MODEL-ASSISTED INTERACTIVE DESIGN
Once a user triggers an interaction with the bar graph of importance scores, we automatically generate \( N = 100 \) new design variants (in the background). In a given variant, every graphical element is adjusted with a probability of \( p = 0.5 \) via positional offsets and scaling factors. We evaluate each design variant by running our importance prediction model and measuring the mean-squared-error (MSE) between the predicted and target importance scores. We add penalty terms for overlapping elements. We keep the top 25 of designs with the lowest MSE. We generate a new set of 75 designs by “genetic crossover”: combining positional offsets and scaling factors for individual design elements across pairs of designs from the top 25, to produce a new “population” of 100 designs. The idea of crossover here is to allow for the effective combination of positive aspects from different variants. We repeat this genetic design breeding process for 20 epochs. After every epoch, we update the canvas with the best design so far.

MODEL-ASSISTED DESIGN REFLOW
All 17 designs and their corresponding reflow variants from our user studies are shown in Figures 1-5.

ADDITIONAL TRAINING DETAILS
We train with KL and CC losses, with coefficients of 10 and -3. A binary cross-entropy loss with a weight of 5 is used for the classification submodule. We obtained these coefficients through grid search and 3-split cross validation, testing values of 1, 3, 5, 10, 15 for each loss (negative values for CC). The learning rate and dropout rate was similarly defined, testing 5 values with 3-split cross validation. The definition of the architectural modules follows insights from previous literature, including image classification [3, 4] and image segmentation work [1, 2].

REFERENCES

Note: This is the author’s preprint copy. This is not the official ACM published version.
Figure 3.
Figure 4.
Figure 5.

Avg. rank (baseline): 1.67  Avg. rank (prior art): 2.00  Avg. rank (UMSI): 2.33