#    install.packages("BiocManager")

# Install EBImage package from Bioconductor
#BiocManager::install("EBImage")
#install.packages("abind")

# Install torch, torchvision, and luz
#install.packages("torch")
#install.packages("torchvision")
#install.packages("luz")
```

```
# load packages
library(ggplot2)
library(gridExtra)
library(imager)
```

```
## Loading required package: magrittr
```

```
##
## Attaching package: 'imager'
```

```
## The following object is masked from 'package:magrittr':
##
##     add
```

```
## The following objects are masked from 'package:stats':
##
##     convolve, spectrum
```

```
## The following object is masked from 'package:graphics':
##
##     frame
```

```
## The following object is masked from 'package:base':
##
##     save.image
```

```
library(jpeg)
library(magick)
```

```
## Linking to ImageMagick 6.9.12.3
## Enabled features: cairo, freetype, fftw, ghostscript, heic, lcms, pango, raw, rsvg, webp
## Disabled features: fontconfig, x11
```

```
library(EBImage)
```

```
##
## Attaching package: 'EBImage'
```

```
## The following objects are masked from 'package:imager':
##
##     channel, dilate, display, erode, resize, watershed
```

```
library(grid)
```

```
##
## Attaching package: 'grid'
```

```
## The following object is masked from 'package:imager':
##
##     depth
```

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following object is masked from 'package:EBImage':
##
##     combine
```

```
## The following object is masked from 'package:imager':
##
##     where
```

```
## The following object is masked from 'package:gridExtra':
##
##     combine
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(abind)
```

```
##
## Attaching package: 'abind'
```

```
## The following object is masked from 'package:EBImage':
##
##     abind
```

Diagnosing Pneumonia from Chest X-Rays

Parsing the data

Today, we are going to look at a series of chest X-rays from children (from this paper (https://www.cell.com/cell/fulltext/S0092-8674(18)30154-5))

and see if we can accurately diagnose pneumonia from them.

Chest X-ray images (anterior-posterior) were selected from retrospective cohorts of pediatric patients of one to five years old from Guangzhou Women and Children's Medical Center, Guangzhou. All chest X-ray imaging was performed as part of patients' routine clinical care. For the analysis of chest x-ray images, all chest radiographs were initially screened for quality control by removing all low quality or unreadable scans. The diagnoses for the images were then graded by two expert physicians before being cleared for inclusion. In order to account for any grading errors, the evaluation set was also checked by a third expert.

We can download, unzip, then inspect the format of this dataset as follows:

"https://drive.google.com/file/d/14H_FilWf12ONOJ_G4vvzNDDGvY7Ccqtm/view?usp=sharing (https://drive.google.com/file/d/14H_FilWf12ONOJ_G4vvzNDDGvY7Ccqtm/view?usp=sharing)"

you can **unzip** the file in a data directory, using the following code: *uncomment it*

```
# Specify the path to the zip file
#zip_file <- "C:/Users/keert/Downloads/lab3_chest_xray.zip"

# Specify the destination directory to extract the files.
#destination_dir <- "Downloads"

# Extract the zip file
#unzip(zip_file, exdir = destination_dir)
```

As with every data analysis, the first thing we need to do is learn about our data. If we are diagnosing pneumonia, we should use the internet to better understand what pneumonia actually is and what types of pneumonia exist.

0_ What is pneumonia and what is the point/benefit of being able to identify it from X-rays automatically?

Pneumonia is an infection that is capable of inflaming the air sacs in both or one of the lungs and is caused by bacteria, virus and is accompanied by symptoms such as cough, cold,fever, chills.

Identifying pneumonia from X-ray is beneficial:

1. We can detect pneumonia in the early stages and timely intervention can improve the life of the patient.

2)Rapidness and Efficacy : The procedure of diagnosing pneumonia from X-rays can be greatly sped up by automation.

3) Human Error: X-ray image interpretation by humans is unpredictable and prone to inaccuracy. Automation reduces the possibility of human error during the identification procedure.

4) Accessibility: Automated detection of pneumonia using X-rays can make diagnostic services more easily accessible, especially in places with little medical resources or areas where radiologists are in low supply.

Exploring dataset

In the provided code snippet, we are exploring the dataset directory structure for a chest x-ray image classification task.

```
data_folder = "C:/Users/keert/Downloads/Downloads/lab3_chest_xray"

files <- list.files(data_folder, full.names=TRUE, recursive=TRUE)
sort(sample(files, 20))
```

```
##  [1] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/test/NORMAL/IM-0050-0001.jpeg"
##  [2] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/test/PNEUMONIA/person113_bacteria_541.jpeg"
##  [3] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/test/PNEUMONIA/person1667_virus_2881.jpeg"
##  [4] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/NORMAL/IM-0128-0001.jpeg"
##  [5] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/NORMAL/IM-0317-0001.jpeg"
##  [6] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/NORMAL/IM-0413-0001.jpeg"
##  [7] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/NORMAL/IM-0433-0001.jpeg"
##  [8] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/NORMAL/IM-0453-0001-0002.jpeg"
##  [9] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/NORMAL/IM-0465-0001.jpeg"
## [10] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/NORMAL/IM-0565-0001.jpeg"
## [11] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/NORMAL/IM-0632-0001.jpeg"
## [12] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/PNEUMONIA/person1014_bacteria_2945.jpeg"
## [13] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/PNEUMONIA/person1051_bacteria_2985.jpeg"
## [14] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/PNEUMONIA/person1074_bacteria_3014.jpeg"
## [15] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/PNEUMONIA/person1107_virus_1831.jpeg"
## [16] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/PNEUMONIA/person1122_virus_1847.jpeg"
## [17] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/PNEUMONIA/person1206_virus_2051.jpeg"
## [18] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/PNEUMONIA/person1220_bacteria_3174.jpeg"
## [19] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/PNEUMONIA/person124_virus_244.jpeg"
## [20] "C:/Users/keert/Downloads/Downloads/lab3_chest_xray/validate/PNEUMONIA/person1950_bacteria_4881.jpeg"
```

In the output above, you can see the filenames for all the chest X-rays. Look carefully at the filenames for the X-rays showing pneumonia (i.e., those in `{train,test}/PNEUMONIA`).

1_ Do these filenames tell you anything about pneumonia? Why might this make predicting pneumonia more challenging? We can see that Normal and Pneumonia are mentioned in the file which are the two classes in the dataset. The files with the term Normal depicts normal x-rays of the chest while the files with the term Pneumonia indicates pneumonia-related conditions, such as bacterial or viral pneumonia. In short, photos labelled “NORMAL” are likely X-rays of individuals without pneumonia, but photos labelled “PNEUMONIA” are likely to be those of individuals with pneumonia.

It can be challenging because: 1.The precise features of pneumonia visible in the photos are not specifically described in the filenames. 2.Chest X-ray scans can show overlapping characteristics in both pneumonia cases and healthy individuals. A model may find it challenging to accurately differentiate between the two classes as a result of this overlap. 3.Even though the filenames can give a broad idea of whether or not an image is related to pneumonia, they do not contain enough details to make precise predictions on their own.

The dataset folder is assumed to contain three subfolders: train, test, and validate. Each of these subfolders further contains two folders representing the two classes or labels in our classification task: “normal” and “pneumonia”. The code provides a way to explore the dataset directory structure and obtain information about the number of images and their distribution across different classes. This information can be helpful in understanding the dataset and planning the subsequent steps of the image classification task.

```
# Exploring dataset
base_dir <- "C:/Users/keert/Downloads/Downloads/lab3_chest_xray"

train_pneumonia_dir <- file.path(base_dir, "train", "PNEUMONIA")
train_normal_dir <- file.path(base_dir, "train", "NORMAL")

test_pneumonia_dir <- file.path(base_dir, "test", "PNEUMONIA")
test_normal_dir <- file.path(base_dir, "test", "NORMAL")

val_normal_dir <- file.path(base_dir, "validate", "NORMAL")
val_pneumonia_dir <- file.path(base_dir, "validate", "PNEUMONIA")

train_pn <- list.files(train_pneumonia_dir, full.names = TRUE)
train_normal <- list.files(train_normal_dir, full.names = TRUE)

test_normal <- list.files(test_normal_dir, full.names = TRUE)
test_pn <- list.files(test_pneumonia_dir, full.names = TRUE)

val_pn <- list.files(val_pneumonia_dir, full.names = TRUE)
val_normal <- list.files(val_normal_dir, full.names = TRUE)

cat("Total Images:", length(c(train_pn, train_normal, test_normal, test_pn, val_pn, val_normal)), "\n")
```

```
## Total Images: 1216
```

```
cat("Total Pneumonia Images:", length(c(train_pn, test_pn, val_pn)), "\n")
```

```
## Total Pneumonia Images: 608
```

```
cat("Total Normal Images:", length(c(train_normal, test_normal, val_normal)), "\n")
```

```
## Total Normal Images: 608
```

Creating training datasets

The provided code segment focuses on creating datasets for training, testing, and validation, as well as assigning labels to the corresponding datasets. Additionally, the code shuffles the data to introduce randomness in the order of the samples. Here’s a breakdown of the code:

`train_dataset` : Combines the lists `train_pn` and `train_normal` to create a single dataset for training.

`train_labels` : Creates a vector of labels for the training dataset by repeating “pneumonia” for the length of `train_pn` and “normal” for the length of `train_normal` .

`shuffled_train_dataset` , `shuffled_train_labels` : Extracts the shuffled training dataset and labels from the shuffled `train_data` data frame.

By creating datasets and assigning labels, this code prepares the data for subsequent steps, such as model training and evaluation. The shuffling of the data ensures that the samples are presented in a random order during training, which can help prevent any biases or patterns that may exist in the original dataset.

```
train_dataset <- c(train_pn, train_normal)
train_labels <- c(rep("pneumonia", length(train_pn)), rep("normal", length(train_normal)))

test_dataset <- c(test_pn, test_normal)
test_labels <- c(rep("pneumonia", length(test_pn)), rep("normal", length(test_normal)))

val_dataset <- c(val_pn, val_normal)
val_labels <- c(rep("pneumonia", length(val_pn)), rep("normal", length(val_normal)))

# Create a data frame with the dataset and labels
train_data <- data.frame(dataset = train_dataset, label = train_labels)
test_data <- data.frame(dataset = test_dataset, label = test_labels)
val_data <- data.frame(dataset = val_dataset, label = val_labels)

# Shuffle the data frame
train_data <- train_data[sample(nrow(train_data)), ]
test_data <- test_data[sample(nrow(test_data)), ]
val_data <- val_data[sample(nrow(val_data)), ]

# Extract the shuffled dataset and labels
shuffled_train_dataset <- train_data$dataset
shuffled_train_labels <- train_data$label

shuffled_test_dataset <- test_data$dataset
shuffled_test_labels <- test_data$label

shuffled_val_dataset <- val_data$dataset
shuffled_val_labels <- val_data$label
```

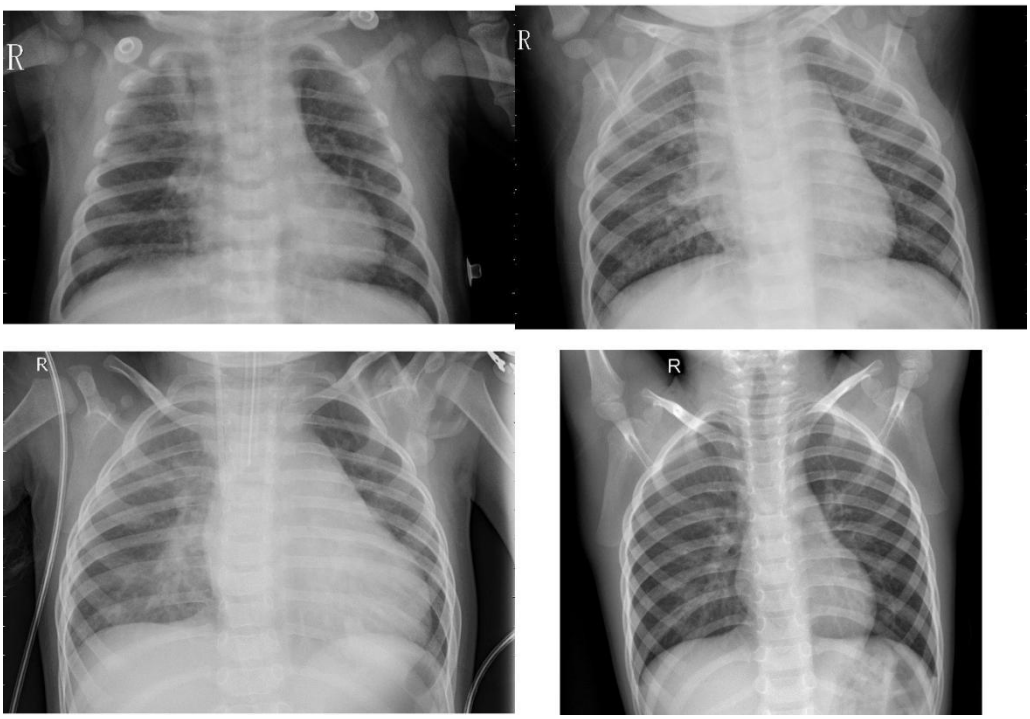
```
#showing a file name from test set
cat("finle name: ", shuffled_train_dataset[5], "\nlabel: ", shuffled_train_labels[5])
```

```
## finle name: C:/Users/keert/Downloads/Downloads/lab3_chest_xray/train/NORMAL/IM-0490-0001.jpeg
## label:  normal
```

Data Visualization

Let's inspect a couple of these files as it is always worth looking directly at data.

```
# Create a list to store the ggplot objects
plots <- list()

# Iterate through the images and labels
for (i in 1:4) {

  image <- readImage(shuffled_train_dataset[i])

  # Create a ggplot object for the image with the corresponding label
  plot <- ggplot() +
    theme_void() +
    annotation_custom(
      rasterGrob(image, interpolate = TRUE),
      xmin = -Inf, xmax = Inf, ymin = -Inf, ymax = Inf
    )

  # Add the ggplot object to the list
  plots[[i]] <- plot
}

# Arrange the plots in a 2x2 grid
grid.arrange(grobs = plots, nrow = 2, ncol = 2)
```



2_ From looking at only 3 images do you see any attribute of the images that we may have to normalise before training a model?

1. Size of the Image(Resizing) : The provided images are in different sizes, we can crop or resize the images to ensure consistency.
2. Adjusting the contrast : By adjusting the contrast, you can make regions of interest or irregularities that might be signs of pneumonia more visible.

Data Pre-processing

The provided code segment presents a function called `process_images` that performs several preprocessing steps on the images. Here's an explanation of each pre-processing step and its purpose:

1. Loading the "imager" library: This line imports the "imager" library, which provides functions for image processing.
2. Setting the desired image size: The variable `img_size` is initialized to 224, indicating the desired size (both width and height) of the processed images. This step ensures that all images are resized to a consistent size.
3. Initializing an empty list for processed images: The variable `X` is initialized as an empty list that will store the processed images.
4. Looping through each image path: The function iterates over each image path in the `shuffled_dataset` input, which represents the paths to the shuffled images.
5. Loading the image: The `imager::load.image()` function is used to read and load the image from its file path.
6. Normalizing the image: The loaded image is divided by 255 to normalize its pixel values. This step scales the pixel values between 0 and 1, which is a common practice in image processing and deep learning.
7. Resizing the image: The `resize()` function from the "imager" library is employed to resize the normalized image to the desired `img_size` . Resizing the images to a consistent size is important for ensuring compatibility with the subsequent steps of the deep learning pipeline.
8. Appending the processed image to the list: The processed image, stored in the variable `img_resized` , is added to the `X` list using the `c()` function and the `list()` function. The resulting `X` list will contain all the processed images.
9. Returning the processed images: Finally, the `X` list, which now holds the processed images, is returned as the output of the `process_images` function.

These preprocessing steps are commonly performed in image classification tasks to prepare the images for training a deep learning model. Normalizing the pixel values and resizing the images ensure that they are in a consistent format and range, which facilitates the learning process of the model. Additionally, resizing the images to a fixed size allows for efficient batch processing and ensures that all images have the same dimensions, enabling them to be fed into the model's input layer.

```
process_images <- function(shuffled_dataset) {

  img_size <- 224  # Desired image size

  # Initialize an empty list to store processed images
  X <- list()

  # Loop through each image path in shuffled_train_dataset
  for (image_path in shuffled_dataset) {
    # Read the image
    img <- imager::load.image(image_path)

    # Normalize the image
    img_normalized <- img / 255

    # Resize the image
    img_resized <- resize(img_normalized, img_size, img_size)

    # Append the processed image to the list
    X <- c(X, list(img_resized))
  }

  return(X)
}
```

In this section, by using the process_images function we will do preprocessing on the training, testing, and validation images.

Then we will encode the labels: The ifelse() function is utilized to encode the labels. If a label in shuffled_train_labels, shuffled_test_labels, or shuffled_val_labels is “normal,” it is assigned a value of 1. Otherwise, if the label is “pneumonia,” it is assigned a value of 2. This encoding scheme allows for easier handling of the labels in subsequent steps.

Finally, We Convert labels to integer type: The labels are converted to the integer data type using the as.integer() function. This ensures that the labels are represented as integers, which is the expected format for the target tensor when using the nn_cross_entropy_loss function.

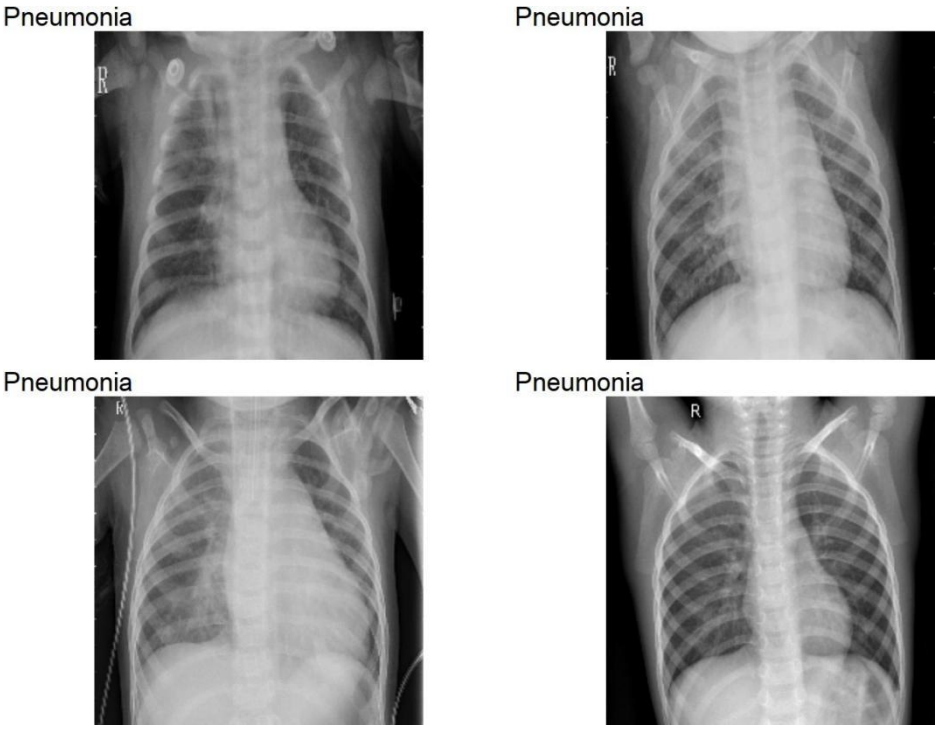
It is important to note that when using the nn_cross_entropy_loss function in R, the target tensor is expected to have a “long” data type, which is equivalent to the integer type in R. Hence, the labels need to be converted to integers.

Furthermore, when working with the Torch package in R, it is essential to ensure that labels start from 1 instead of 0. In binary classification problems, the labels should be 1 and 2, representing the two classes. This adjustment is necessary to avoid errors when using the labels as indices for the output tensor.

```
train_X <- process_images(shuffled_train_dataset)
test_X <- process_images(shuffled_test_dataset)
val_X <- process_images(shuffled_val_dataset)

train_y <- ifelse(shuffled_train_labels == "normal", 1, 2)
test_y <- ifelse(shuffled_test_labels == "normal", 1, 2)
val_y <- ifelse(shuffled_val_labels == "normal", 1, 2)

train_y <- as.integer(train_y)
test_y <- as.integer(test_y)
val_y <- as.integer(val_y)
```

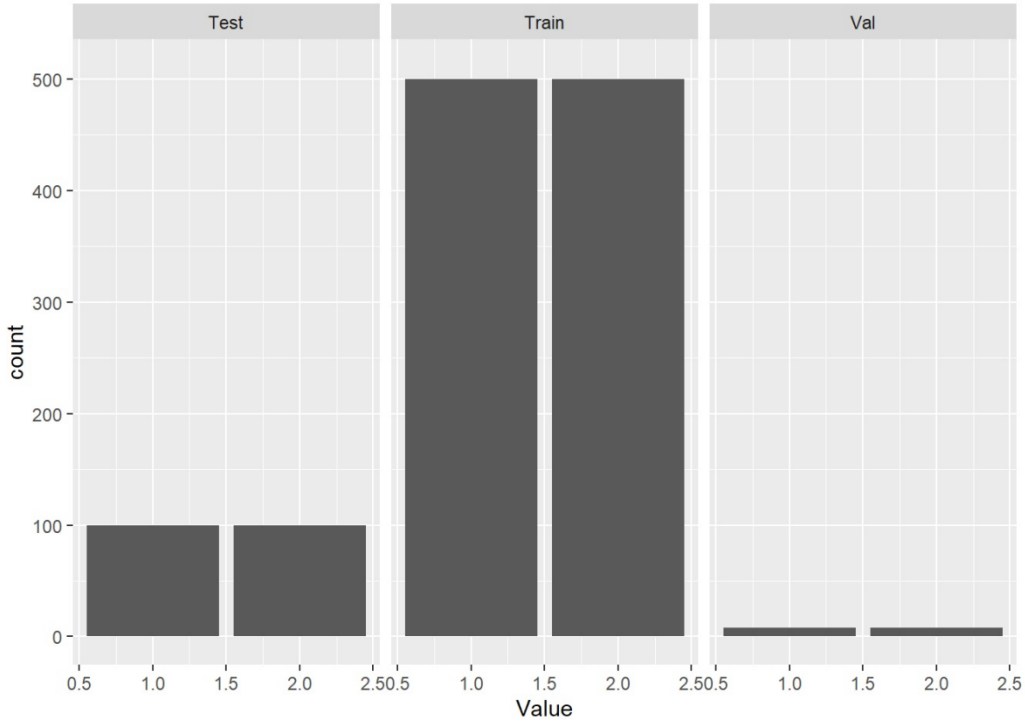
Now let’s have an other look at images after doing pre processing.

```
# Create a list to store the ggplot objects
plots <- list()

# Iterate through the images and labels
for (i in 1:4) {
  if (train_y[i] == 0) {
    label <- "Normal"
  } else {
    label <- "Pneumonia"
  }

  # Create a ggplot object for the image with the corresponding label
  plot <- ggplot() +
    theme_void() +
    ggtitle(label) +
    annotation_custom(
      rasterGrob(train_X[[i]], interpolate = TRUE),
      xmin = -Inf, xmax = Inf, ymin = -Inf, ymax = Inf
    )

  # Add the ggplot object to the list
  plots[[i]] <- plot
}

# Arrange the plots in a 2x2 grid
grid.arrange(grobs = plots, nrow = 2, ncol = 2)
```



Let's count and display the number of images in each dataset to examine the distribution of labels in the data. This will help us understand the ratio of "normal" and "pneumonia" labels in the dataset.

```
# Combine train, test, and val vectors into a single data frame
df <- data.frame(
  Data = rep(c("Train", "Test", "Val"), times = c(length(train_y), length(test_y), length(val_y))),
  Value = c(train_y, test_y, val_y)
)

# Create a single bar plot with facets
fig <- ggplot(df, aes(x = Value)) +
  geom_bar() +
  ylim(0, 510) +
  facet_wrap(~Data, ncol = 3)

# Arrange the plot
grid.arrange(fig, nrow = 1)
```



As you can see, the provided dataset is completely balanced in all sets. **3**_ if the dataset was not balanced, what kind of techniques could be useful?

If the dataset is imbalanced, we can perform the following:

1. Weighting Classes : In order to address the class imbalance, different weights might be assigned to the classes during model training. If we focus more on the minority classes, we can properly classify them
2. Data Augmentation : By applying different changes to existing samples, such as rotation, scaling, or flipping, augmentation techniques can artificially increase the number of instances in the minority class
3. Undersampling: Randomly remove instances from the majority class to reduce its dominance in the dataset 4.Ensemble approaches: For addressing imbalanced datasets, ensemble techniques like bagging or boosting can be helpful. 5.Oversampling :Apply oversampling techniques, such as random oversampling or SMOTE, to increase the percentage of the minority class.

Training

In the next step, we need to reshape the dataset to ensure it is in the appropriate format for feeding into deep learning models. Reshaping involves modifying the structure and dimensions of the data to match the expected input shape of the model.

```
train_X <- array(data = unlist(train_X), dim = c(1000, 224, 224, 1))
test_X <- array(data = unlist(test_X), dim = c(200, 224, 224, 1))
val_X <- array(data = unlist(val_X), dim = c(16, 224, 224, 1))
```

```
print(dim(train_X))
```

```
## [1] 1000  224  224    1
```

```
print(length(train_y))
```

```
## [1] 1000
```

```
print(dim(test_X))
```

```
## [1] 200 224 224   1
```

```
print(length(test_y))
```

```
## [1] 200
```

```
print(dim(val_X))
```

```
## [1]  16 224 224   1
```

```
print(length(val_y))
```

```
## [1] 16
```

The last dimension of an image represents the color channels, typically RGB (Red, Green, Blue) in color images or grayscale in black and white images. In our case, since we are working with black and white images, there is only one channel, hence the value 1.

However, the deep learning framework expects the input tensor to have a specific shape, with the color channels as the second dimension. The desired shape is (batch_size x channels x height x width), but our current data has the shape (batch_size x height x width x channels).

To rearrange the dimensions of our data to match the expected shape, we use the aperm function in R. The aperm function allows us to permute the dimensions of an array. In this case, we are permuting the dimensions of train_X to change the order of the dimensions, so that the channels dimension becomes the second dimension.

```
train_X <- aperm(train_X, c(1,4,2,3))
test_X <- aperm(test_X, c(1,4,2,3))
val_X <- aperm(val_X,c(1,4,2,3))

dim(train_X)
```

```
## [1] 1000    1  224  224
```

In order to train a Convolutional Neural Network (CNN), we will utilize the torch package in R. Torch is a powerful deep learning library that provides a wide range of functions and tools for building and training neural networks.

CNNs are particularly effective for image-related tasks due to their ability to capture local patterns and spatial relationships within the data. Torch provides a high-level interface to define and train CNN models in R.

By using torch, we can leverage its extensive collection of pre-built layers, loss functions, and optimization algorithms to construct our CNN architecture. We can define the network structure, specifying the number and size of convolutional layers, pooling layers, and fully connected layers.

```
# Load the torch package
library(torch)
library(torchvision)
library(luz)
```

In this code, we are defining a custom dataset class called “ImageDataset” to encapsulate our training, testing, and validation data. The purpose of the dataset class is to provide a structured representation of our data that can be easily consumed by deep learning models.

The “ImageDataset” class has three main functions: 1. “initialize”: This function is called when creating an instance of the dataset class. It takes the input data (X) and labels (y) as arguments and stores them as tensors. 2. “.getitem”: This function is responsible for retrieving a single sample and its corresponding label from the dataset. Given an index (i), it returns the i-th sample and label as tensors. 3. “.length”: This function returns the total number of samples in the dataset.

After defining the dataset class, we create instances of it for our training, testing, and validation data: “train_dataset”, “test_dataset”, and “val_dataset”. We pass the respective input data and labels to each dataset instance.

Next, we create dataloader objects for each dataset. A dataloader is an abstraction that allows us to efficiently load and iterate over the data in batches during the training process. The batch size (16 in this case) determines the number of samples that will be processed together in each iteration. It helps in optimizing memory usage and can speed up the training process by leveraging parallel computation.

Finally, the code visualizes the size of the first batch by calling “batch[[1]]$size()”. This can be useful for understanding the dimensions of the data and ensuring that the input shapes are consistent with the network architecture.

```
# Define a custom dataset class
ImageDataset <- dataset(
  name = "ImageDataset",
  initialize = function(X, y) {
    # Store the data as tensors
    self$data <- torch_tensor(X)
    self$labels <- torch_tensor(y)
  },
  .getitem = function(i) {
    # Return a single sample and label
    x <- self$data[i,,,]
    y <- self$labels[i]
    list(x = x, y = y)
  },
  .length = function() {
    # Return the number of samples
    dim(self$data)[1]
  }
)

# Create a dataset object from your data
train_dataset <- ImageDataset(train_X, train_y)
test_dataset <- ImageDataset(test_X, test_y)
val_dataset <- ImageDataset(val_X, val_y)

# Create a dataloader object from your dataset
train_dataloader <- dataloader(train_dataset, batch_size = 16)
test_dataloader <- dataloader(test_dataset, batch_size = 16)
val_dataloader <- dataloader(val_dataset, batch_size = 16)

# Iterate over batches of data
batch = train_dataloader$.iter()$.next()

# Visualize the first batch size
batch[[1]]$size()
```

```
## [1]  16   1 224 224
```

creat the CNN model

The input image has one channel and a size of 224 x 224 pixels. The first convolutional layer has 32 filters with a kernel size of 3 x 3 and a stride of 1. The output of this layer has a size of 32 x 222 x 222. The second convolutional layer has 64 filters with the same kernel size and stride. The output of this layer has a size of 64 x 220 x 220. The max pooling layer has a kernel size of 2 x 2 and reduces the spatial dimensions by half. The output of this layer has a size of 64 x 110 x 110. The dropout layer randomly sets some elements to zero with a probability of 0.25. The flatten layer reshapes the output into a vector with a length of 774400. The first fully connected layer has 128 neurons and applies a ReLU activation function. The second dropout layer randomly sets some elements to zero with a probability of 0.5. The second fully connected layer has 2 neurons and produces the final output for the classification task.

Input Image: 1 channel, 224 x 224

Layer Type	Output Size	Parameters
Conv2D	32 x 222 x 222	32 x 3 x 3
		(weights)
Conv2D	64 x 220 x 220	64 x 3 x 3
		(weights)
MaxPooling2D	64 x 110 x 110	2 x 2
		(kernel size)
Dropout	64 x 110 x 110	0.25
		(dropout rate)
Flatten	774400	-
FullyConnected	128	-
(ReLU)		
Dropout	128	0.5
		(dropout rate)
FullyConnected	2	-

```
net <- nn_module(
  "Net",

  initialize = function() {
    self$conv1 <- nn_conv2d(1, 32, 3, 1)
    self$conv2 <- nn_conv2d(32, 64, 3, 1)
    self$dropout1 <- nn_dropout2d(0.25)
    self$dropout2 <- nn_dropout2d(0.5)
    self$fc1 <- nn_linear(774400, 128)  # Adjust the input size based on your image dimensions
    self$fc2 <- nn_linear(128, 2)             # Change the output size to match your classification task
  },

  forward = function(x) {
    x %>%                                    # N * 1 * 224 * 224
      self$conv1() %>%                       # N * 32 * 222 * 222
      nnf_relu() %>%
      self$conv2() %>%                       # N * 64 * 220 * 220
      nnf_relu() %>%
      nnf_max_pool2d(2) %>%                  # N * 64 * 110 * 110
      self$dropout1() %>%
      torch_flatten(start_dim = 2) %>%       # N * 64 * 110 * 110 --> N * 774400
      self$fc1() %>%                         # N * 128
      nnf_relu() %>%
      self$dropout2() %>%
      self$fc2()                             # N * 2 (change the output size to match your classification tas
k)
  }
)
```

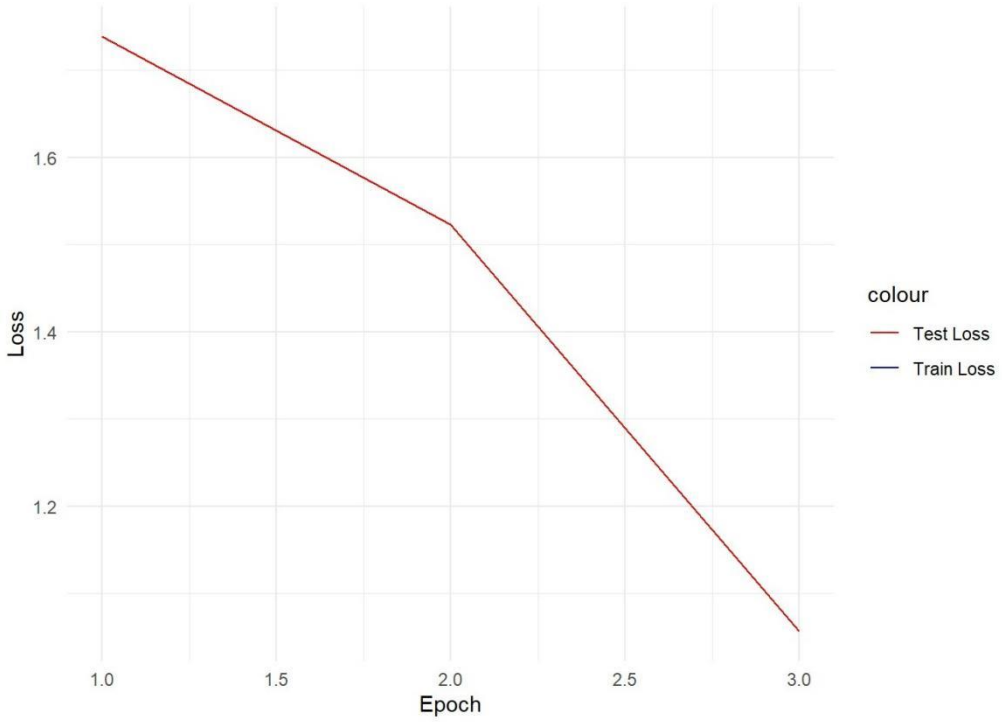
Train model

```
# Set the number of epochs
num_epochs <- 3

train_loss <- numeric(num_epochs)
train_acc <- numeric(num_epochs)
test_loss <- numeric(num_epochs)
test_acc <- numeric(num_epochs)

# Loop through the epochs
for (epoch in 1:num_epochs) {
  # Perform training and validation for each epoch
  fitted <- net %>%
    setup(
      loss = nn_cross_entropy_loss(),
      optimizer  =  optim_adam,
      metrics = list(
        luz_metric_accuracy()
      )
    ) %>%
    fit(train_dataloader, epochs = 1, valid_data = test_dataloader)

  # Print the metrics for the current epoch
  cat("Epoch ", epoch, "/", num_epochs, "\n")
  cat("Train metrics: Loss: ", fitted$records$metrics$train[[1]]$loss, " - Acc: ", fitted$records$metrics$train[[
1]]$acc, "\n")
  cat("Valid metrics: Loss: ", fitted$records$metrics$valid[[1]]$loss, " - Acc: ", fitted$records$metrics$valid[[
1]]$acc, "\n")
  cat("\n")

  # Store the loss and accuracy values
  train_loss[epoch] <- fitted$records$metrics$train[[1]]$loss
  train_acc[epoch] <- fitted$records$metrics$train[[1]]$acc
  test_loss[epoch] <- fitted$records$metrics$train[[1]]$loss
  test_acc[epoch] <- fitted$records$metrics$valid[[1]]$acc
}
```

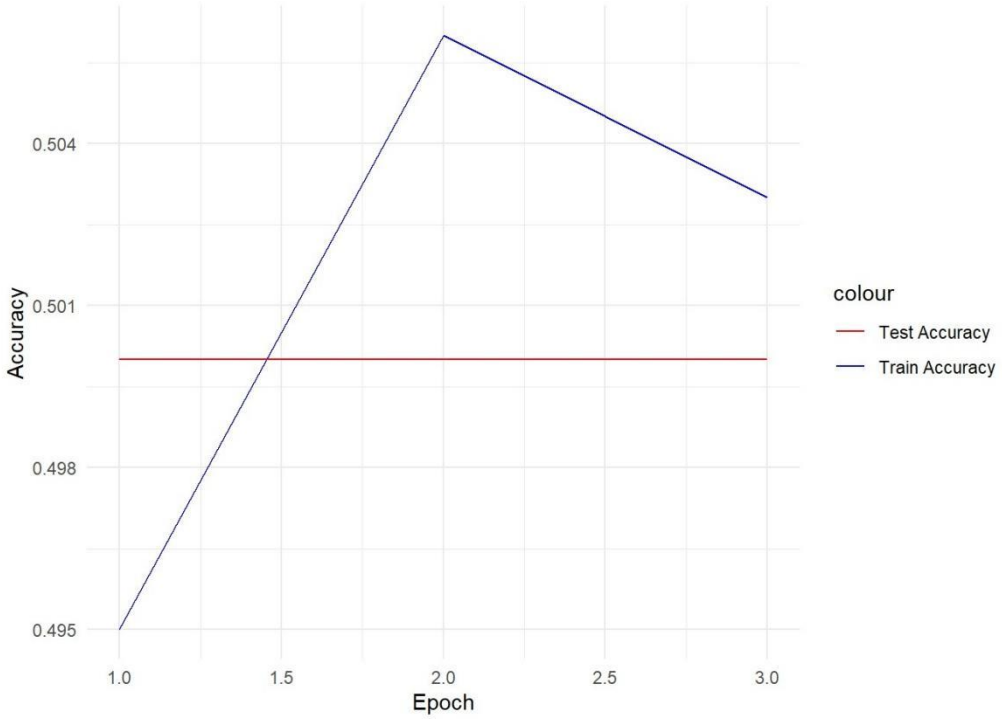
```
## Epoch  1 / 3
## Train metrics: Loss:  1.738474  - Acc:  0.495
## Valid metrics: Loss:  0.6933246  - Acc:  0.5
##
## Epoch  2 / 3
## Train metrics: Loss:  1.522781  - Acc:  0.506
## Valid metrics: Loss:  0.6933338  - Acc:  0.5
##
## Epoch  3 / 3
## Train metrics: Loss:  1.056429  - Acc:  0.503
## Valid metrics: Loss:  0.6937919  - Acc:  0.5
```

Plot learning curves

```
# Plot the train and test loss
loss_df <- data.frame(
  Epoch = 1:num_epochs,
  Train_Loss = train_loss,
  Test_Loss = test_loss
)
loss_plot <- ggplot(data = loss_df) +
  geom_line(aes(x = Epoch, y = Train_Loss, color = "Train Loss")) +
  geom_line(aes(x = Epoch, y = Test_Loss, color = "Test Loss")) +
  labs(x = "Epoch", y = "Loss") +
  scale_color_manual(values = c("Train Loss" = "blue", "Test Loss" = "red")) +
  theme_minimal()

# Plot the train and test accuracy
acc_df <- data.frame(
  Epoch = 1:num_epochs,
  Train_Accuracy = train_acc,
  Test_Accuracy = test_acc
)
acc_plot <- ggplot(data = acc_df) +
  geom_line(aes(x = Epoch, y = Train_Accuracy, color = "Train Accuracy")) +
  geom_line(aes(x = Epoch, y = Test_Accuracy, color = "Test Accuracy")) +
  labs(x = "Epoch", y = "Accuracy") +
  scale_color_manual(values = c("Train Accuracy" = "blue", "Test Accuracy" = "red")) +
  theme_minimal()

# Print the plots
print(loss_plot)
```




```
print(acc_plot)
```



4_ Based on the training and test accuracy, is this model actually managing to classify X-rays into pneumonia vs normal? What do you think contributes to this? why?

1. Model complexity and architecture: A model's capacity to effectively categorise X-rays can be considerably impacted by the architecture it is built on.

2. Class imbalance: The performance of the model may be hampered by the dataset's class imbalance. The model may have a bias towards the majority class if the dataset contains noticeably more instances of one class (for example, normal X-rays) than the other (for example, pneumonia X-rays).

3. Performance Metrics : We can use appropriate performance metrics to evaluate the performance of the model.

4. Feature Selection: The features extracted from the X-ray images can greatly influence the model's performance.

5. Hyperparameter Tuning: To optimise the model's classification performance, the best hyperparameters—such as learning rate and batch size—should be selected.

It seems that the model is not training that effectively the model is struggling to learn from the data and is not generalizing well to unseen examples. It suggests that the model may be too complex or the training process needs adjustments.

5_ what is your suggestions to solve this problem? How could we improve this model? We can perform the following:

1.Data Augmentation : Data augmentation is a powerful technique that can be used to improve the model's performance

2. Ensemble approaches: If you want to integrate numerous models for better performance, think about employing ensemble methods like bagging or boosting.

3. Class Imbalance : If there is a substantial class imbalance, use strategies to rectify it, such as oversampling the minority class, undersampling the majority class, or employing class weights during training.

4. Enhance Data Diversity : Increase the quantity and diversity of the dataset by accumulating X-ray images from various populations, sources.

5.Monitoring and evaluating the model continuously: Analyse the model's effectiveness on both training and validation datasets.

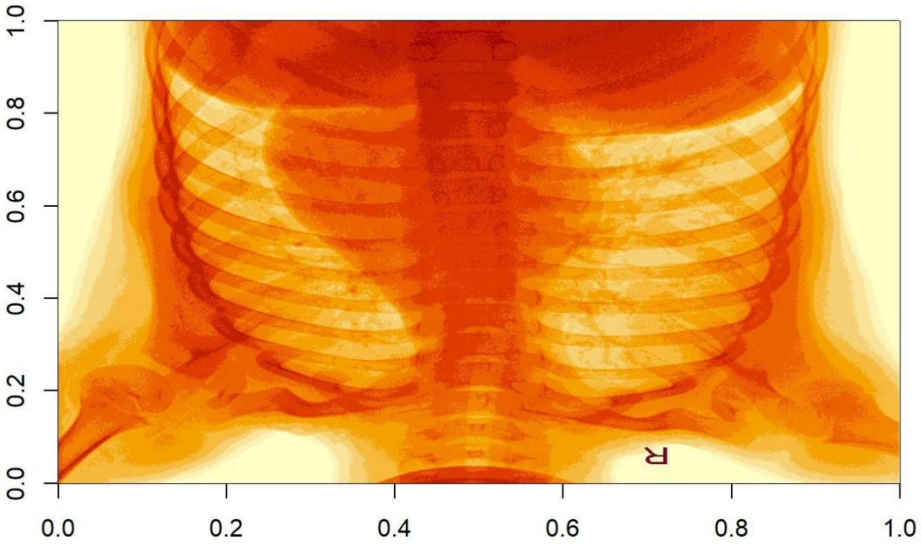
Data Augmentation

Data augmentation is one of the solutions to consider when facing training difficulties. Data augmentation involves applying various transformations or modifications to the existing training data, effectively expanding the dataset and introducing additional variations. This technique can help improve model performance and generalization by providing the model with more diverse examples to learn from.

By applying data augmentation, we can create new training samples with slight modifications, such as random rotations, translations, flips, zooms, or changes in brightness and contrast. These modifications can mimic real-world variations and increase the model's ability to handle different scenarios. Data augmentation increased dataset size, improved generalization, and reduced overfitting.

Below is an example that demonstrates how we can augment the data.

```
img <- readImage(shuffled_train_dataset[5])

T_img <- torch_squeeze(torch_tensor(img)) %>%
        # Randomly change the brightness, contrast and saturation of an image
        transform_color_jitter() %>%
        # Horizontally flip an image randomly with a given probability
        transform_random_horizontal_flip() %>%
        # Vertically flip an image randomly with a given probability
        transform_random_vertical_flip(p = 0.5)

image(as.array(T_img))
```



We can also add the data transofmrations to our dataloader:

```
# Define a custom dataset class with transformations
ImageDataset_augment <- dataset(
  name = "ImageDataset",
  initialize = function(X, y, transform = NULL) {
    self$transform <- transform
    self$data <- X
    self$labels <- y
  },
  .getitem = function(i) {
    # Return a single sample and label
    x  <-  self$data[i,,,]
    x <- self$transform(x)
    y <- self$labels[i]

    list(x = x, y = y)
  },
  .length = function() {
    dim(self$data)[1]
  }
)

# Define the transformations for training data
train_transforms <- function(img) {
  img <- torch_squeeze(torch_tensor(img)) %>%
    transform_color_jitter() %>%
    transform_random_horizontal_flip() %>%
    transform_random_vertical_flip(p = 0.5) %>%
    torch_unsqueeze(dim = 1)

  return(img)
}

# Apply the transformations to your training dataset
train_dataset <- ImageDataset_augment(train_X, train_y, transform = train_transforms)
test_dataset <- ImageDataset(test_X, test_y)
val_dataset <- ImageDataset(val_X, val_y)

# Create a dataloader for training
train_dataloader <- dataloader(train_dataset, batch_size = 16)
test_dataloader <- dataloader(test_dataset, batch_size = 16)
val_dataloader <- dataloader(val_dataset, batch_size = 16)

# Iterate over batches of data
batch = train_dataloader$.iter()$.next()

# Visualize the first batch size
batch[[1]]$size()
```

```
## [1]  16   1 224 224
```

6_ What are the potential drawbacks or disadvantages of data augmentation?

1. The information could be altered : In some cases, when we apply data augmentation techniques, it might distort the integral features in the dataset which could lead to false conclusions.

2. Increase in computational needs: Increasing the dataset results in more training instances overall, which raises the amount of computer power needed for training.

3. Limited Diversity: Data augmentation techniques rely on predefined transformations applied to the original data, resulting in the generation of additional examples

4. Imbalance: : Data augmentation should be applied uniformly across classes to maintain class balance.

Mobile net

Transfer learning is another technique in machine learning where knowledge gained from solving one problem is applied to a different but related problem. It involves leveraging pre-trained models that have been trained on large-scale datasets and have learned general features. By utilizing transfer learning, models can benefit from the knowledge and representations learned from these pre-trained models.

Torchvison provides versions of all the integrated architectures that have already been trained on the ImageNet dataset.

7_ What is ImageNet aka “ImageNet Large Scale Visual Recognition Challenge 2012”? How many images and classes does it involve? Why might this help us?

The 2012 ImageNet Large Scale Visual Recognition Challenge is a well-known dataset used for image classification tasks. The challenge focuses on a portion of the dataset called ILSVRC2012, which has about 1.2 million photos(50,000 validation images, and 150,000 test images) and 1,000 classes out of the dataset’s roughly 14 million labelled images.

1. Scalability and Diversity:Its importance stems from its size and diversity, which offer plenty of data for deep learning model training with millions of parameters.

2. Benchmark for evaluation: For computer vision research, the availability of ImageNet and the performance of models built using it, including AlexNet and later designs like VGG, ResNet, and Inception, served as benchmarks.

3. Training Neural Networks: Improving picture classification accuracy through learning of complicated patterns and hierarchical representations.

MobileNet is a pre-trained model that can be effectively utilized in transfer learning scenarios. Do some research about this model.

8_ Why do you think using this architecture in this practical assignment can help to improve the results? Hint: See MobileNet publication

MobileNet is a lighweight deep neural network with very less paramateres and higher classification accuracy.

1. Reduction in size : Compared to the conventional Convolutional Neural Networls, MobileNet are small deep learning architecture which optimizes the memory requirements espcially when we have limited resources.

2. Efficient: For use in mobile vision applications, MobileNet is a straightforward but effective convolutional neural network that requires little computer power.

3. Applications in real-life: The pre-trained network can categorise photos into 1000 different object categories, including several animals, a keyboard, a mouse, and a pencil.

4. Faster: MobileNet uses a new type of convolutional layer and is a significantly faster and smaller version of the CNN architecture.

9_ How many parameters does this network have? How does this compare to better performing networks available in torch?

There are typically 4.2 million parameters in a MobileNet model but it can vary based on hyper parameters and design.

MobileNet contains less parameters than other networks in PyTorch like ResNet-50,VGG-16 or AlexNet, VGG-16 has over 138 million parameters, AlexNet has 61 million parameters. One of MobileNet's benefits is the smaller number of parameters, which minimises model complexity, memory needs, and computational expense.As a result, MobileNet is better suited for circumstances with limited resources or applications that require efficient and lightweight models.

In the following you can see an example of how we can load pre-trained models in our codes.

```
# Load the pre-trained MobileNet model
mobilenet <- model_mobilenet_v2(pretrained = TRUE)

# Modify the last fully connected layer to match your classification task

#in_features <- mobilenet$classifier$in_features
mobilenet$classifier <- nn_linear(224*224*3, 2)
print(mobilenet)
```

```
## An `nn_module` containing 2,524,930 parameters.
##
## ── Modules ──────────────────────────────────────────────────────────────────
## • features: <nn_sequential> #2,223,872 parameters
## • classifier: <nn_linear> #301,058 parameters
```

10_ Using the provided materials in this practical, train a different network architecture. Does this perform better?

The RESNET Model performs better. ResNet is well-known for producing good outcomes when it comes to improving performance, particularly in terms of accuracy. ResNet's deep architecture with residual connections allows it to handle complicated and large-scale information successfully, getting good accuracy.

Contrary to this, MobileNet's efficiency and compactness make it ideal for mobile and embedded devices with minimal processing resources. MobileNet is especially useful when performing real-time or on-device inference with low processing resource,Efficiency and compactness are crucial factors.

```
#Loading the pre-trained resnet model
resnet <- model_resnet34(pretrained = TRUE)
resnet$classifier <- nn_linear(224*224*3, 2)
print(resnet)
```

```
## An `nn_module` containing 22,098,730 parameters.
##
## ── Modules ──────────────────────────────────────────────────────────────────
## • conv1: <nn_conv2d> #9,408 parameters
## • bn1: <nn_batch_norm2d> #128 parameters
## • relu: <nn_relu> #0 parameters
## • maxpool: <nn_max_pool2d> #0 parameters
## • layer1: <nn_sequential> #221,952 parameters
## • layer2: <nn_sequential> #1,116,416 parameters
## • layer3: <nn_sequential> #6,822,400 parameters
## • layer4: <nn_sequential> #13,114,368 parameters
## • avgpool: <nn_adaptive_avg_pool2d> #0 parameters
## • fc: <nn_linear> #513,000 parameters
## • classifier: <nn_linear> #301,058 parameters
```

Useful links

https://medium.com/@kemalgunay/getting-started-with-image-preprocessing-in-r-52c7d153b381 (https://medium.com/@kemalgunay/getting-started-with-image-preprocessing-in-r-52c7d153b381) https://cran.r-project.org/web/packages/magick/vignettes/intro.html (https://cran.r-project.org/web/packages/magick/vignettes/intro.html) https://www.datanovia.com/en/blog/easy-image-processing-in-r-using-the-magick-package/ (https://www.datanovia.com/en/blog/easy-image-processing-in-r-using-the-magick-package/) https://dahtah.github.io/imager/imager.html (https://dahtah.github.io/imager/imager.html) https://rdrr.io/github/mlverse/torchvision/api/ (https://rdrr.io/github/mlverse/torchvision/api/) https://github.com/brandonyph/Torch-for-R-CNN-Example (https://github.com/brandonyph/Torch-for-R-CNN-Example)