Supplementary Materials for Evolved and Transparent Pipelines for Biomedical Image Classification

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1 More Irace details

1.1 Sampling frequency for all parameters

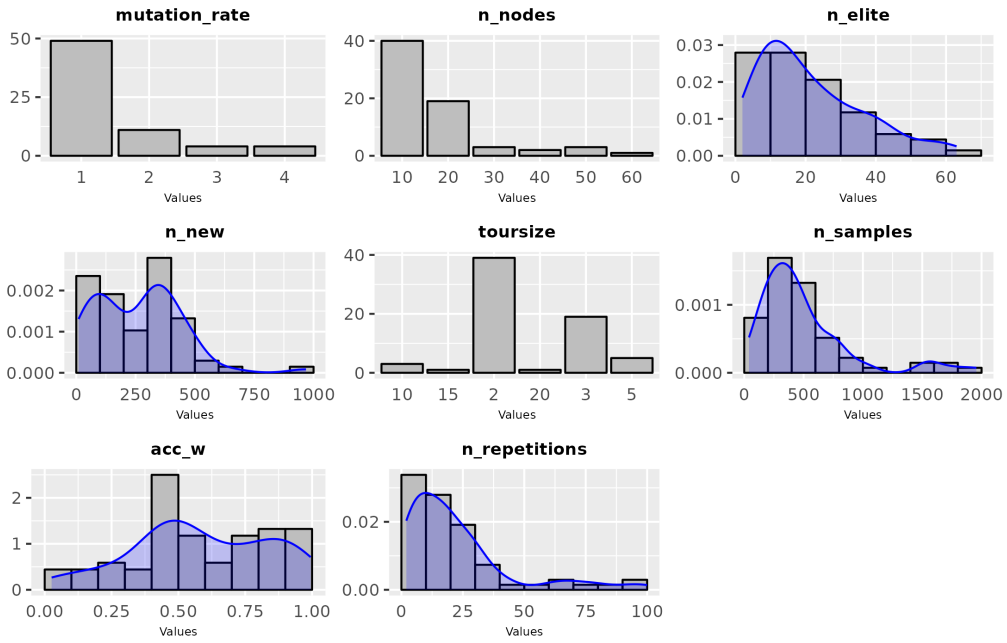

Figure 1: Distribution of sampling frequency for each parameter over the racing procedure.

1.2 Sampling frequency for ρ

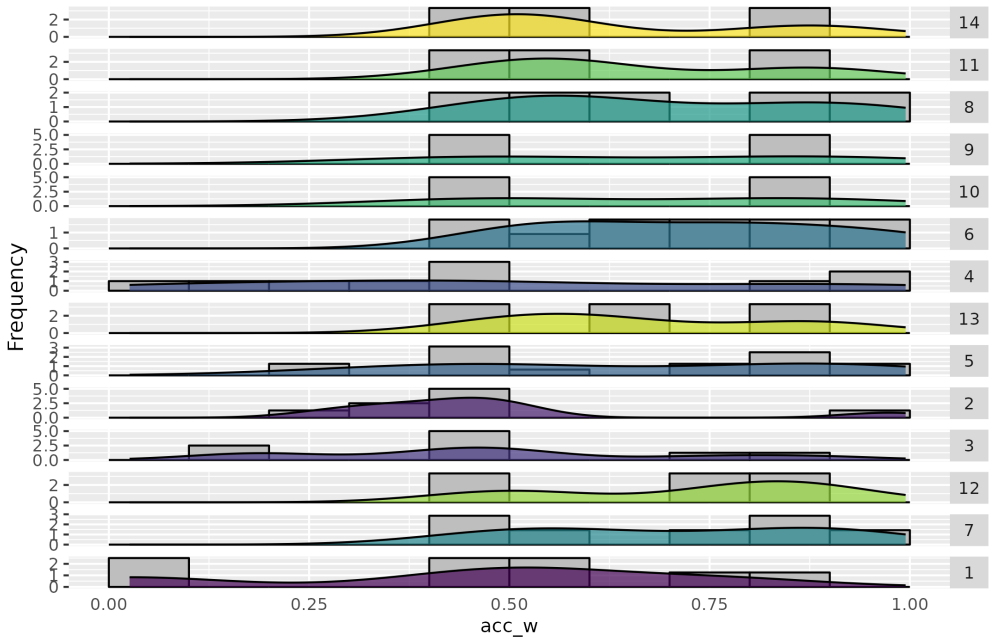

Figure 2: Sampling frequency across Irace iterations for ρ : Accuracy weight in loss

1.3 Sampling frequency for μ

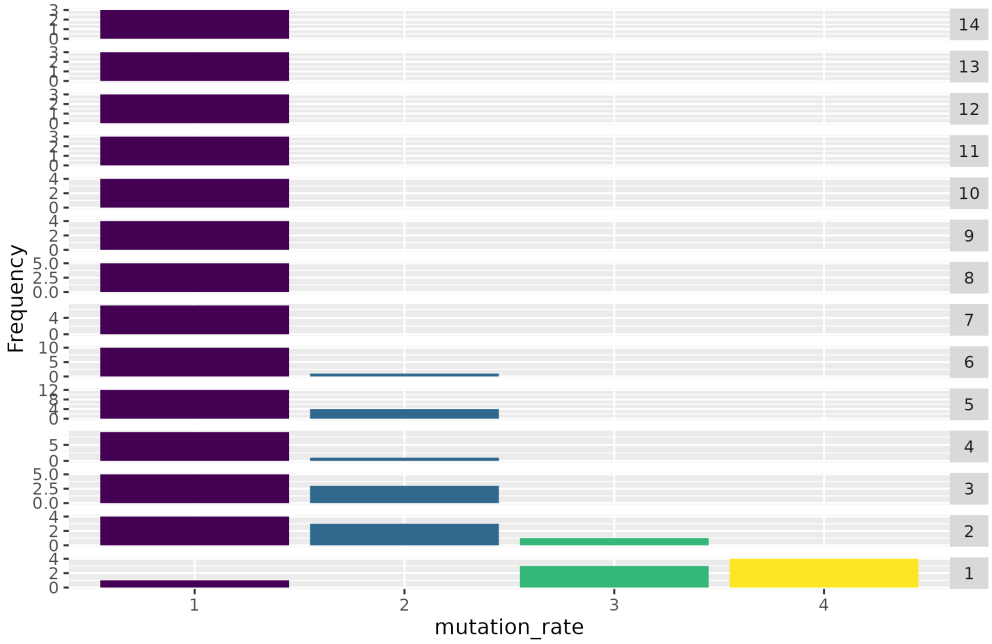

Figure 3: Sampling frequency across Irace iterations for μ : Mutation rate

1.4 Sampling frequency for e

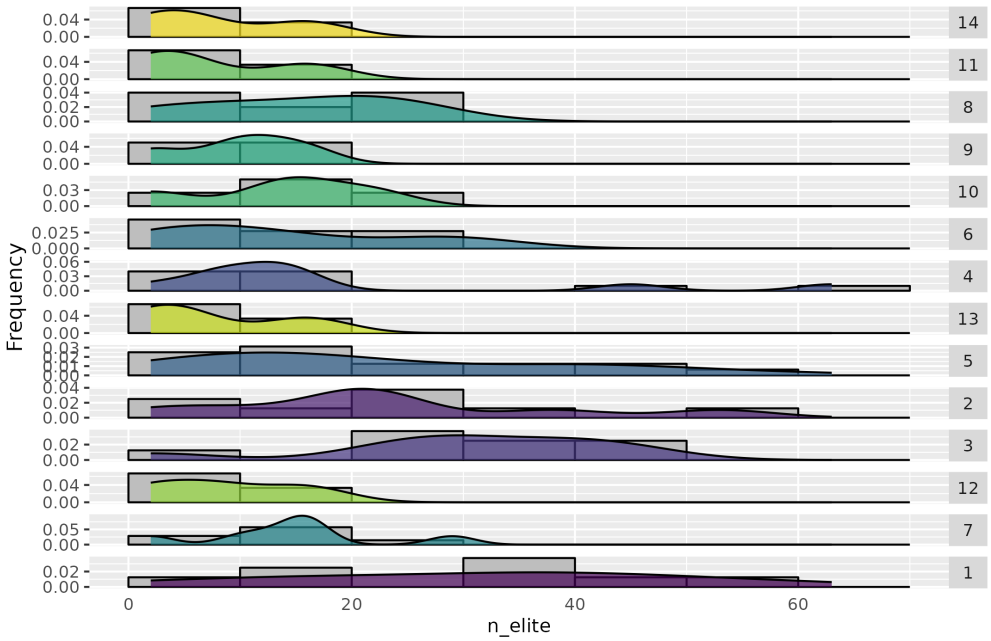

Figure 4: Sampling frequency across Irace iterations for e : Elite pop. size

1.5 Sampling frequency for $news$

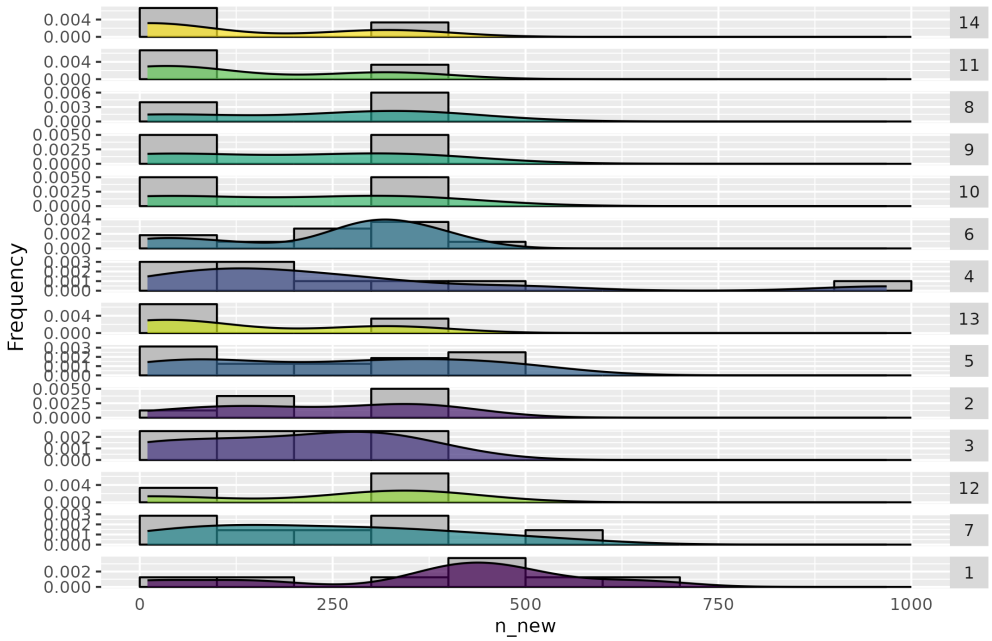

Figure 5: Sampling frequency across Irace iterations for $news$: # of offspring

1.6 Sampling frequency for n

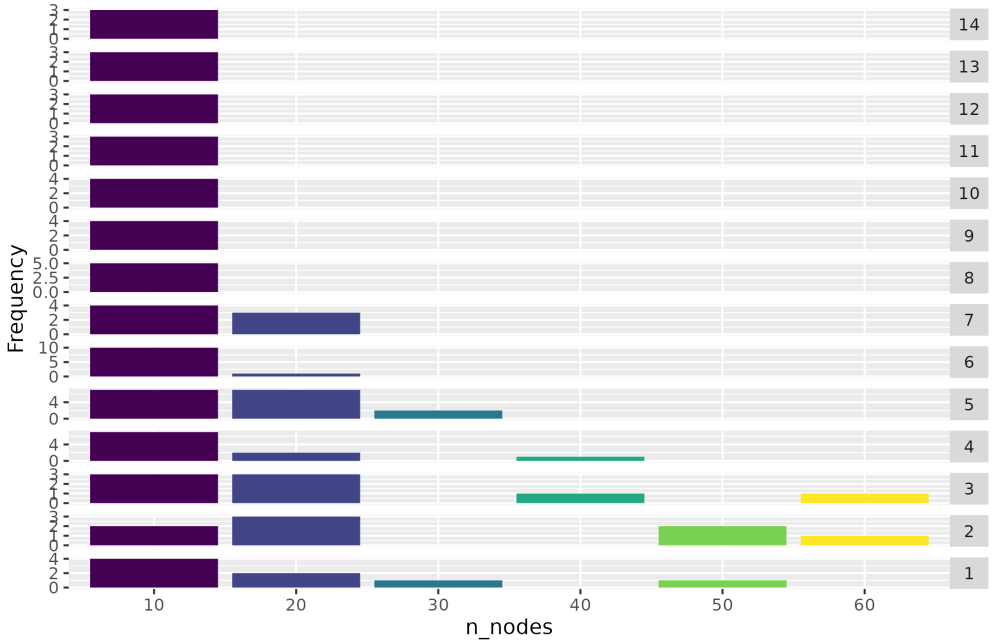

Figure 6: Sampling frequency across Irace iterations for n : # of nodes

1.7 Sampling frequency for $reps$

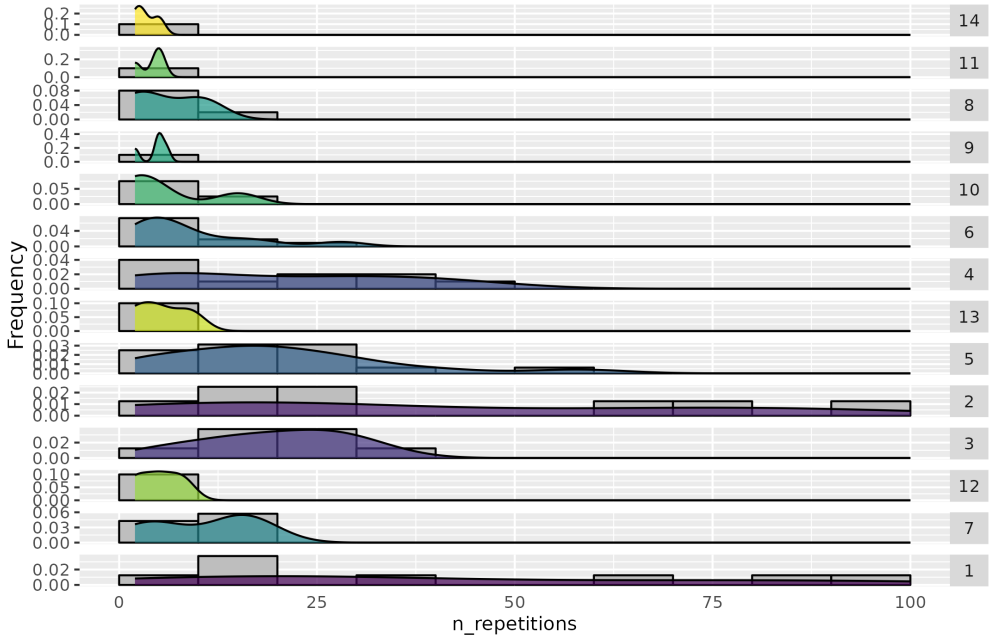

Figure 7: Sampling frequency across Irace iterations for $reps$: # of sampling repetitions per iteration

1.8 Sampling frequency for bs

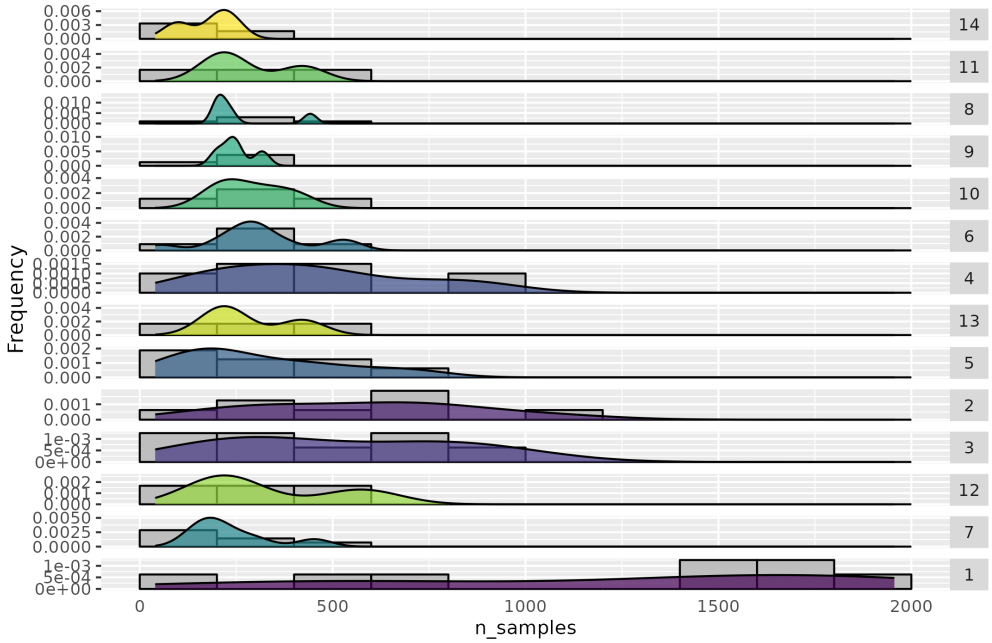

Figure 8: Sampling frequency across Irace iterations for bs : # of images per sample

1.9 Sampling frequency for ts

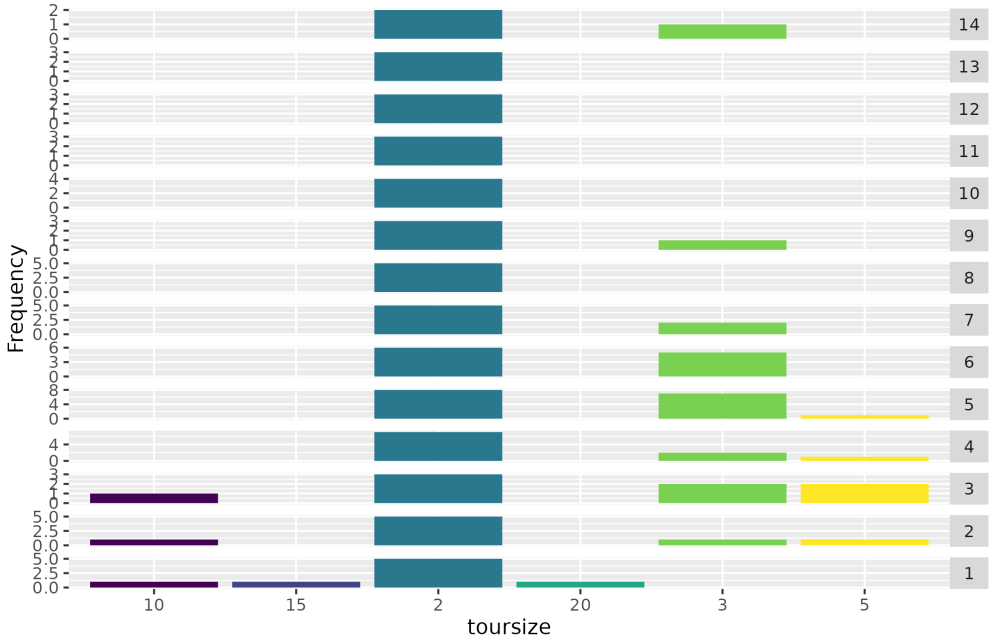

Figure 9: Sampling frequency across Irace iterations for ts : size of the tournament

2 Program Interpretability

Below you will find several examples of malignant and benign patches as well as the predictions made by the top 3 models based on validation accuracy across the 100 MAGE runs.

The model interpreted in the paper correspond to the "Third best model".

2.1 Malignant Example 1

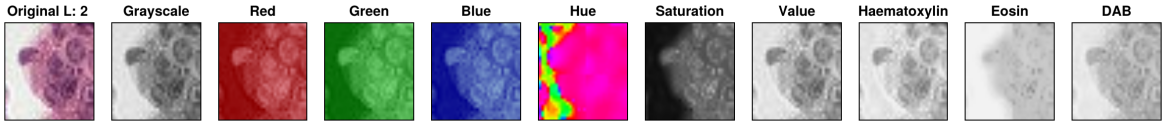

Figure 10: Example 1 of a malignant patch

2.1.1 Best model

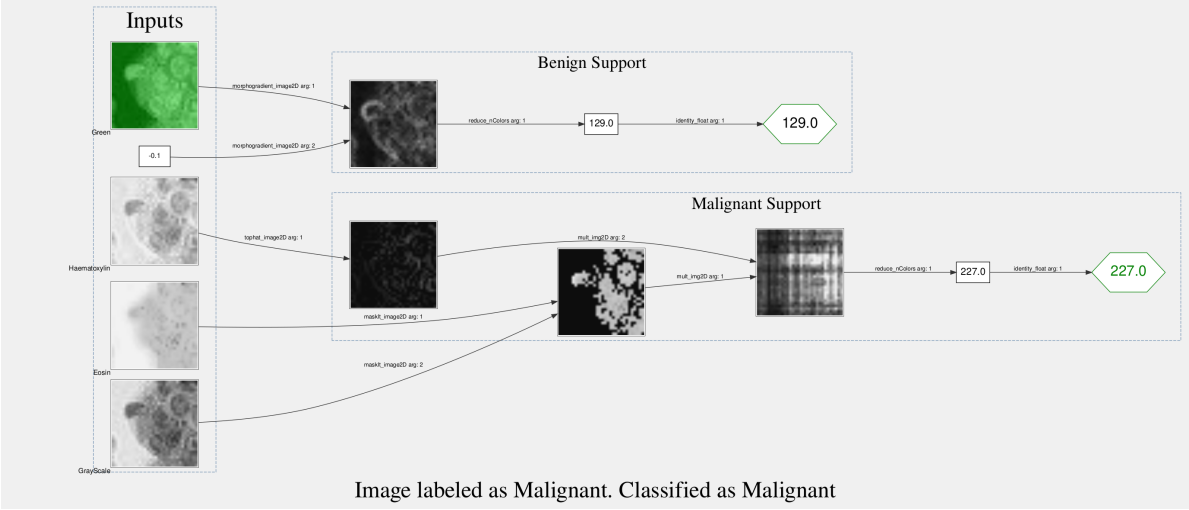

Figure 11: Prediction made by the Best model (TP)

2.1.2 Second best model

Figure 12: Prediction made by the second best model (FN)

2.1.3 Third best model

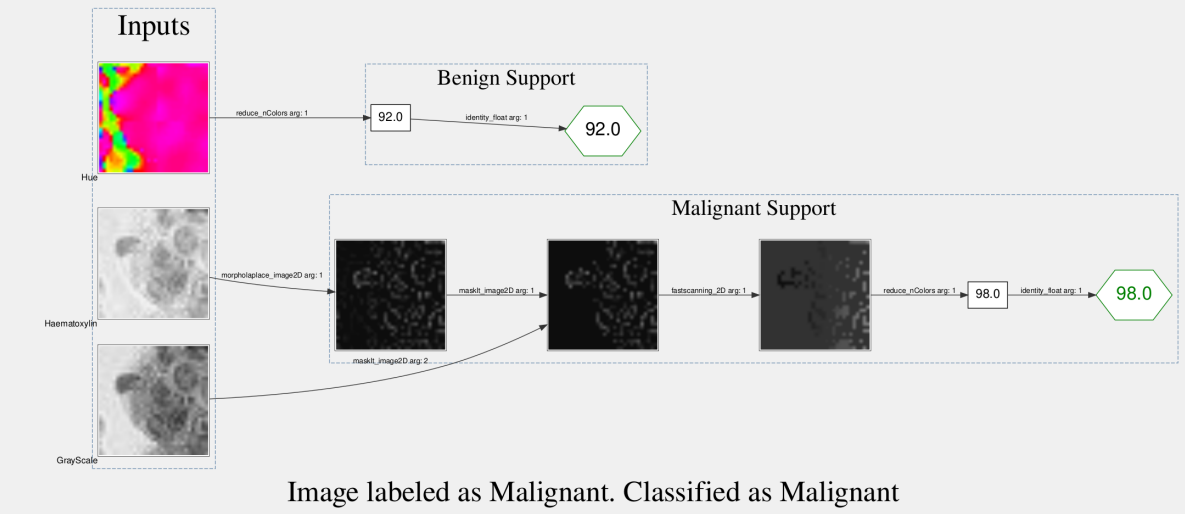

Figure 13: Prediction made by the third best model (TP)

2.2 Malignant Example 2

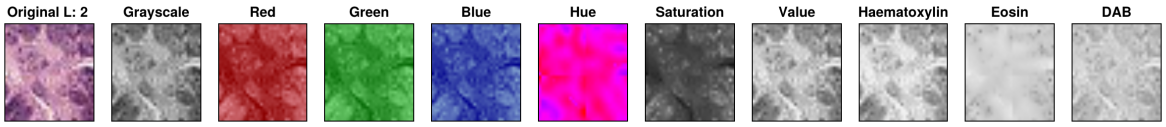

Figure 14: Example 2 of a malignant patch

2.2.1 Best model

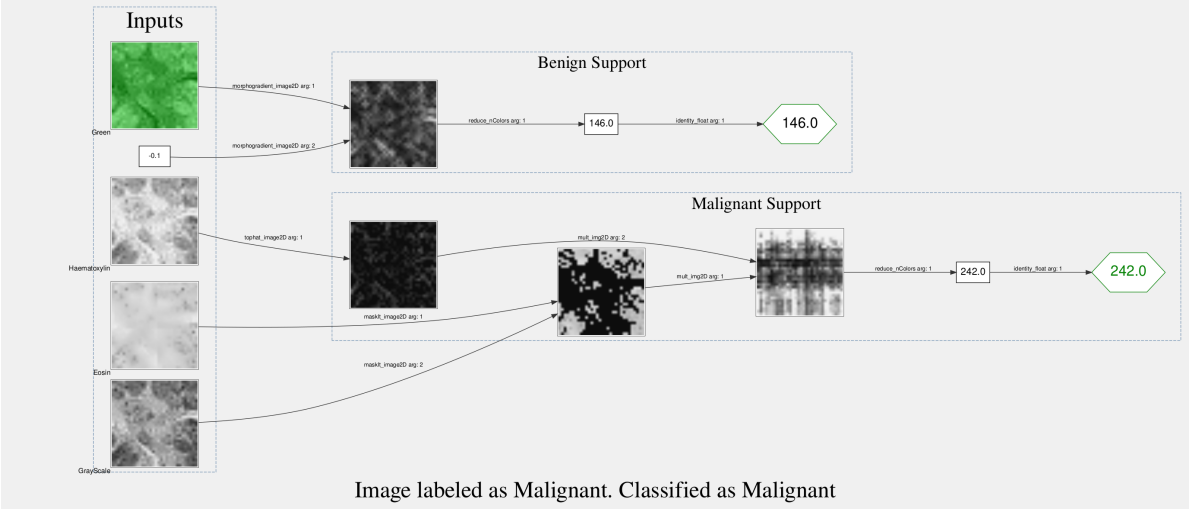

Figure 15: Prediction made by the best model (TP)

2.2.2 Second best model

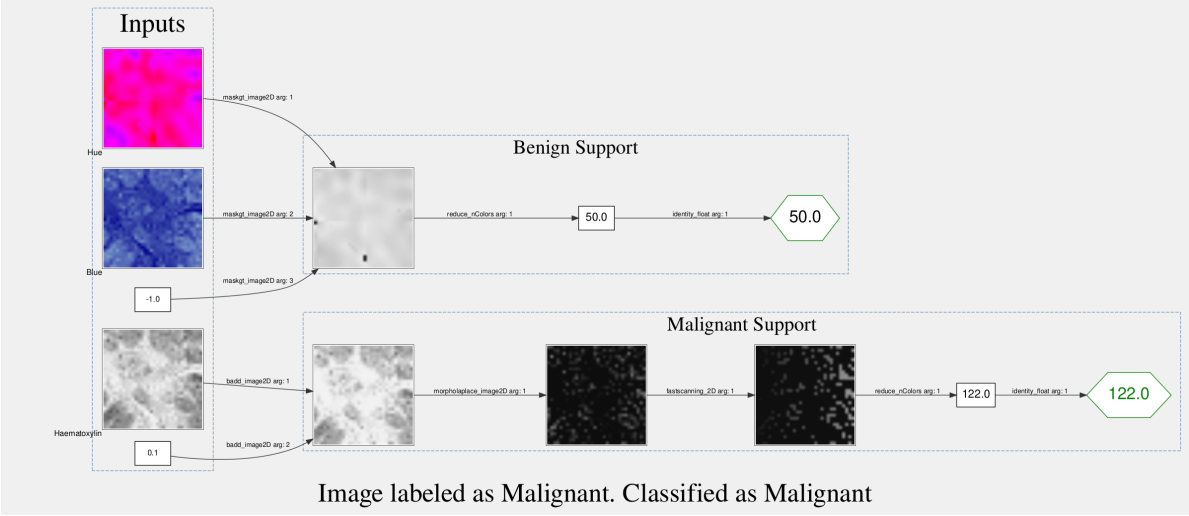

Figure 16: Prediction made by the second best model (TP)

2.2.3 Third best model

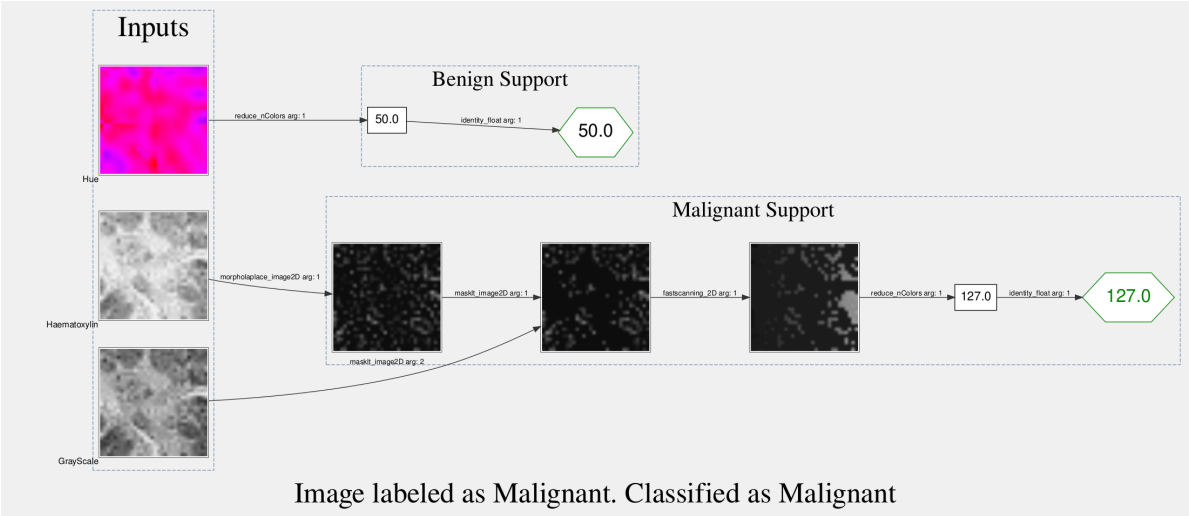

Figure 17: Prediction made by the third best model (TP)

2.3 Malignant Example 3

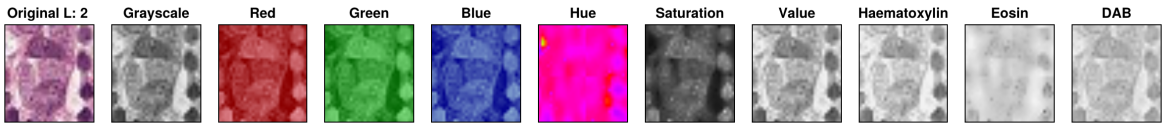

Figure 18: Example 3 of a malignant patch

2.3.1 Best model

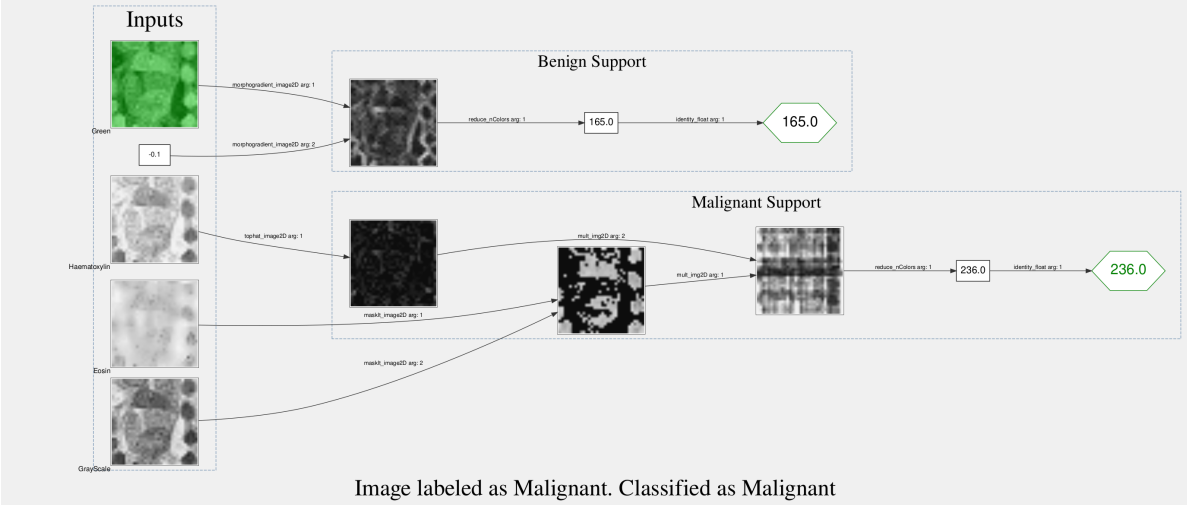

Figure 19: Prediction made by the best model (TP)

2.3.2 Second best model

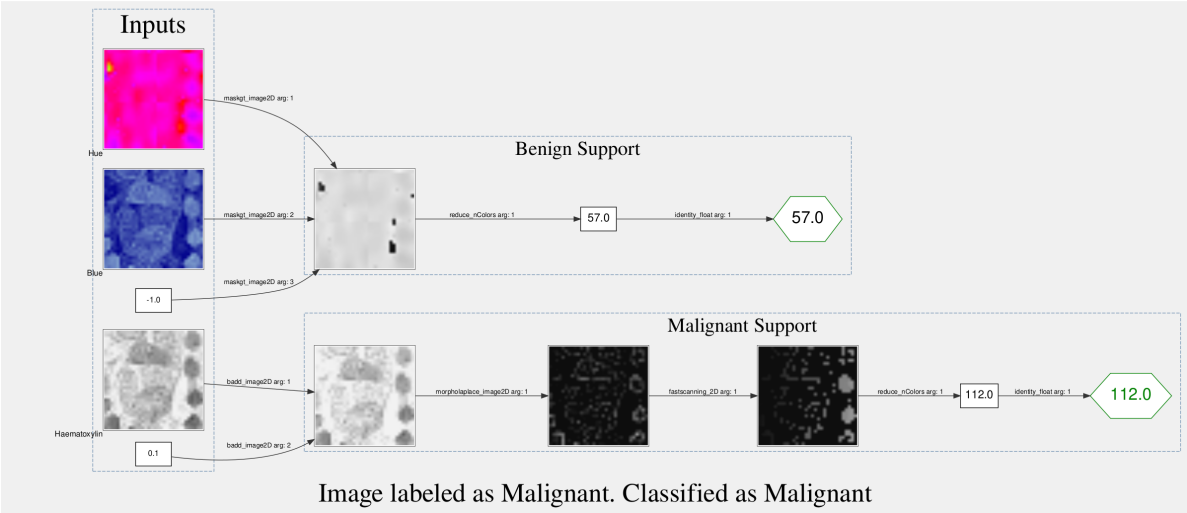

Figure 20: Prediction made by the second best model (TP)

2.3.3 Third best model

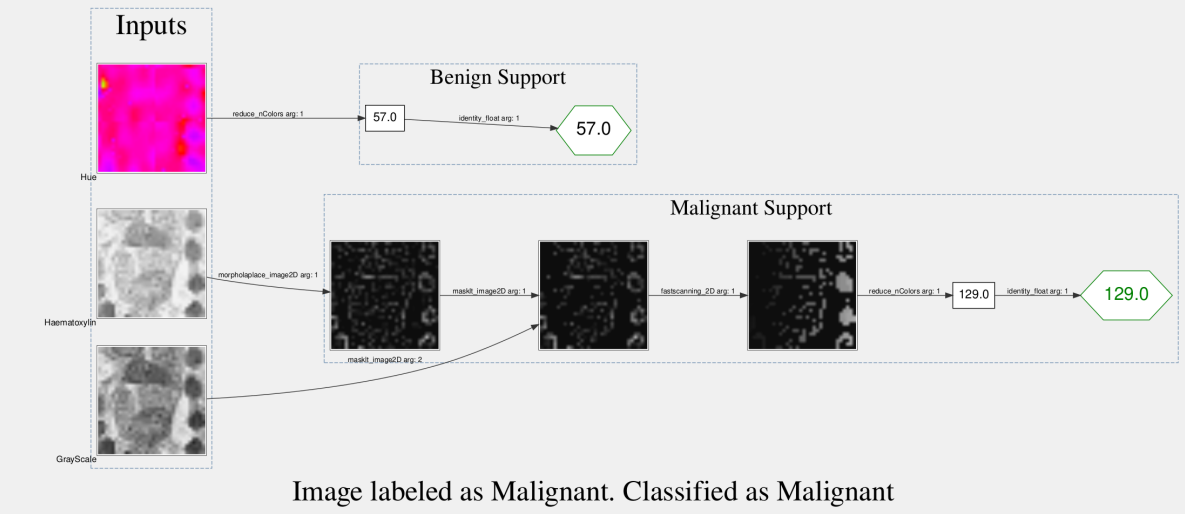

Figure 21: Prediction made by the third best model (TP)

2.4 Benign Example 1

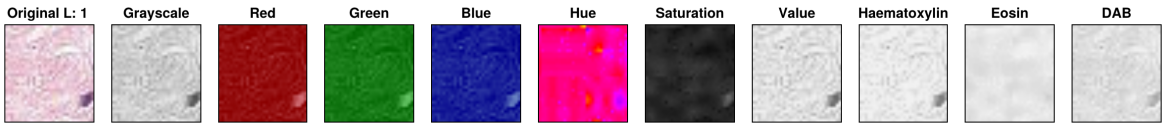

Figure 22: Example 1 of a benign patch

2.4.1 Best model

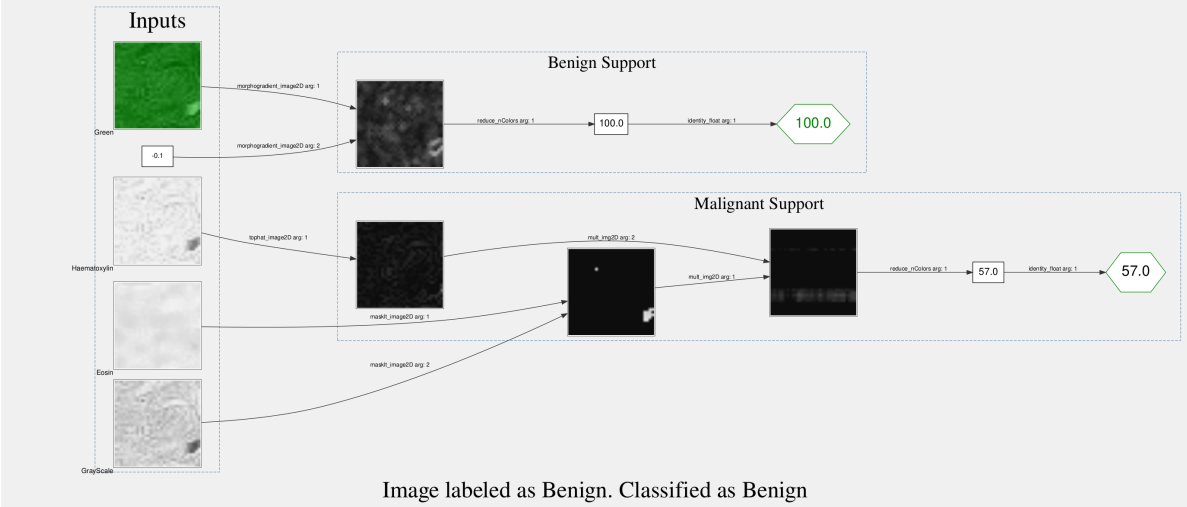

Figure 23: Prediction made by the best model (TN)

2.4.2 Second best model

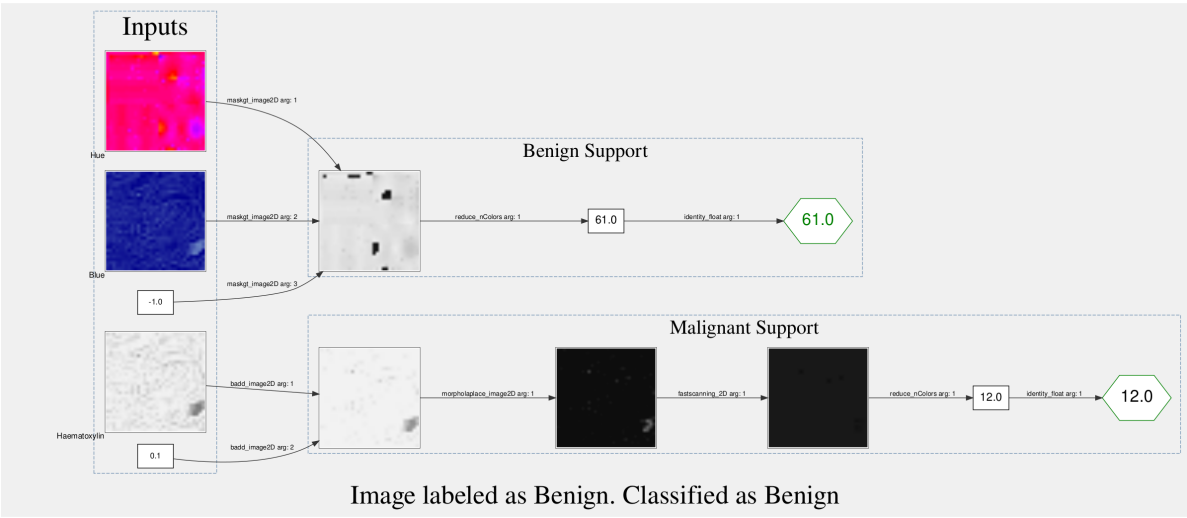

Figure 24: Prediction made by the second best model (TN)

2.4.3 Third best model

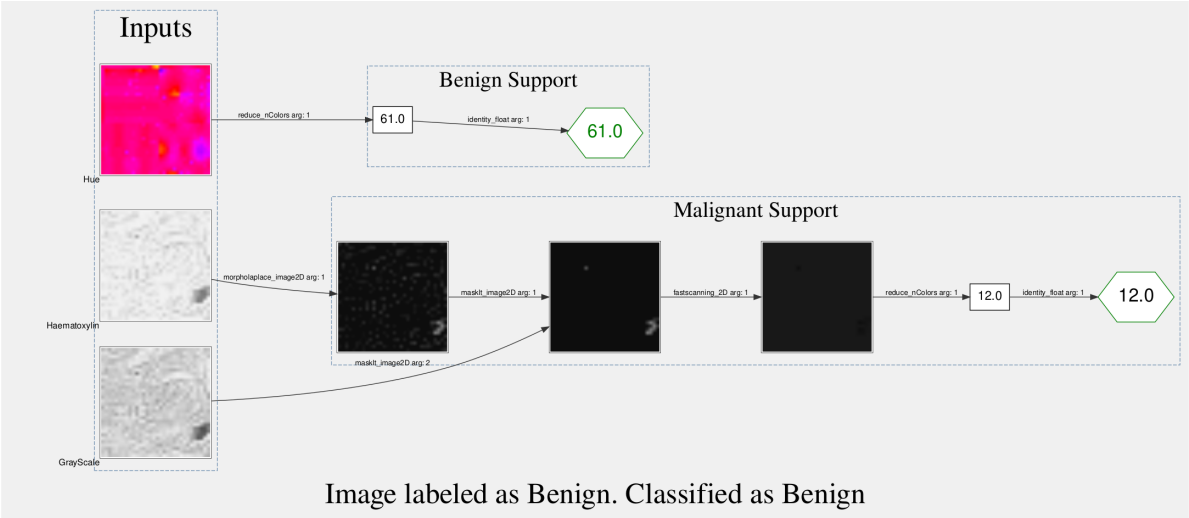

Figure 25: Prediction made by the third best model (TN)

2.5 Benign Example 2

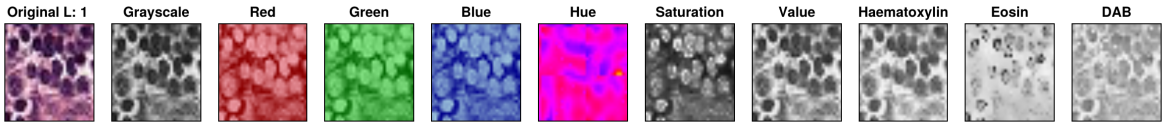

Figure 26: Example 2 of a benign patch

2.5.1 Best model

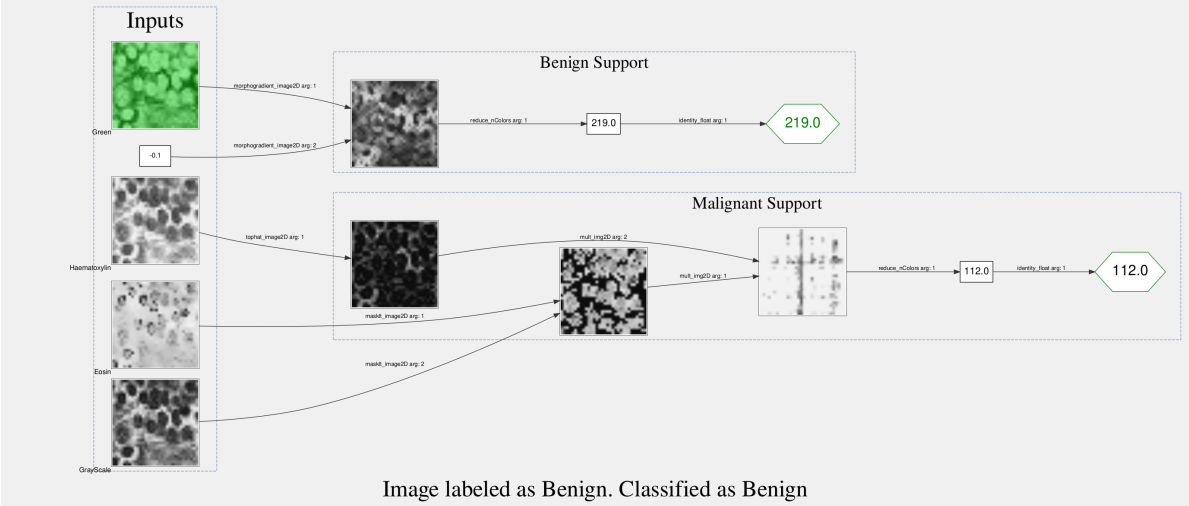

Figure 27: Prediction made by the best model (TN)

2.5.2 Second best model

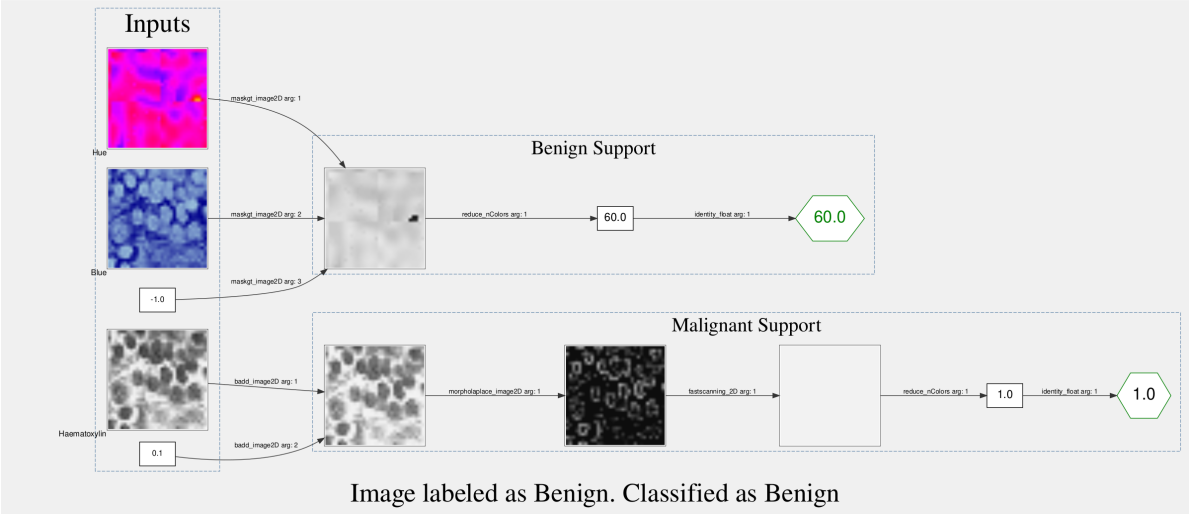

Figure 28: Prediction made by the second best model (TN)

2.5.3 Third best model

This is an example of the overflowing by "fastscanning", explained in the paper, because of previous numerous nuclei edges detected. Hence, the support for malignancy is lower than the

support for benign.

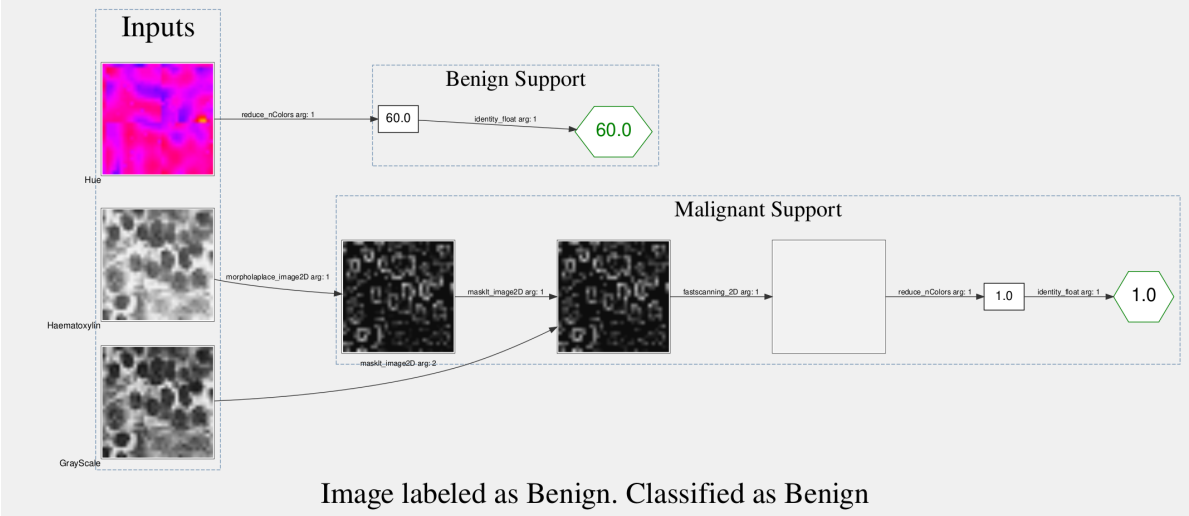

Figure 29: Prediction made by the third best model (TN)

2.6 Benign Example 3

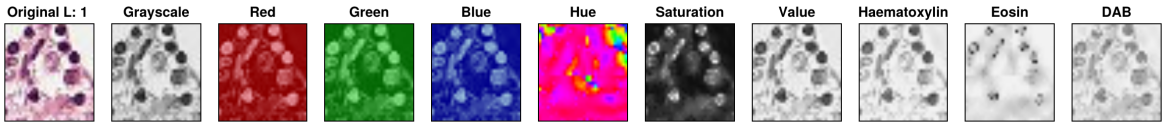

Figure 30: Example 3 of a benign patch

In this case all models produced wrong predictions.

2.6.1 Best model

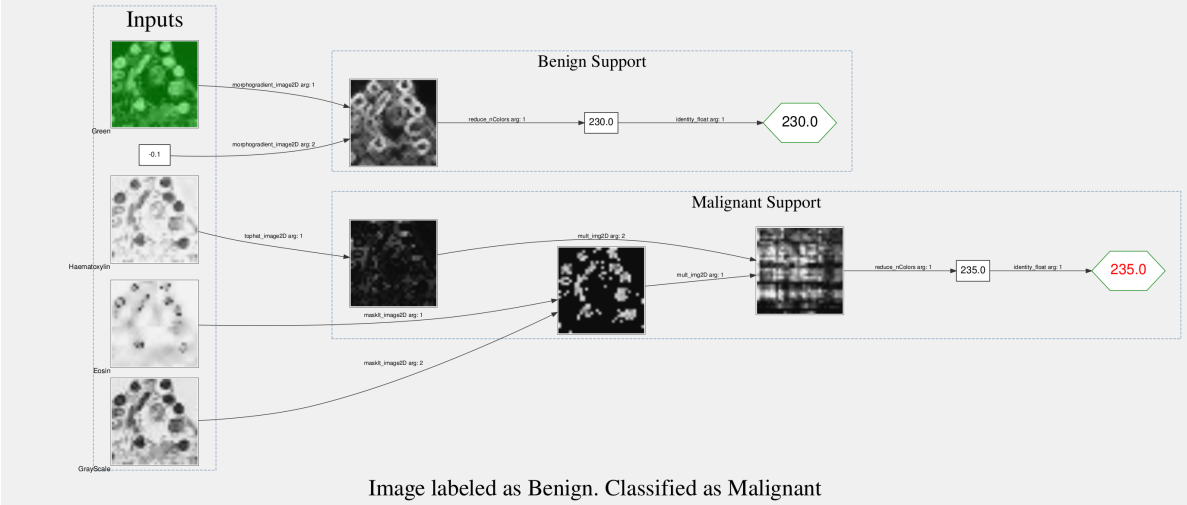

Figure 31: Prediction made by the best model (FP)

2.6.2 Second best model

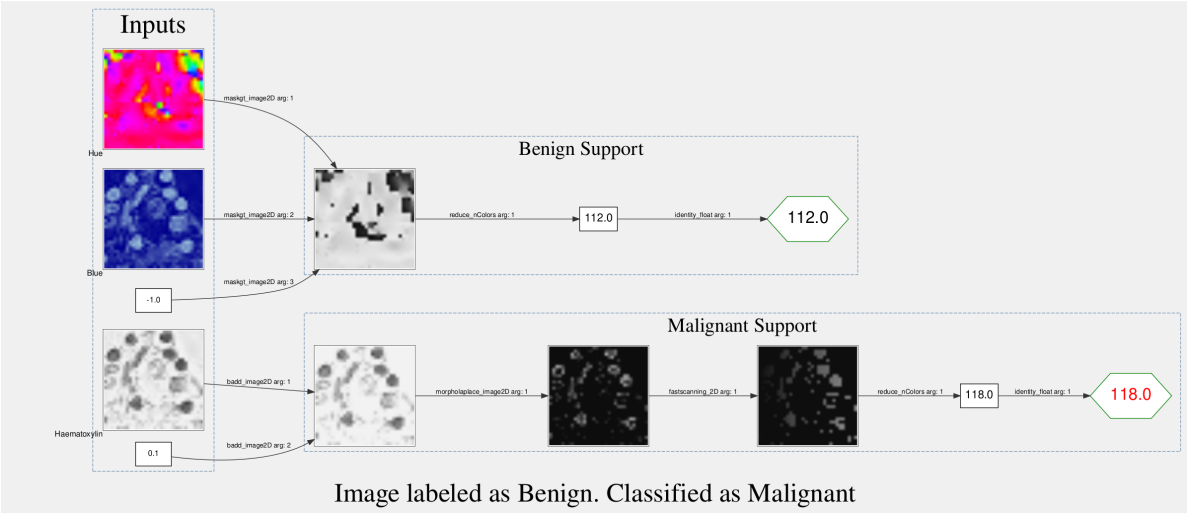

Figure 32: Prediction made by the second best model (FP)

2.6.3 Third best model

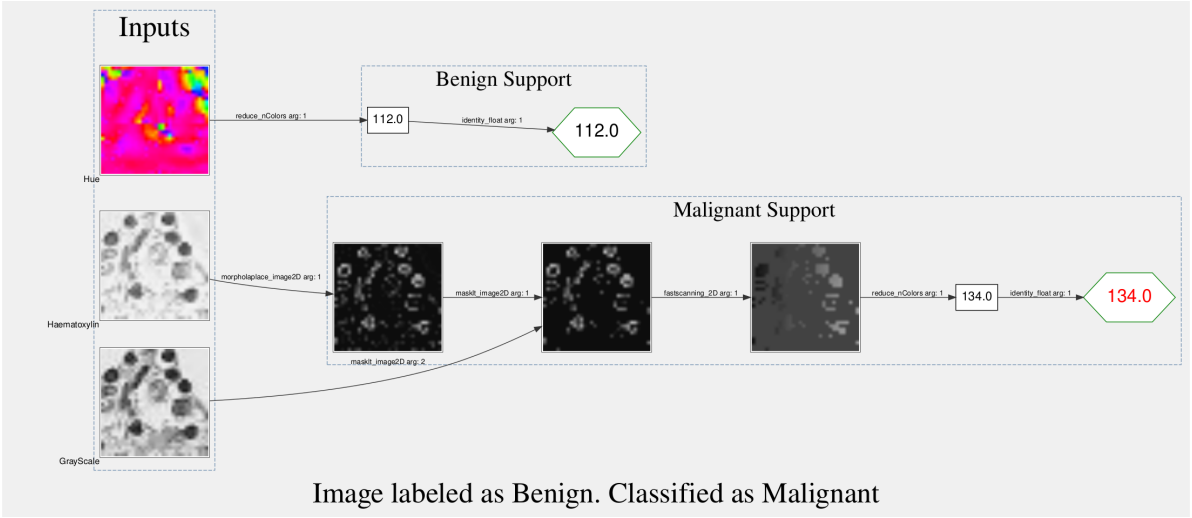

Figure 33: Prediction made by the third best model (FP)