DEEP
LEARI
INSTIT

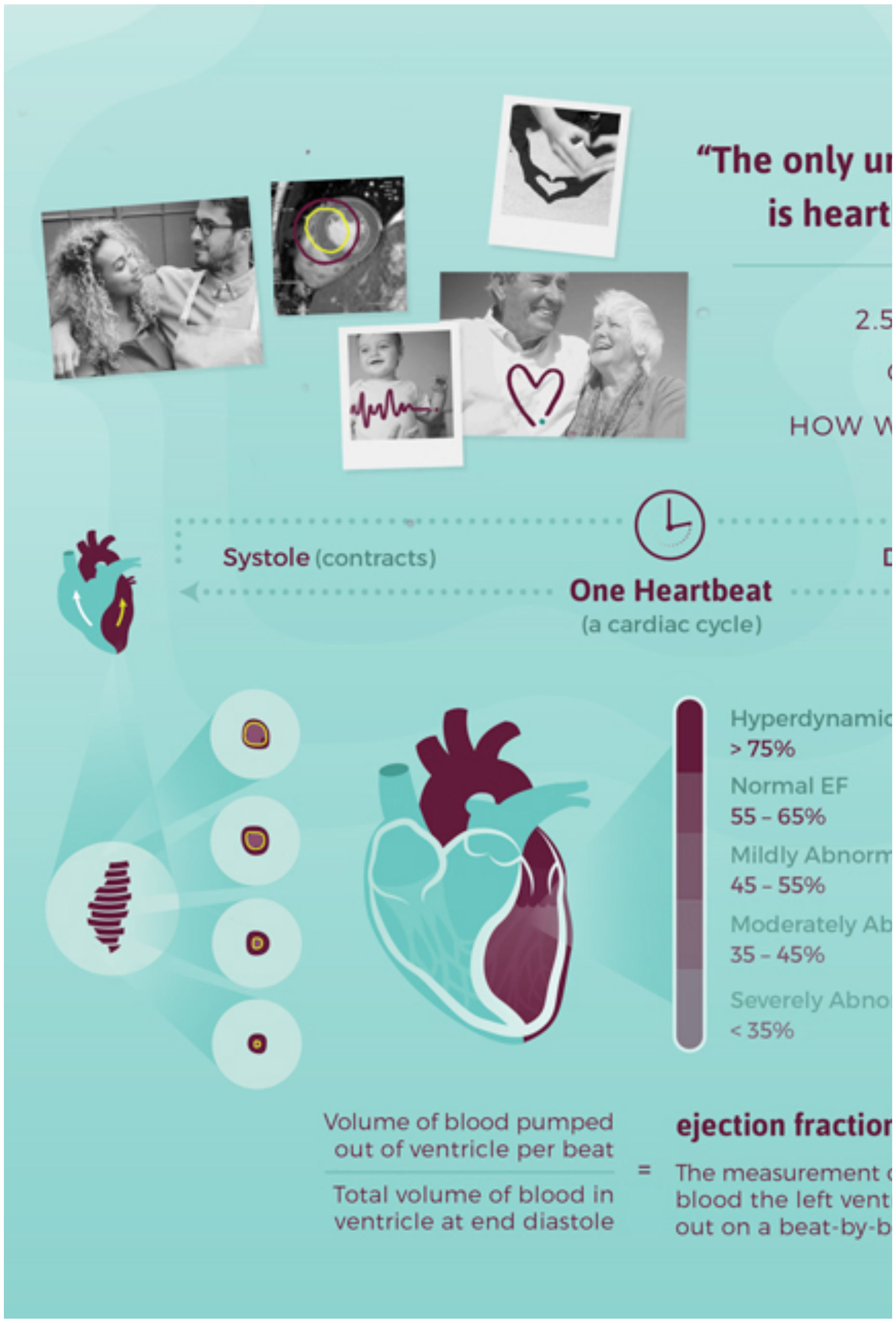
(https://www.nvidia.com/dli)

Transforming How We Diagnose Heart Disease

Cardiovascular disease, also commonly referred to as heart disease, takes on many forms - heart a
According to a report published on behalf of the American Heart Association, 610,000 Americans di

Booz | Allen | Hamilton and Kaggle offered the 2015 Data Science Bowl (https://www.kaggle.com/c/
scientist to help automate the diagnosis of heart disease through a competition.

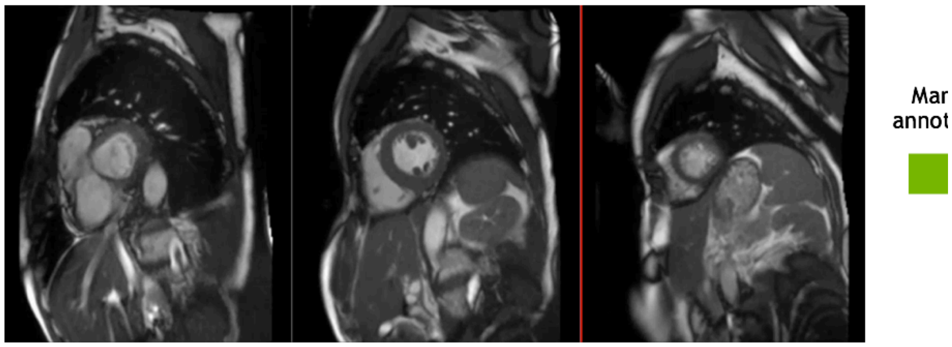
Two indicators of the presense of heart disease are "volumes" (both end-systolic and end-diastolic)
challenge included the following image:

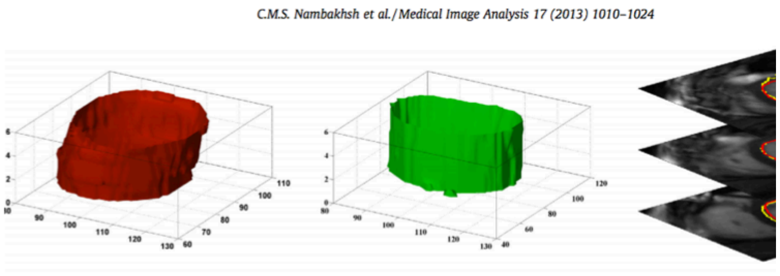


End-systolic and end-diastolic volumes yield the ejection fraction (EF) noted above in the image anc volumes at systole and V_D denotes the volumes at diastole.

$$100 \cdot \frac{V_D - V_S}{V_D}$$

In addition, Magnetic Resonance Imaging (MRI) correctly assess the heart's squeezing ability. Howe deep neural networks can automate this process. Variations in anatomy, function, image quality, anc a challenging problem. You will encounter this variation in the competition dataset, which aims to pr

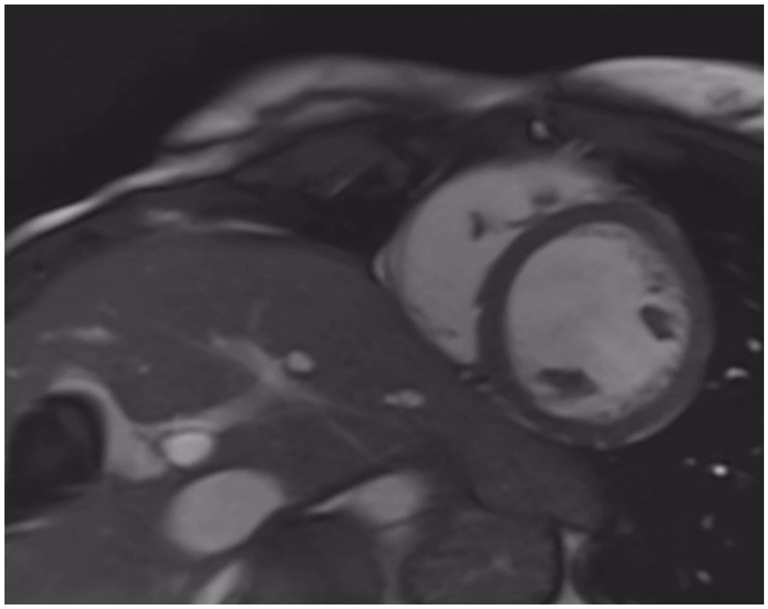



C.M.S. Nambakhsh et al. / Medical Image Analysis 17 (2013) 1010–1024

C.M.S Nambakhsh et al., Medical Image Analysis 17

The Dataset

The National Heart, Lung, and Blood Institute (NHLBI) provided the MRI images for the Data Scienc
data-science-bowl/data) consists of hundreds of cardiac MRI images in DICOM (https://en.wikipedi
approximately 30 images across the cardiac cycle. Each slice is acquired on a separate breath hold
expected to be imperfect.



The dataset contains patients from young to old, images from numerous hospitals, and hearts from which is robust to these variations could both validate and automate the cardiologists' manual mea directory of DICOM files. The exact number of images will differ from case to case, either varying in number of frames in the time sequences.

The main view for assessing ventricle size is the short axis stack (PSAX), which contains images tak ventricle:

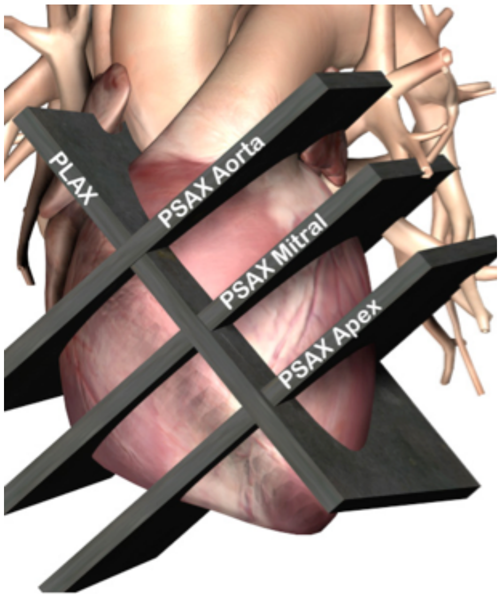


image credit: fpnotebook.com

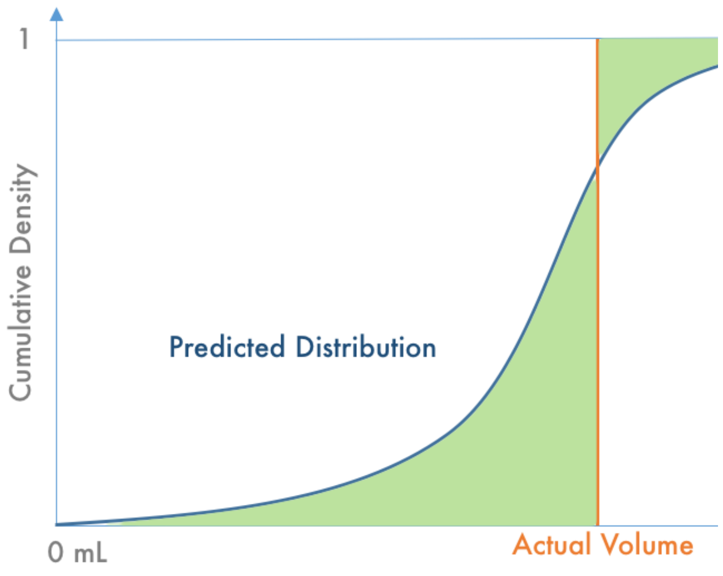
These have the prefix "sax_" in the dataset. Most cases also have alternative views.

Evaluation

Performance is evaluated using the Continuous Ranked Probability Score (CRPS). For each MRI, a
systolic and diastolic volumes (two separate distributions per case). The CRPS is computed as follo

$$CRPS = \frac{1}{600 \cdot N} \sum_{m=1}^{N} \sum_{n=0}^{599} (P(y \leq n) - H($$

where P is the predicted distribution, N is the number of rows in the test set (equal to twice the nur
Heaviside step function ($H(x < 0) = 0$ and $H(x \geq 0) = 1$). While it is not simple to visualize the C
guide for understanding the error term between the predicted distribution and actual volume:



Note that the entry will not score if any of the predicted values has $P(y \leq k) > P(y \leq k + 1)$ for a

End-to-End Deep Learning for NDSB-II

In this example, we will show how to use GPU accelerated MXNet library to build an end-to-end de
this is a very simple model without any network structure optimizations or hyper parameter tuning. I
example solution.

About MXNet

MXNet (https://github.com/dmlc/mxnet) is a deep learning framework designed for both efficiency a
resources to solve the problem under limited resource constraint, with a flexible programming interf
learning tasks with R, Julia, Python and more. To run on multiple GPU with huge network, or questio

docs (https://mxnet.readthedocs.org/en/latest/)

General Overview of Model

Input Data

The dataset itself contains 500 training studies with on average 10 unique SAX observation at variou
5000 observations in total. Each of these SAX observation usually contain 30 DICOM images ("fram
(expansion and contraction). The idea here is to pack each of the 30 image frames of an observatio
just think of stacking playing cards to form a deck. Each card has the same rectangular dimensions
to form a deck. It's the same thing here. We're going to take each of the 30 square image frames of
"deck" to the deep neural network. The only difference with the card deck analogy is that the image
heartbeat is not all garbled. This tutorial is based on this simple idea: we first accumulate all suitabl
network to learn the target directly.

The label data set contains only 500 labels. That is, each of the roughly 10 SAX observation for a pa
each SAX observation of a study is just a different view of the same heart (i.e. a single heartbeat as
axis of the heart). Therefore, in the data preprocessing step, each label must be duplicated for each

Additionally, the same 64x64x30 deck of images is used to predict both systole and diastole volume
observation tensor to predict systole volume. Then a separate network that ingests that same imag

Another idea used in this tutorial is taking a frame-by-frame difference to measure change per fram
dynamically difference the input inside of the network. It helps a little in the final result.

Network Objective

For the network, we use the well documented LeNet style convolution network with batch normaliz
configuration. In this challenge, we are asked to predict a CDF value of 600 data-point. Therefore th
neural-net that given a stack of images 64x64x30 to output 600x1 vector - one predicted value for e
a single floating point value like 83.3 (mL). This label is transformed into a step function having 600
83 are 0 and all y-values with x greater than 83 are 1.

Preprocessing

We first run a preprocessing step, to pack the data into a csv file (`train-64x64-data.csv`). Each
gives 30 frames of images. We can also use other inputs besides csv. The CSV is used here since t

The input dataset is quite big (5293 observations of size 64x64x30). While this data set can likely fit
use the `CSVIter` from `mxnet` to load data from disk on-the-fly during training, without loading all t

The labels for the training data are stored in `train-systole.csv` and `train-diastole.csv` wh
Line `i` in the training CSV data file is label by the associated line `i` in the label CSV files. Again, whe
`systole.csv` and likewise when training the diastole network we will use labels from `train-dias`

Code

First we load the necessary libraries

In [1]:
```
# import libraries
require(mxnet)
require(data.table)
require(ggplot2)
```

```
Loading required package: mxnet
Loading required package: data.table
Loading required package: ggplot2
```

Next we define a function that will architect (not trained yet) neural networks. This network is a class
years ago and hence has the nostalgic name "LeNet".

Notice here that we create a variable using `mx.symbol.Variable` which *represents* the input data
variable. For example, the first thing we do to the image data input is to normalize the pixel values. I
actually access each individual frame of the input. Recall that the input is 64x64x30 so that each inc
so that differences between successive frames can be calculated. That is, instead of training the ne
trained on the differences between each successive frame. This is pretty cool since we can actually
having to preprocess the whole dataset when we want to experiment with a new idea. Once each fr
into a 64x64x29 tensor input using `mxnet:::mx.varg.symbol.Concat`. Since we've taken succ

From here we just chain various layers together, such as `mx.symbol.Convolution`, to form the n
free to add layers in between or remove layers etc. That's part of the fun of working with DL; various
you're free to construct anything you'd like. Play with the network structure to get a feel for how trai

In [2]:
```
# Create LeNet style network
get.lenet <- function() {

    # create data variable (i.e. symbol)
    source <- mx.symbol.Variable("data")

    # normalize values of input data
    source <- (source-128) / 128

    # SliceChannel is a symbol that can be indexed just like an array
    frames <- mx.symbol.SliceChannel(source, num.outputs = 30);

    # init list of differences
    # init list of differences
    diffs <- list()

    # compute differences for each "frame"
    for (i in 1:29) {
        diffs <- c(diffs, frames[[i + 1]] - frames[[i]])
    }

    # set the property for number of arugments in diffs variable
    diffs$num.args = 29

    # concatonate frame variables into single variable
    source <- mxnet:::mx.varg.symbol.Concat(diffs)

    # convolution layer with 5x5 kernel dimention
    net <- mx.symbol.Convolution(source, kernel = c(5, 5), num.filter = 4C

    # normalization layer: simply subtract mean divide by std
    net <- mx.symbol.BatchNorm(net, fix.gamma = TRUE)

    # activation layer using Rectified Linear Unit (relu) activation funct
    net <- mx.symbol.Activation(net, act.type = "relu")

    # Max pooling layer with a 2x2 kernel and no overlap since stride is 2
    net <- mx.symbol.Pooling(net, pool.type = "max", kernel = c(2, 2), str

    # continue building the network ...
    net <- mx.symbol.Convolution(net, kernel = c(3, 3), num.filter = 40)
    net <- mx.symbol.BatchNorm(net, fix.gamma = TRUE)
    net <- mx.symbol.Activation(net, act.type = "relu")
    net <- mx.symbol.Pooling(net, pool.type = "max", kernel = c(2, 2), str

    # flatten the features to single variable
    flatten <- mx.symbol.Flatten(net)

    # add a drop out layer where 50% of data gets dropped out at training

    flatten <- mx.symbol.Dropout(flatten)

    # add the final fully connected layer for output of dimension 600
    fc1 <- mx.symbol.FullyConnected(data = flatten, num.hidden = 600)

    # Name the final layer as softmax so it auto matches the naming of dat
    # Otherwise we can also change the provide_data in the data iter
    return(mx.symbol.LogisticRegressionOutput(data = fc1, name = 'softmax'
}
```

If you want to know more about a particular layer, pull up the help listing for that layer. For example, activation layer where additional functions are listed for use such as 'sigmoid', 'tanh' and so on.

In [3]:
```
?mx.symbol.Activation
```

Next the training batch size is specified. The size can be smaller or larger arbitrarily but since we're
really large batch size since the GPU has limited memory. The batch size is also a factor of how larg
16 is a good size. It is not the end of the world if batch size is too large. If the batch size is too large
something like "device out of memory" which is likely your queue to reduce the batch size.

In [4]:
```
batch_size <- 16
```

Next we load the training data using an iterator so that we use host memory efficiently. This is nice s
off is that it does increase the training time since we have to keep loading data over and over.

In [5]:
```
# CSVIter is used here, since the data can't fit into memory
data_train <- mx.io.CSVIter(
   data.csv  = "./train-64x64-data.csv", data.shape  = c(64, 64, 30),
  label.csv  = "./train-systole.csv"   , label.shape = 600,
  batch.size = batch_size
)
```

Lets now initialize a LeNet style network using our network function. This network has structure but
materials that will be shaped into meaningful values/parameters during the training phase. Notice th
to random values which does actually consume memory on the system. If the network has 10 millio
memory. Also, all the network parameters must actually fit into the GPU memory (with the input data
run out of memory on the GPU. So, start conservatively and grow the network as you work through

In [7]:
```
network <- get.lenet()
network
```

```
C++ object <0x4c7cc00> of class 'MXSymbol' <0x4b905b0>
```

Before we can train the network parameters we must specify a *loss function* also called a *cost funct*
current set of parameters reproduce the target output. In general, for a given cost function the traini
function is minimized. That is, a lower cost is better than higher cost.

In [8]:
```
# Custom evaluation metric using CRPS.
costfun <- function(label, pred) {
  pred  <- as.array(pred )
  label <- as.array(label)
  return(sum((label - pred) ^ 2) / length(label))
}

# create custom mxnet metric for training
mx.metric.CRPS <- mx.metric.custom("CRPS", costfun)
```

Now you are ready to train your architected network with training data to build a model. Below we c
code block below that was created with 65 training rounds (epochs) or train your own model in the s
rounds (five training rounds will likely take 10+ minutes to execute). Once you feel comfortable, feel
see how the training performance changes.

NOTE: No changes are needed in the first of two code blocks that follow this explanation and you o

Notice that one of the arguments provided is `ctx = mx.gpu(0)` which effectively tells MXNet to u
training with the CPU instead then set the context to `ctx=mx.cpu()`. Furthermore, an array of GPU
there are more than one GPU devices present on the machine. Keep in mind here that using multipl
with large datasets. It's not unusual that training time actually increases when using multiple GPU d
small and grow the training strategy and always profile execution times etc. to keep an eye on learn

If you want to save some time, simply load the pretrained model using the cell below and skip the c

In [9]:
```
# load the pretrained result
systole_model <- mx.model.load("stytole_model_BN",65)
```

Execute the cell above if you would like to use the pretrained results OR execute the code below if y

In [10]:
```
# Training the systole model (this takes a long time).

# set the random seed so the results are reproducible
mx.set.seed(0)

# start the clock
start_time <- proc.time()

# train the model parameters with the data
systole_model <- mx.model.FeedForward.create(
  X             = data_train,
  ctx           = mx.gpu(0) ,
  symbol        = network   ,
  num.round     = 5         ,
  learning.rate = 0.01      ,
  wd            = 0.0001    ,
  momentum      = 0.9       ,
  eval.metric   = mx.metric.CRPS
)

# get the time delta
proc.time() - start_time
```

```
Start training with 1 devices
[1] Train-CRPS=0.0481668175688349
[2] Train-CRPS=0.0343573634394582
[3] Train-CRPS=0.03320528982994l
[4] Train-CRPS=0.032136443729039
[5] Train-CRPS=0.0310192129196943
```

```
   user  system elapsed
182.556  16.500 336.316
```

If you've trained a network and want to save the results then export the trained model so it can be r

In [11]:
```
# Save the trained neural network model to disk.
# This creates two files:
#    1. systole_model-0005.params
#    2. systol_model-symbol.json
#
# WARNING: the 5 here must match num.rounds parameter provided to mx.model
#          So if the model was saved at 5, then it must be loaded with 5.
#
mx.model.save(systole_model,"systole_model_BN",5)
```

Just to get a better feel for the data, lets extract it using the CSV iterator. Doing this reads in the ent
large dataset.

In [12]:
```
# this reads in all the data at once (not a great idea, but we can do it)
labels <- mx.io.extract(data_train,"label")
data   <- mx.io.extract(data_train,"data" )
```

Once the data has been loaded we can check the dimensions. As advertised we have ~ 5000 trainir

In [13]:
```
#
dim(labels)
dim(data)
```

```
600   5293

64   64   30   5293
```

Using the trained model we can pass input samples into the model to predict their systolic volume. `data[,,,1:20]` to extract some samples. Notice here we're selecting input data along the 4th dim 64x64x30 and by leaving the first three index empty we are effectively saying "give me everything" a

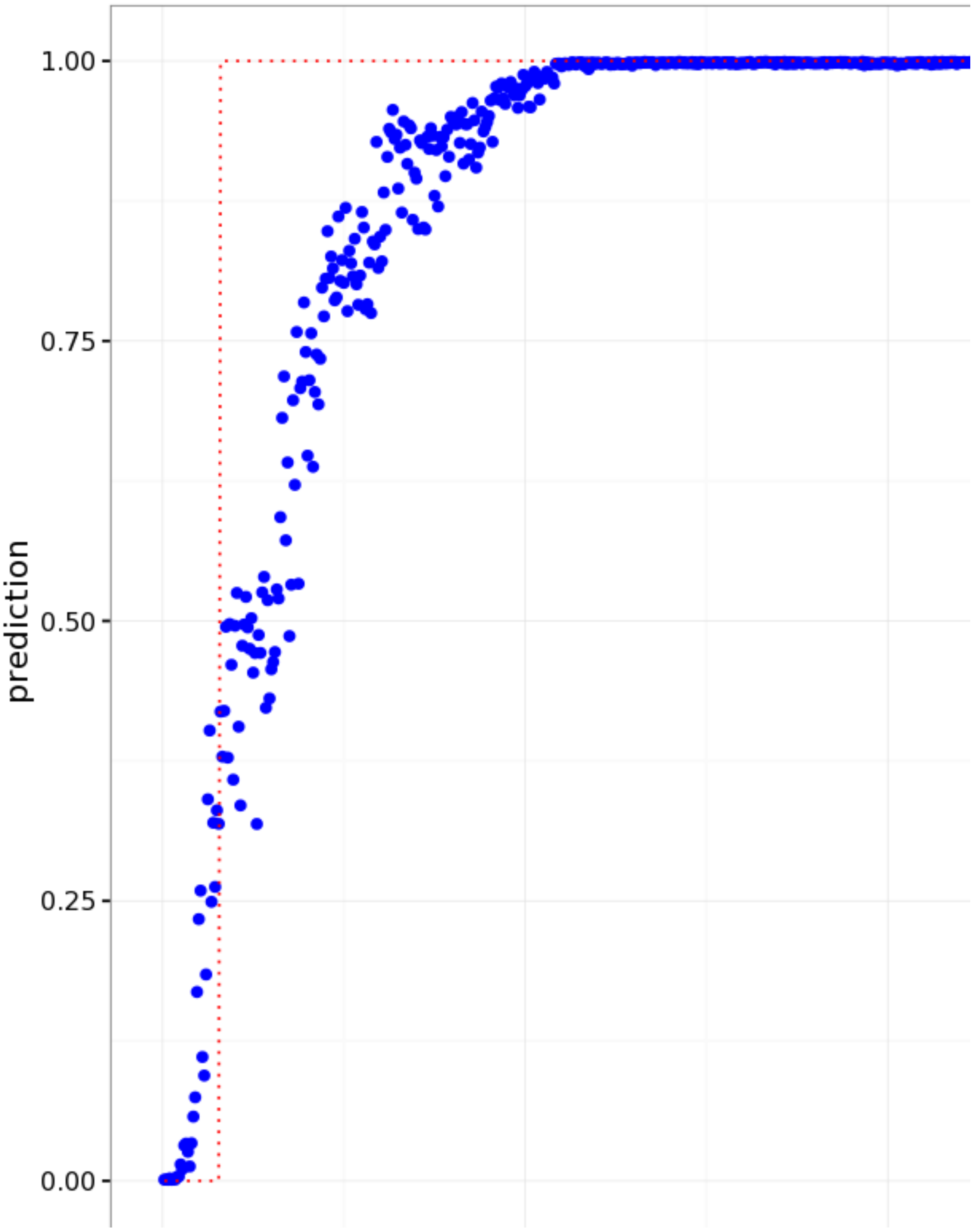
In [14]:
```
# create index for selecting samples
sample_index = c(1:20);

# apply the model to just a few data to generate some predictions
model_predictions <- predict(systole_model, data[,,,sample_index])
```

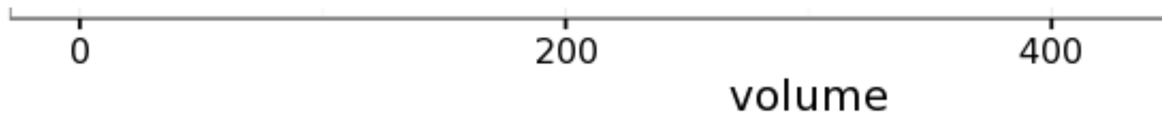
Now lets have a look at what was predicted by the model for these input. Try selecting a different in hesitate to predict more input in the cell above to investigate even further.

In [15]:
```
# have a look at what the label and associated prediction looks like
ix = 14;
x  <- seq(1, 600, 1)
y1 <- model_predictions[,ix]
y2 <- labels[,ix]
df <- data.frame(volume=x,prediction=y1,label=y2)

# basic graphical object
ggplot(df, aes(volume)) +

  # the predicted CDF using the trained model
  geom_point(aes(y=prediction), color="blue") +

  # the label for this set of images (i.e. systole volume)
  geom_line(aes(y=label), color="red", linetype="dotted") +

  # make the plot theme simple
  theme_bw()
```

```
# evaluate the cost function for this prediction
costfun(labels[,ix],model_predictions[,ix])
```

```
0.0248231752989287
```





Notice how the prediction (blue curve) is a logistic like curve (CDF) while the label is a step function. "close" the set of predictions are to their labels. However, notice with this formulation of the problen actual volume predicted is.

In [16]:
```
costfun(labels[,sample_index],model_predictions[,sample_index])
```

0.0260655184942826

OK Now it is your Turn!

Lets use what we've learned from creating the `systole_network` and create a network to predict

Step 1. Create a training data set using the diastole labels

Step 2. Create network

Step 3. Train the network

In [19]:
```
# step 1
# CSVIter is used here, since the data can't fit into memory
data_train_diastole <- mx.io.CSVIter(
   data.csv  = "./train-64x64-data.csv", data.shape  = c(64, 64, 30),
  label.csv  = "./train-diastole.csv"   , label.shape = 600,
  batch.size = batch_size
)
data_train_diastole
```

```
C++ object <0x1b2f7fd0> of class 'MXNativeDataIter' <0x4ba5ff0>
```

In [21]:
```
# step 2
network_diastole <- get.lenet()
print(network_diastole)

# set the random seed so the results are reproducible
mx.set.seed(0)

# start the clock
start_time <- proc.time()

# train the model parameters with the data
diastole_model <- mx.model.FeedForward.create(
  X             = data_train_diastole,
  ctx           = mx.gpu(0) ,
  symbol        = network_diastole,
  num.round     = 5          ,
  learning.rate = 0.01       ,
  wd            = 0.0001     ,
  momentum      = 0.9        ,
  eval.metric   = mx.metric.CRPS
)

# get the time delta
proc.time() - start_time
```

```
C++ object <0x219ad950> of class 'MXSymbol' <0x4b905b0>
Start training with 1 devices
[1] Train-CRPS=0.0652898599732858
[2] Train-CRPS=0.0512829253625502
[3] Train-CRPS=0.0493174068008693
[4] Train-CRPS=0.0475295476931218
[5] Train-CRPS=0.0456691814859295
```

```
   user  system elapsed
106.456  15.600  54.561
```

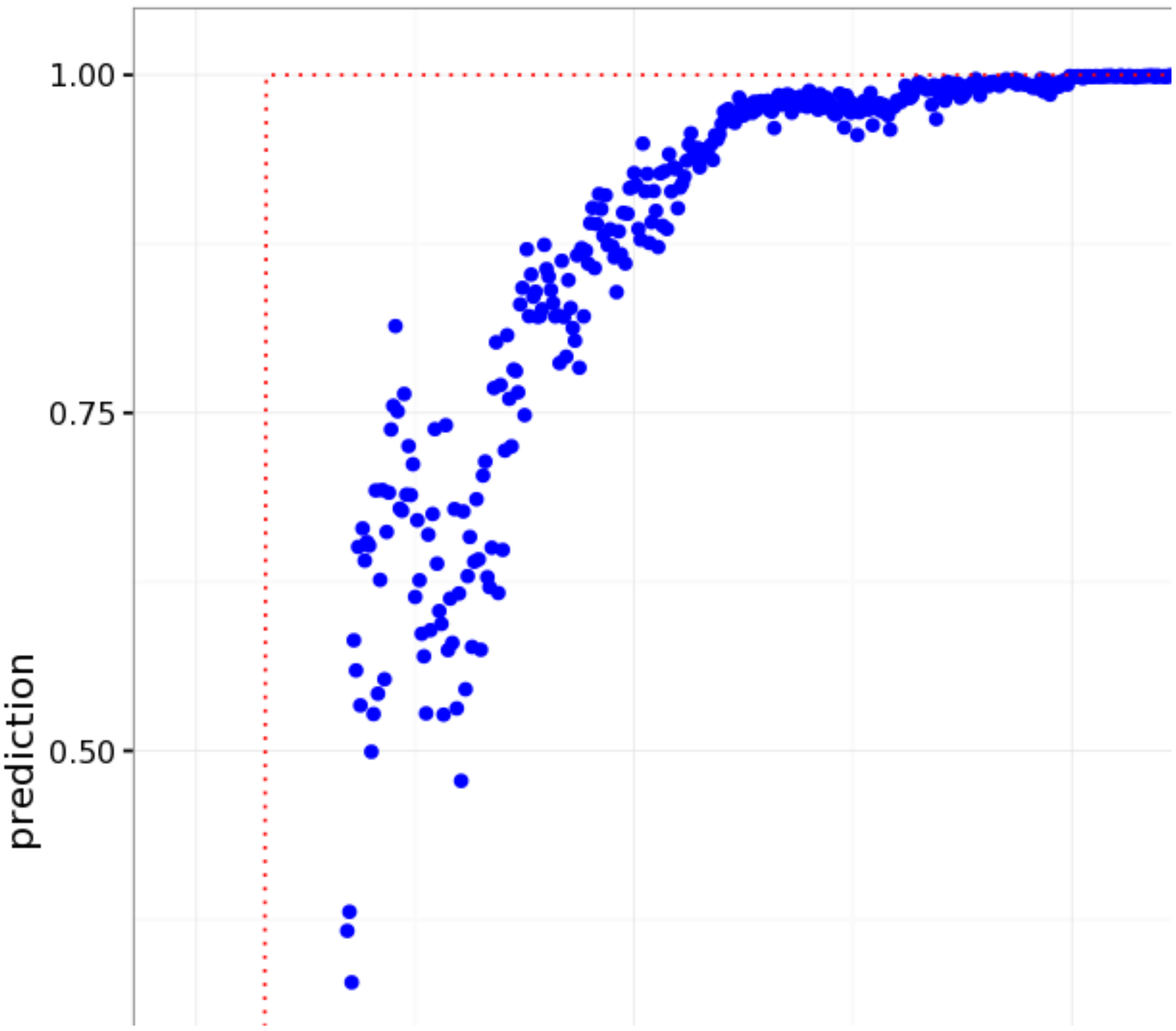
In [22]:
```
# step 3
# this reads in all the data at once (not a great idea, but we can do it)
labels_diastole <- mx.io.extract(data_train_diastole,"label")
data_diastole   <- mx.io.extract(data_train_diastole,"data" )
```

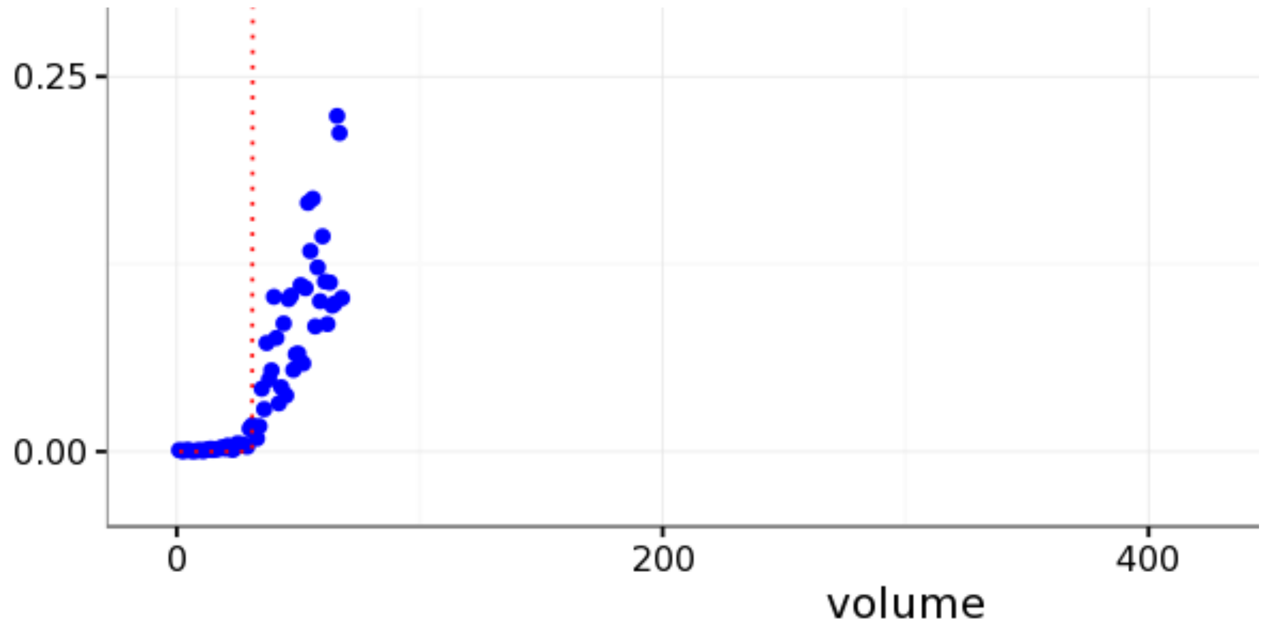
In [23]:
```
# apply the model to just a few data to generate some predictions
model_predictions_diastole <- predict(diastole_model, data_diastole[,,,sam
```

In [24]:
```
# have a look at what the label and associated prediction looks like
ix = 14;
x  <- seq(1, 600, 1)
y1 <- model_predictions_diastole[,ix]
y2 <- labels[,ix]
```

```
df <- data.frame(volume=x,prediction=y1,label=y2)

# basic graphical object
ggplot(df, aes(volume)) +

  # the predicted CDF using the trained model
  geom_point(aes(y=prediction), color="blue") +

  # the label for this set of images (i.e. systole volume)
  geom_line(aes(y=label), color="red", linetype="dotted") +

  # make the plot theme simple
  theme_bw()

# evaluate the cost function for this prediction
costfun(labels[,ix],model_predictions_diastole[,ix])
```

```
0.0718063186435208
```





In [25]:
```
costfun(labels_diastole[,sample_index],model_predictions_diastole[,sample_
```

```
0.0503821121021908
```

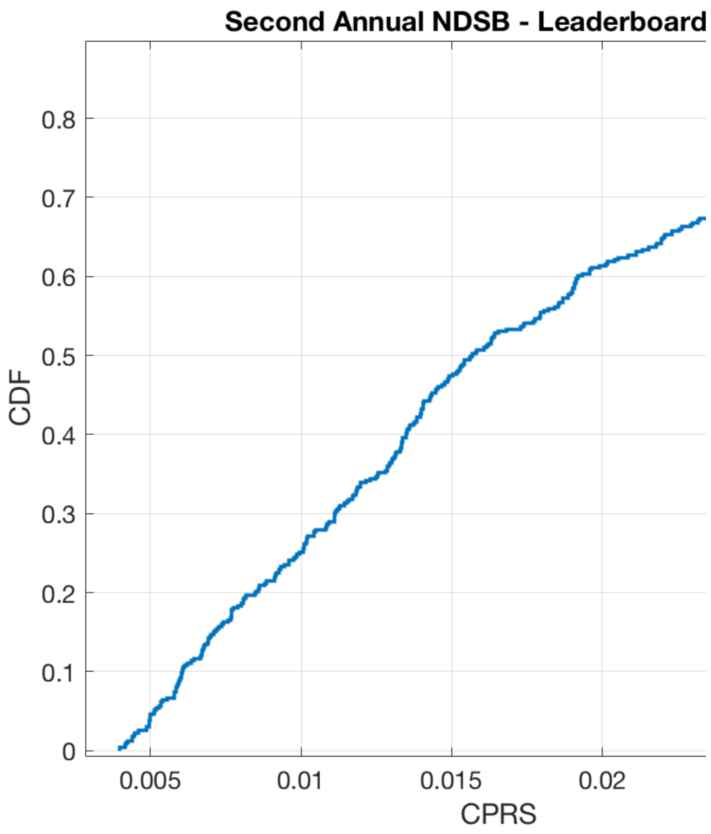
Discovery Requires Experimentation ...

There are many ways to explore and even improve this model:

1. Maybe try removing batch normalization layers (ref (https://arxiv.org/abs/1502.03167)) [hint: mo
2. Try increasing or decreasing the number of features in the convolution layer [hint: modify `num.f`
3. How does batch size effect training?
4. Have a go at modifying the learning rate and momentum of the training phase [hint: learning.rat
5. Notice that the CRPS function uses the residual squared. What else might we try (hint: try abs i
6. Try using different activation functions (i.e. other than relu). How does this effect performance?
7. Maybe try using different pooling functions (i.e. other than max) [hint: use help to see other func
8. Maybe try removing dropout layer or modifying the percentage dropout (i.e. default is 50%)
9. Maybe try double differencing the data or not differencing the data at all
10. What are other ways we could formulate the network output (i.e. other than discrete CDF)?

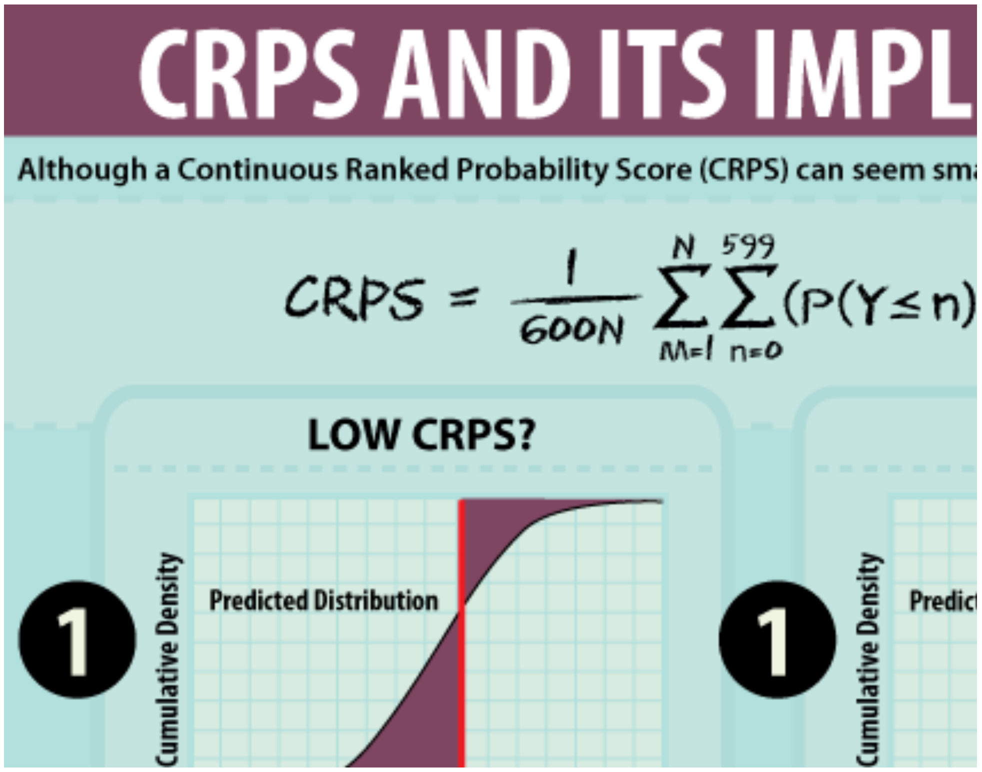
NDSB Competition Results

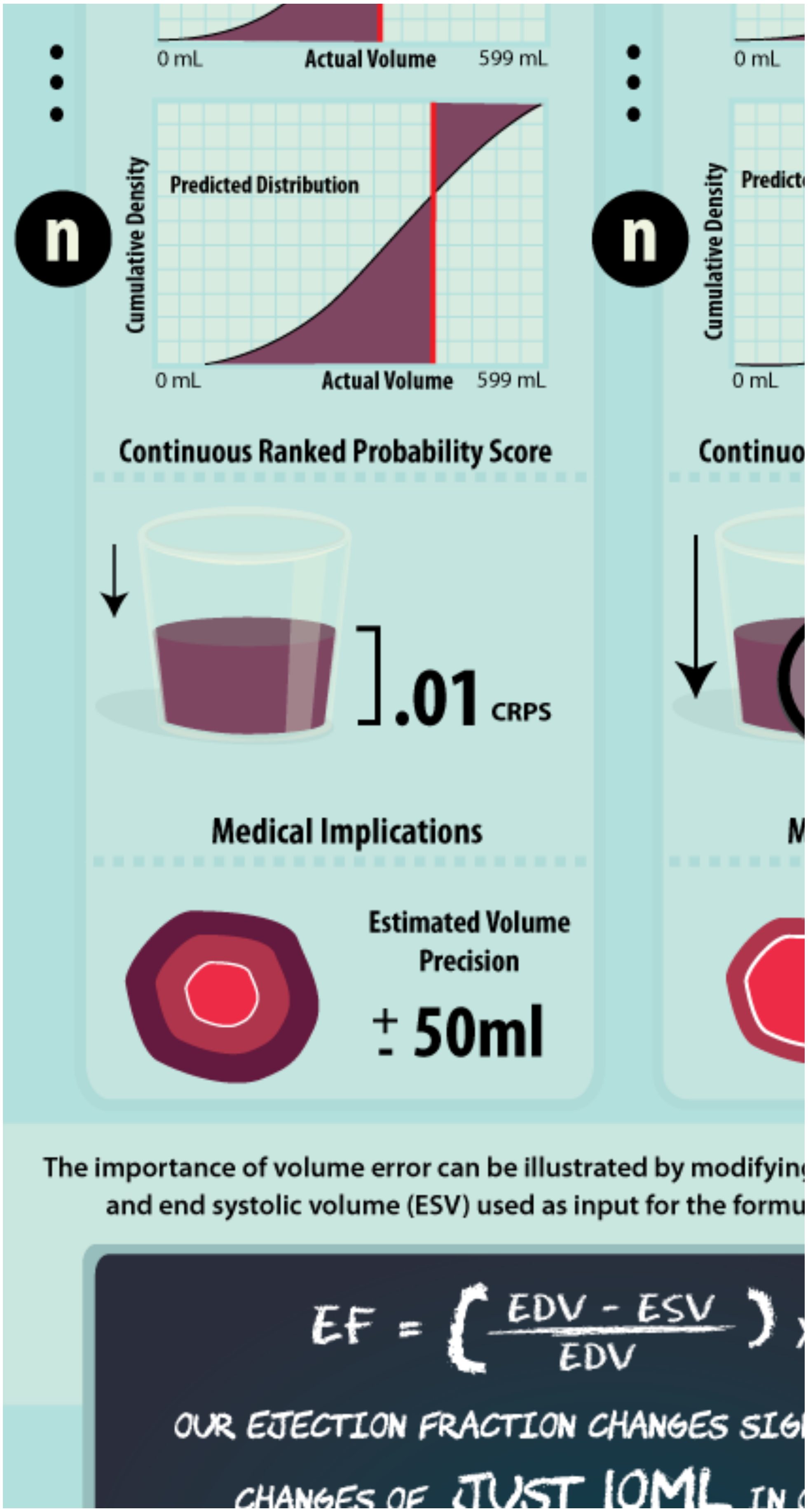
There were nearly 200 participants (https://www.kaggle.com/c/second-annual-data-science-bowl/le
to solving this challange. The CRPS scores for the leaderboard top ten ranged from 0.009485 in firs
your results stackup against the competion, we created an empirical CDF from the leaderboard CRI



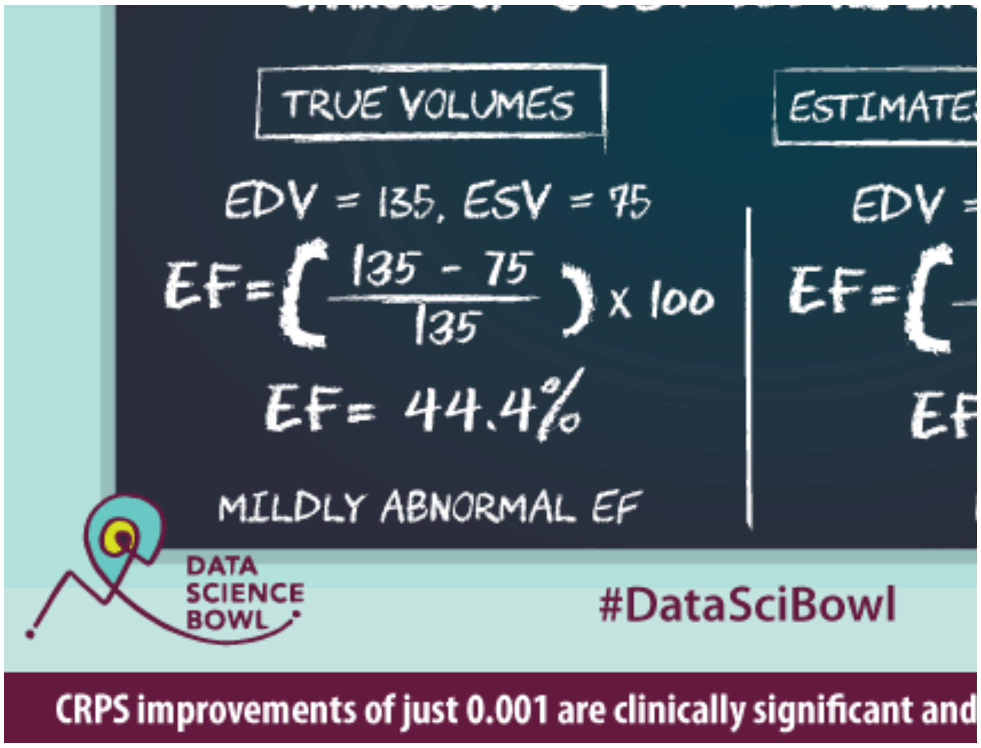
Therefore, achieving a CRPS score of 0.03 is at about the 80th percentile w.r.t. the overall competiti

So how much better is a CRPS of 0.009485 than 0.012611? To get a loose sense for how CRPS eff infographic to performers:


CRPS AND ITS IMPL
Although a Continuous Ranked Probability Score (CRPS) can seem sma
CRPS = 1/600N ∑_{M=1}^{N} ∑_{n=0}^{599} (P(Y≤n)
LOW CRPS?
1
Cumulative Density
Predicted Distribution
1
Cumulative Density
Predict



The importance of volume error can be illustrated by modifyin
and end systolic volume (ESV) used as input for the formu



Analysis of the competition results seem more favorable than this graphic might imply and noted th
human performance. For a medical perspective on the competion results check out this kaggle blog
bowl/forums/t/19839/a-medical-perspective-on-the-quality-of-the-left-ventricular-volume-and) by D
applicability provided by Jonathan Mulholland of Booze Allen Hamilton here (http://www.datascienc
These analysis conclude, based on the top four models submitted to the competion, that "*The mod*
While the models are not right 100% the time, there is a very low probability of a severely abnormal
range. The normal to mild diagnoses are very likely to stay within their domain ... This is a pretty goo

```
In [ ]:
```