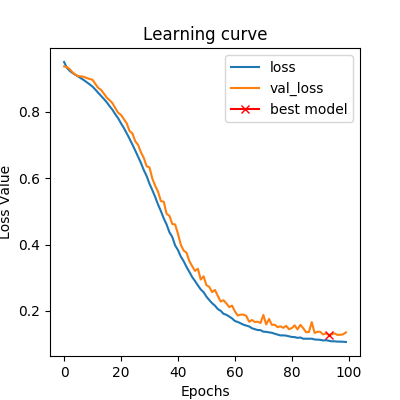
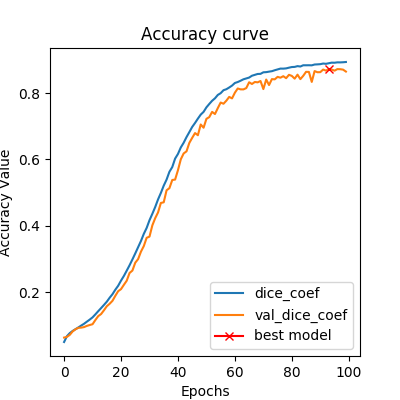
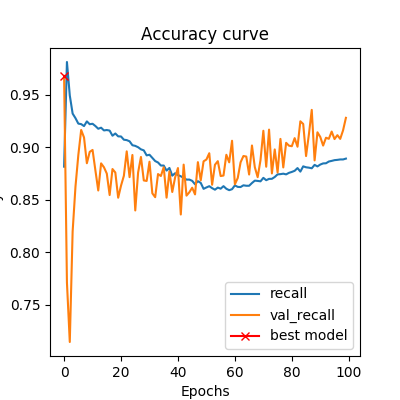
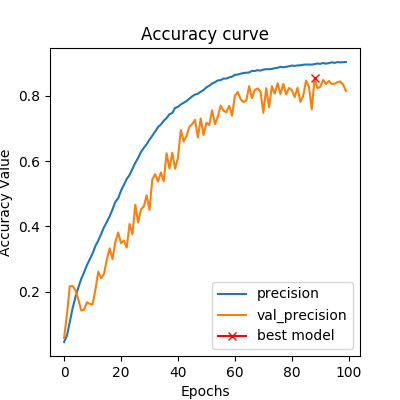
Lab 4

Task 1

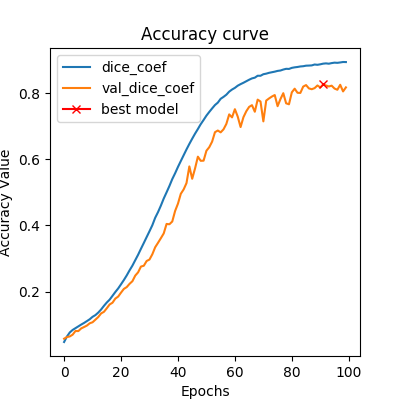
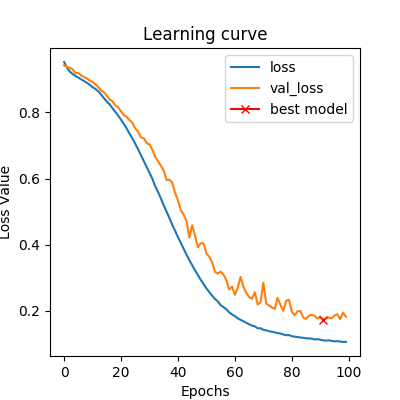
Training U-Net using three-fold cross validation on the brain tumor MRI dataset.

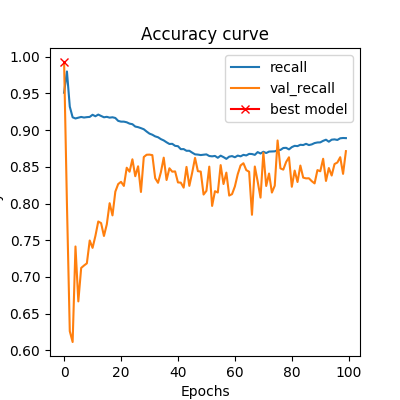
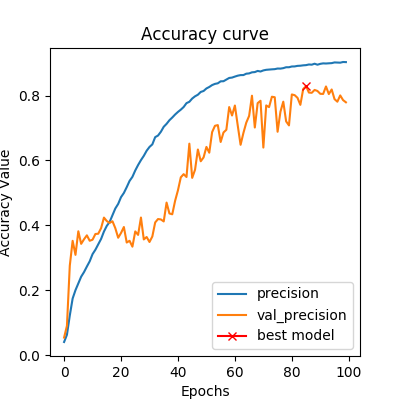


First Fold - Dice Coefficient First Fold - Loss Curve

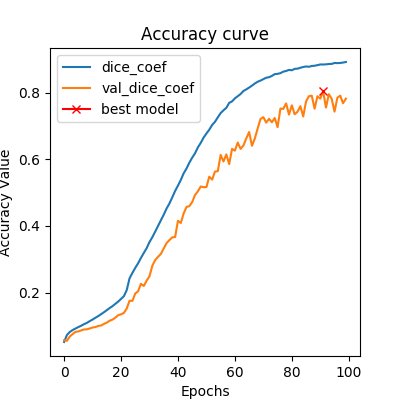
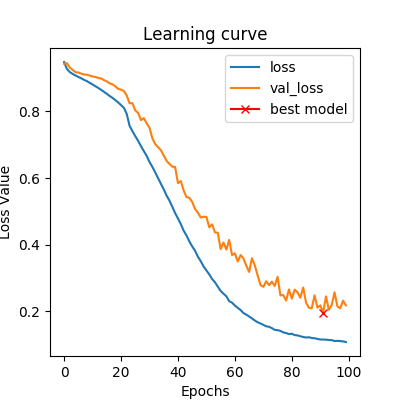
 

First Fold - Recall First Fold - Precision

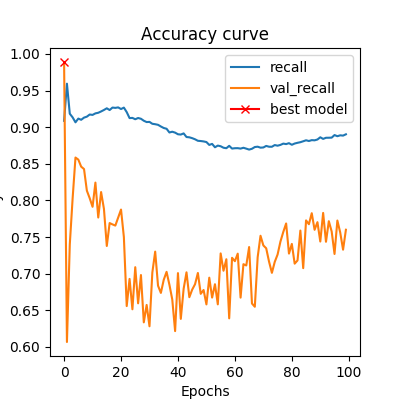
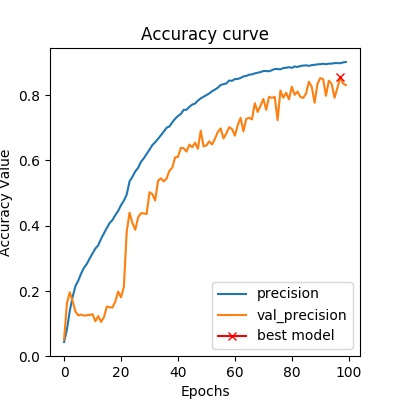
 

Second Fold – Dice Coefficient Second Fold – Loss Curve  

Second Fold – Recall Second Fold – Precision

Third Fold – Dice Coefficient Third Fold – Loss Curve

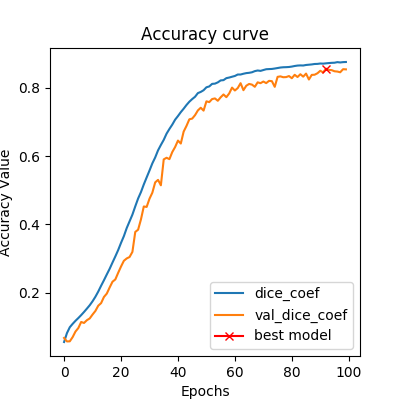
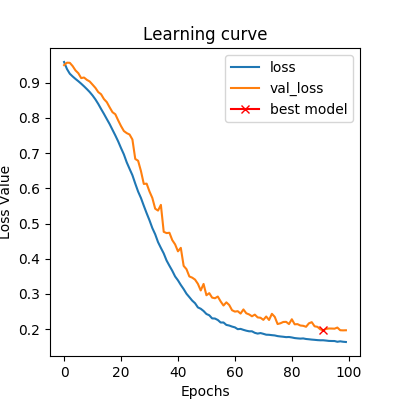
 

Third Fold – Recall Third Fold – Precision

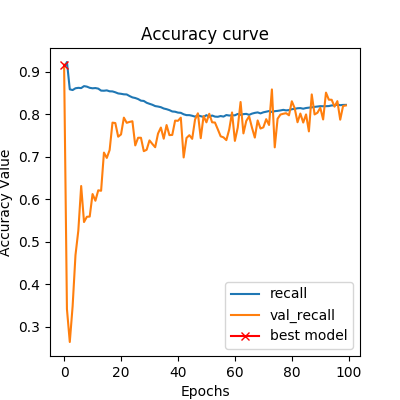
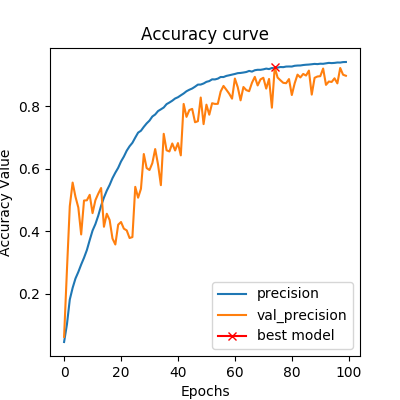
As we can observe from the Accuracy curves (dice coefficient), the perfomance is almost consistant across all folds. There is a very minor difference between the validation accuracies (dice\_coef) obtained after each fold.

In general there are two main ways in which such a problem could be handled. One way consists of increasing the amount of data (if possible) to see if this can help to generalize more. Otherwise, you could also shuffle the data that you already had and try a different "fold splitting": this could help if the problem is not really the amount of data itself, but rather the choice of some training sets that are not "representative" enough.

Task 2

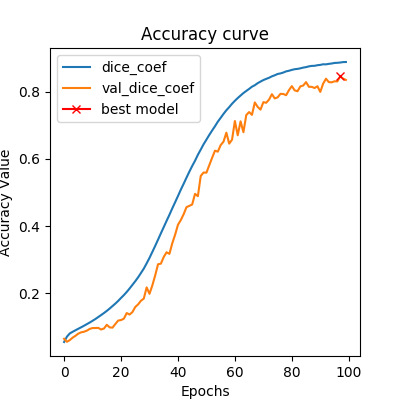
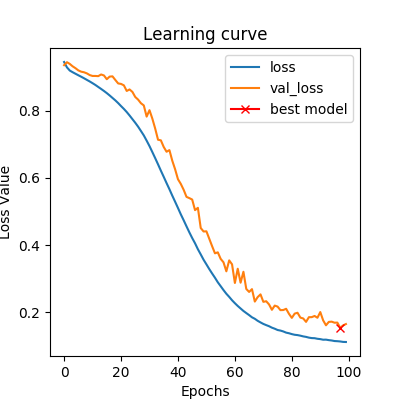
 

Dice Coefficient Loss Curve

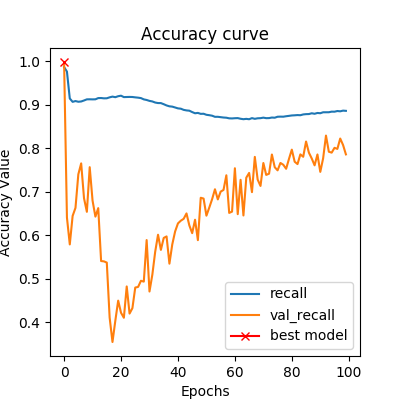
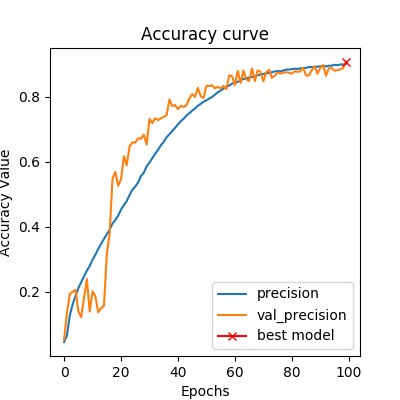
 

Recall Precision

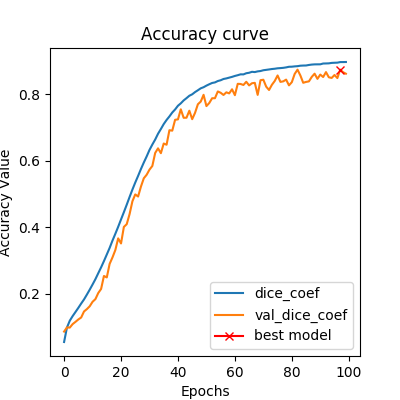
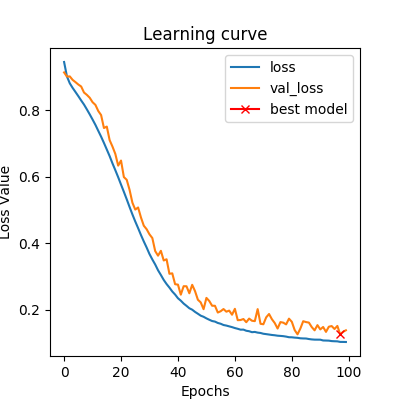
Task 3

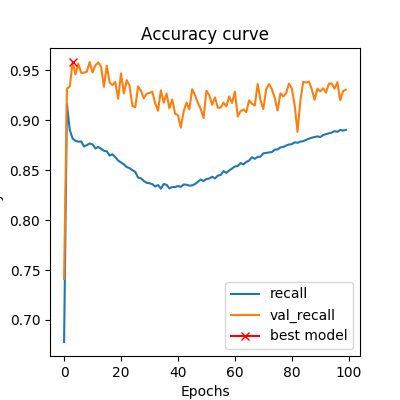
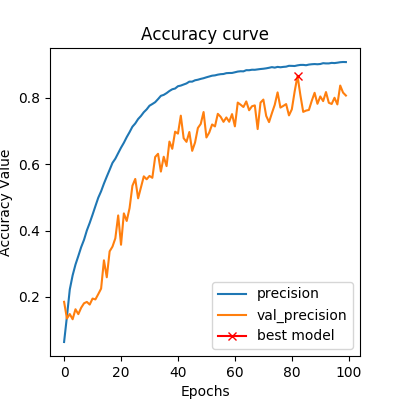
Step 0 -First Fold - Dice Coefficient Step 0- First Fold - Loss Curve

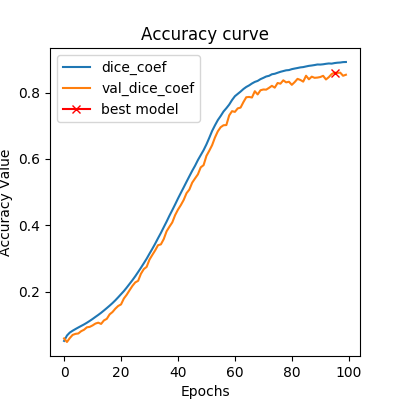
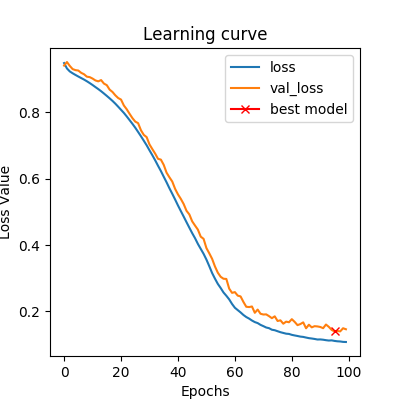
Step 0 -First Fold - Recall Step 0- First Fold – Precision

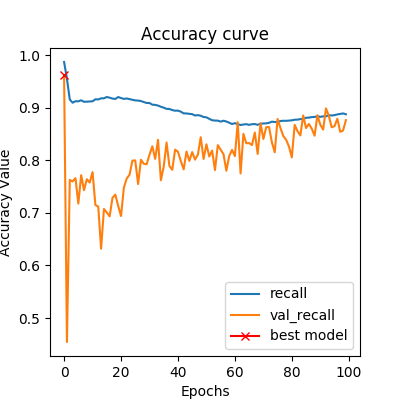
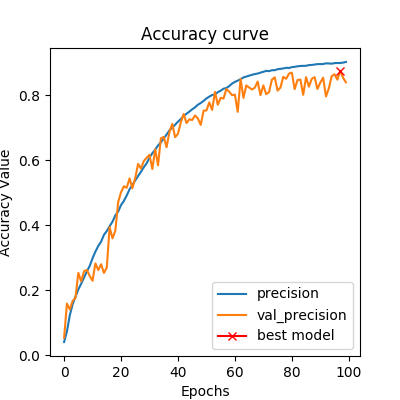
Step 0 -Second Fold - Dice Coefficient Step 0- Second Fold - Loss Curve

Step 0 -Second Fold - Recall Step 0- Second Fold – Precision

Step 0 -Third Fold - Dice Coefficient Step 0- Third Fold - Loss Curve

Step 0 -Third Fold - Recall Step 0- Third Fold – Precision