Online Appendix for: Disentangling Suboptimal Updating: Structure, Sequencing, and Complexity

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Contents

1 Instructions

1.1 Common Instructions

The instructions shown in this subsection were seen by participants regardless of their treatment. These initial instructions aimed to familiarize participants with the mechanism through which they submitted their posteriors.

Figure 1: Initial Instructions I

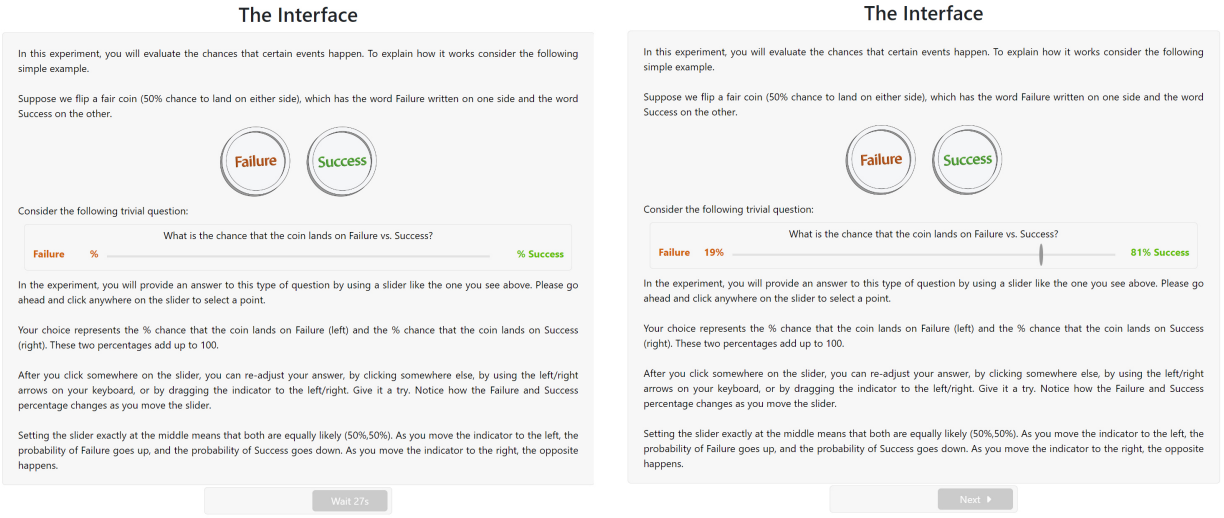
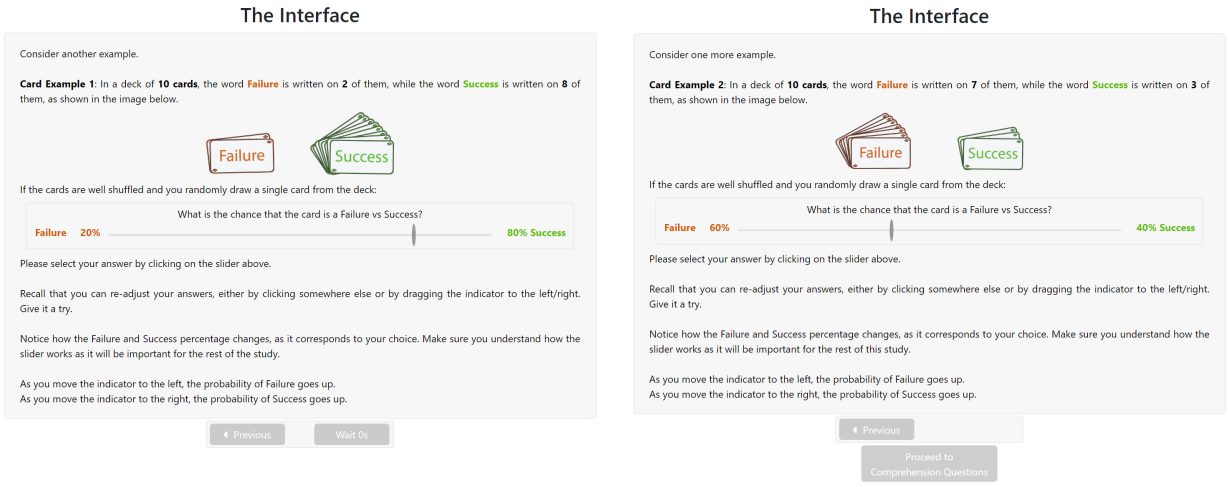


Figure 1 shows the initial page presented to the participants. To ensure that participants spend time internalizing the information, the *Next* button was made available only after a countdown of 30 seconds.[1] On this, and every other page, there is initially no indicator on the slider via which participants submit their probabilities. We made this decision to prevent participants from being anchored. The indicator and accompanying probabilities show up only after participants click somewhere on the slider. Compare the left (before clicking) and right (after clicking) screenshots in Figure 1.

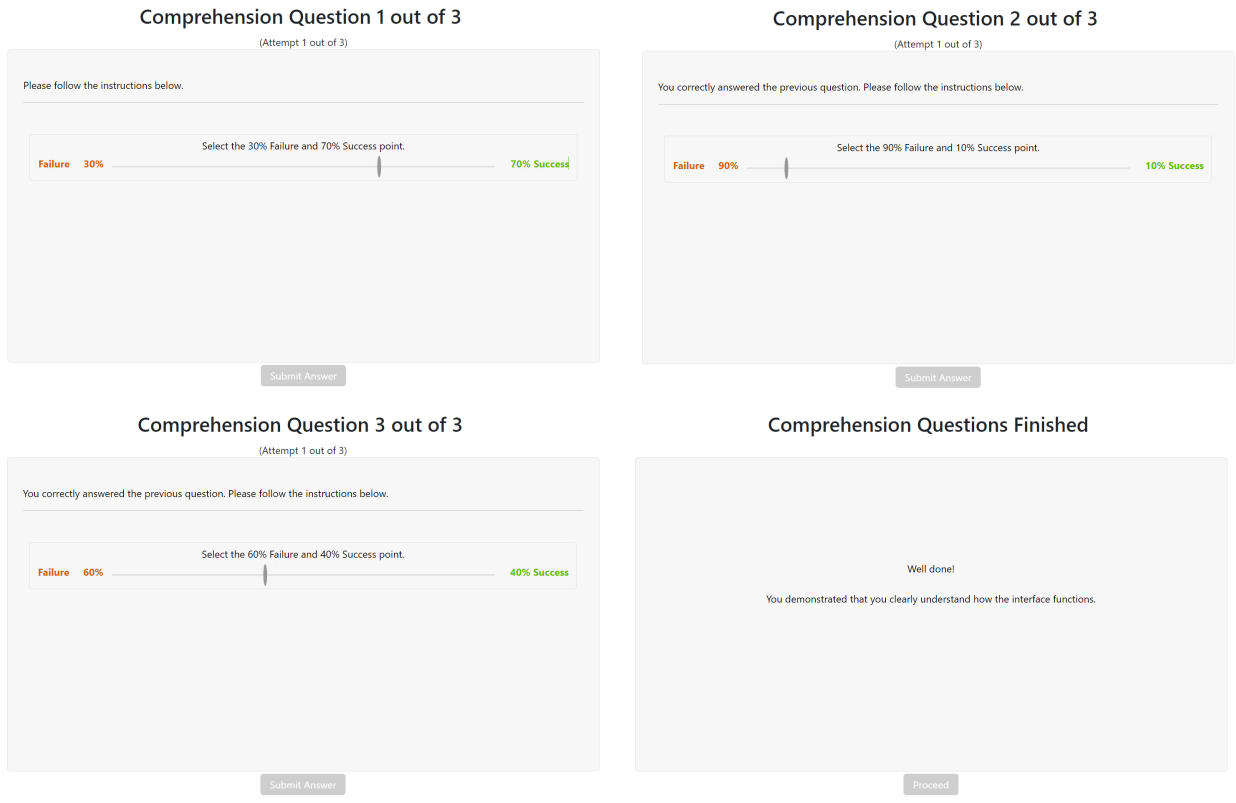
[1] Compare buttons on the bottom of the left and right screenshots shown in Figure 1. The left screenshot is taken 3 seconds after the page was loaded, whereas the right screenshot is taken after at least 30 seconds.

Figure 2: Initial Instructions II



Instructions continue by giving participants two more examples and reminding them how the mechanism works; see Figure 2. After these examples, participants are invited to start a simple comprehension test to ensure they know how to use the slider properly, see Figure 3.

Figure 3: Initial Instructions II

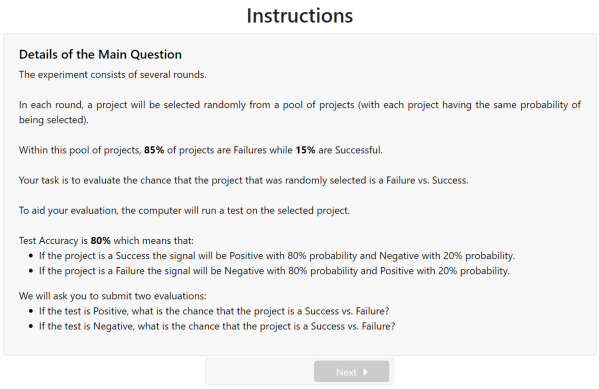


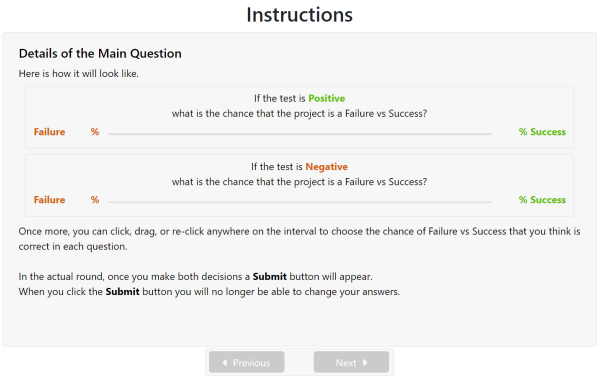
If participants submitted wrong answers more than twice, they were not allowed to

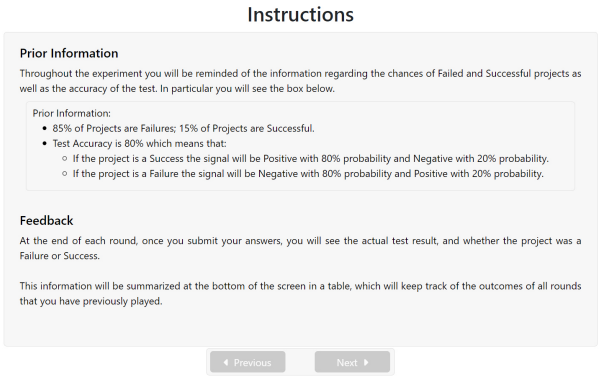
continue the study. Succesful participants continued with treatment-specific instructions.

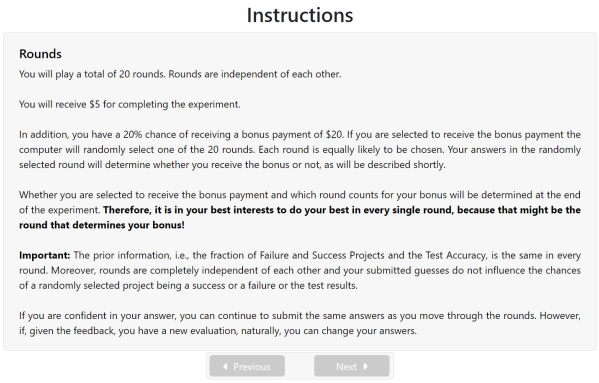
1.2 Baseline Treatment Instructions

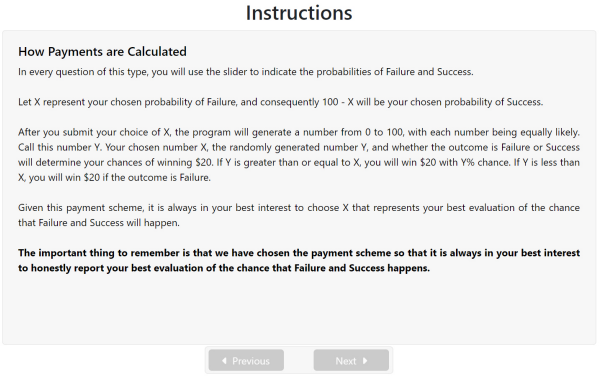
Figure 4: Baseline Treatment Instructions

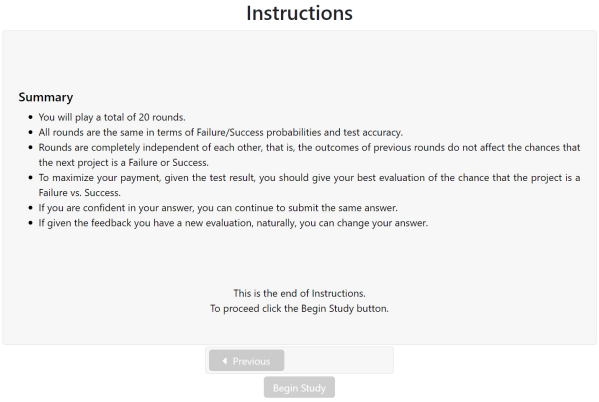






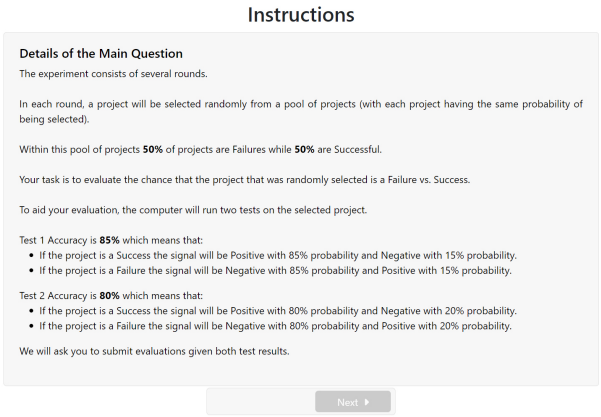


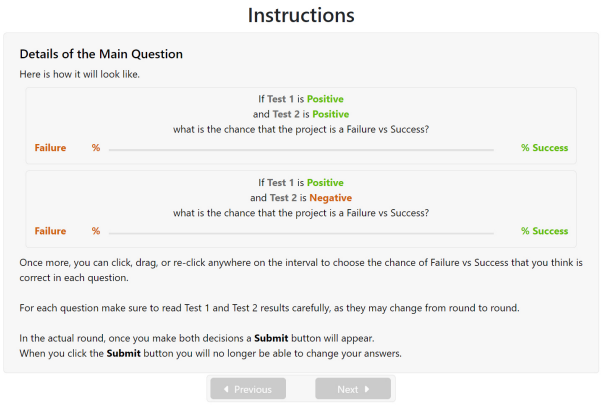


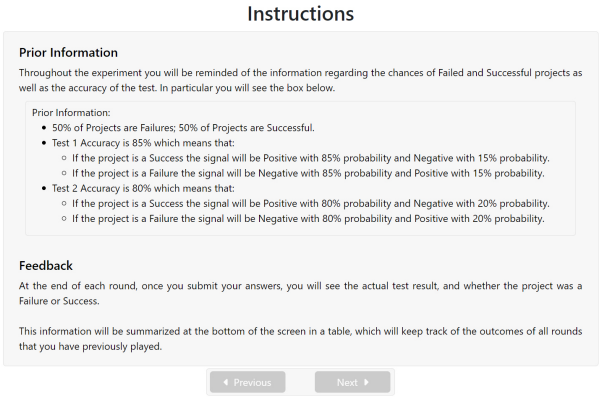


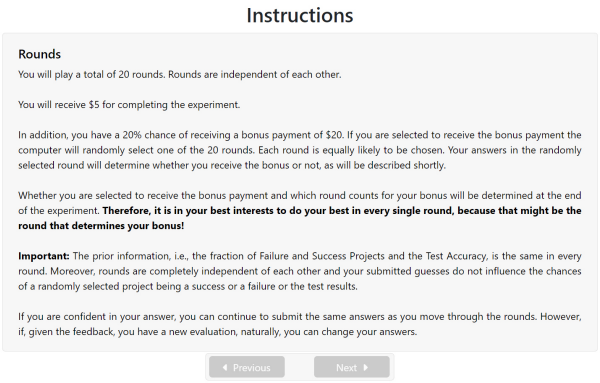
1.3 Simultaneous Treatment Instructions

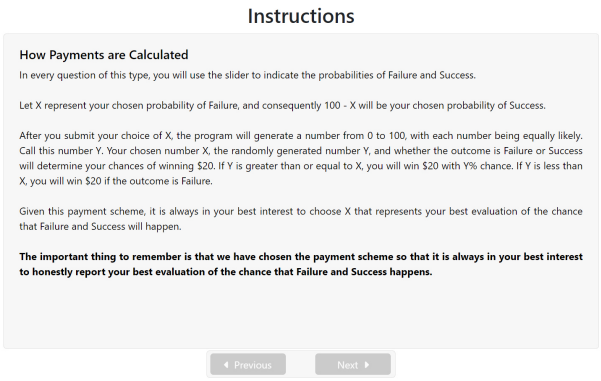
Figure 5: Simultaneous Treatment Instructions

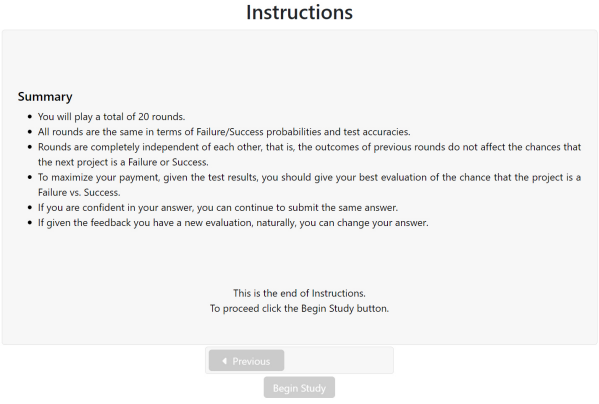






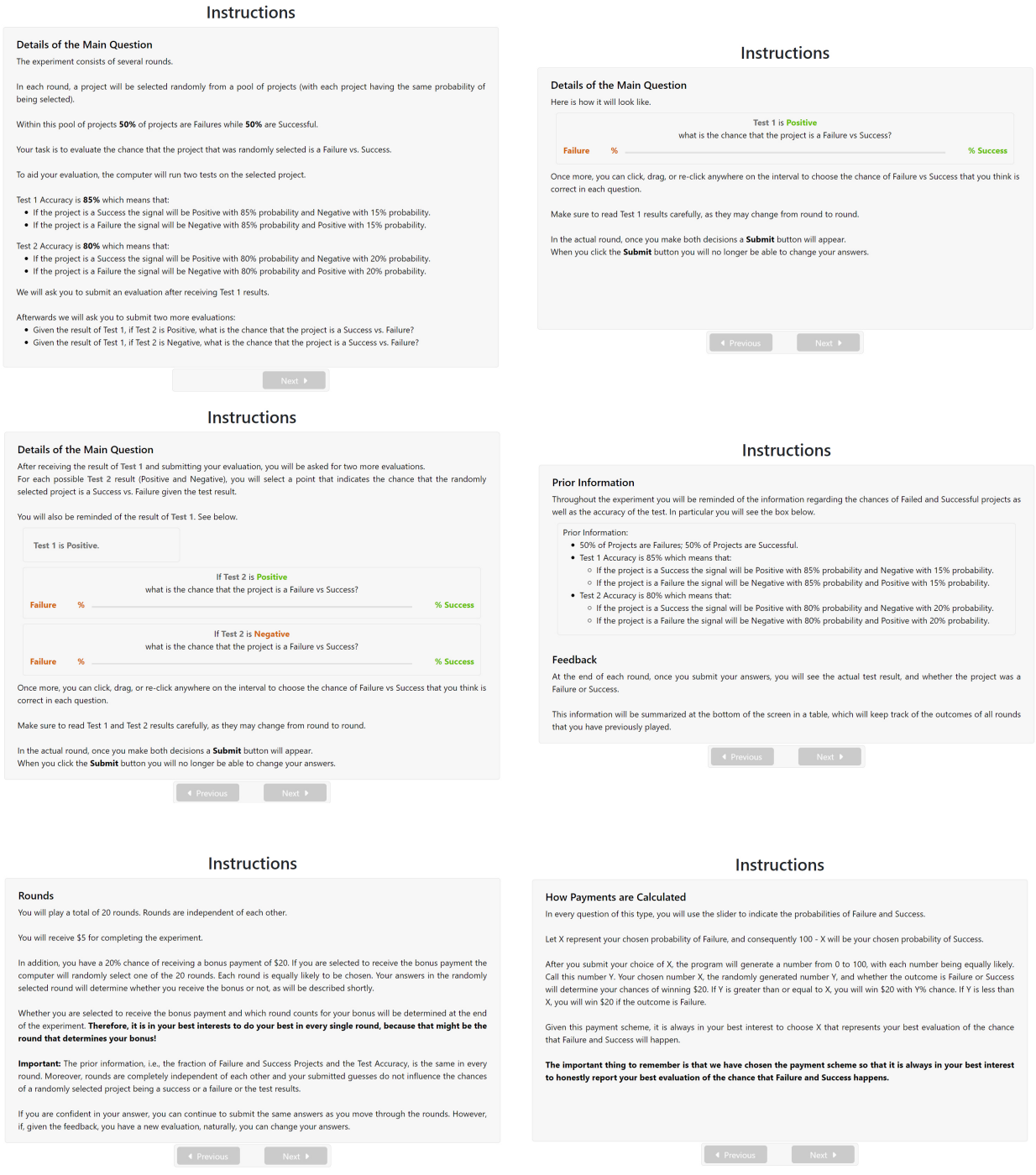






1.4 Sequential Treatment Instructions

Figure 6: Sequential Treatment Instructions

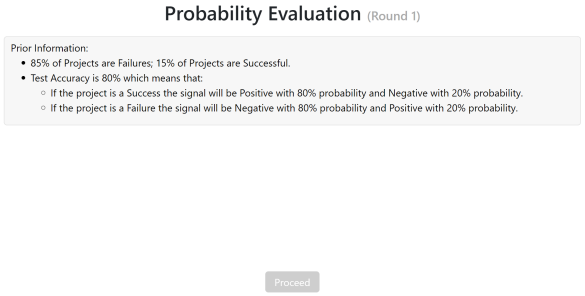


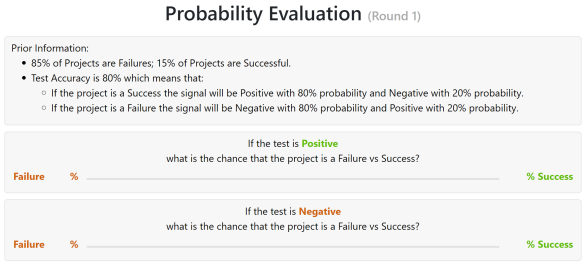
2 Interface

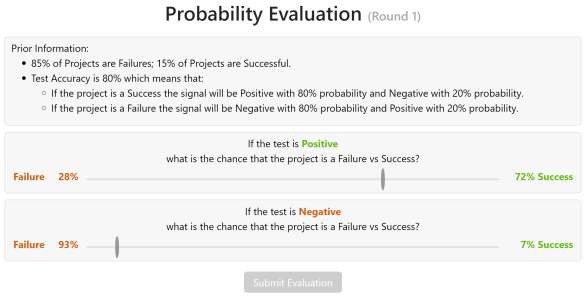
2.1 Baseline Treatment Interface

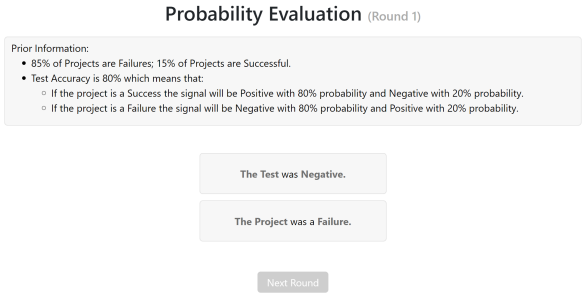
We present various screenshots of the interface presented to participants in the baseline treatments at different stages of the study. We highlight important features below.

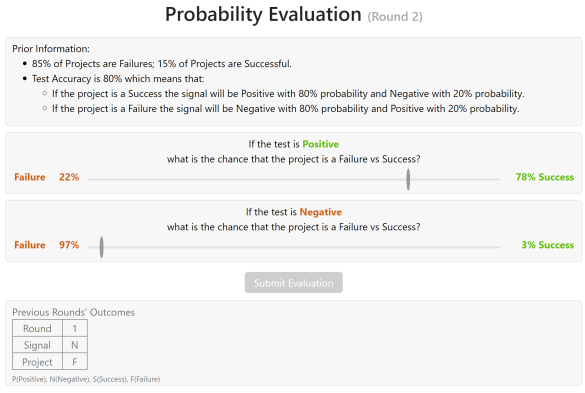
Figure 7: Baseline Treatment Interface

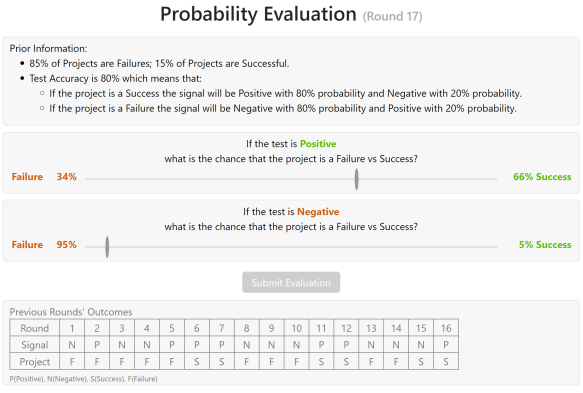










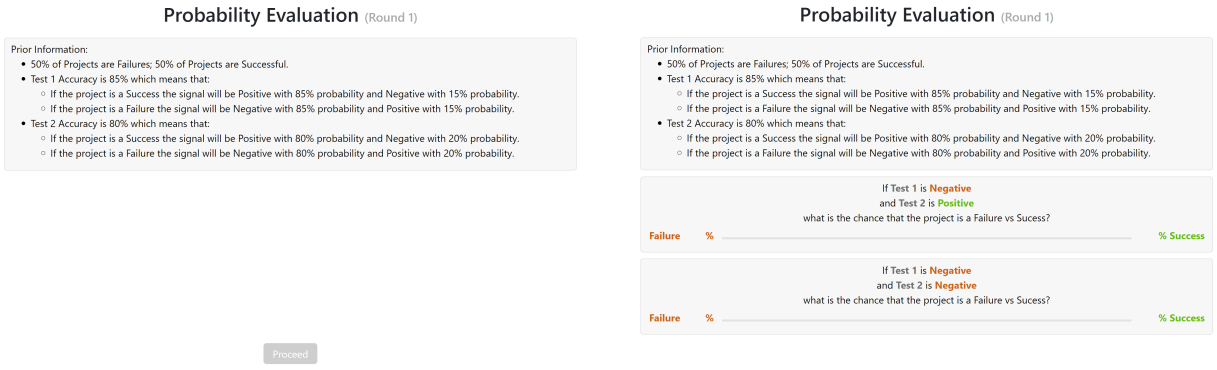


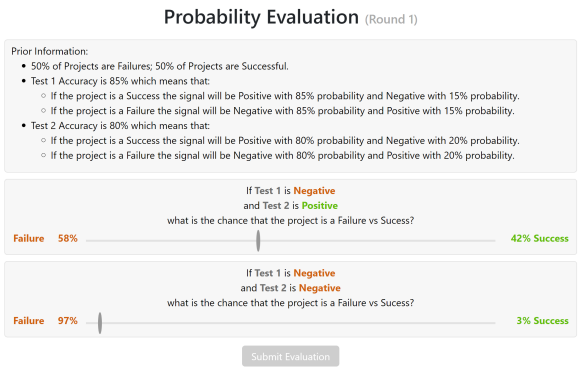
- As clarified in the instructions, throughout the experiment, at the top, participants

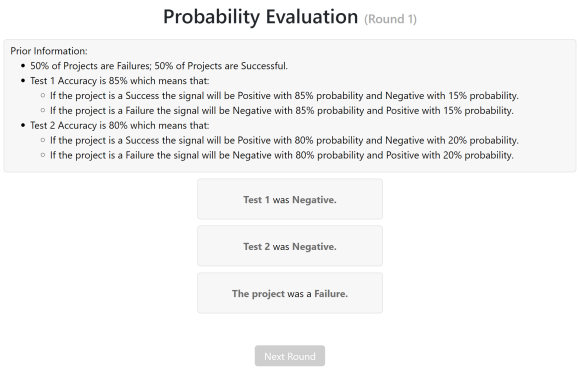
see information regarding the prior probability of successful/failed projects as well as the signal accuracy.

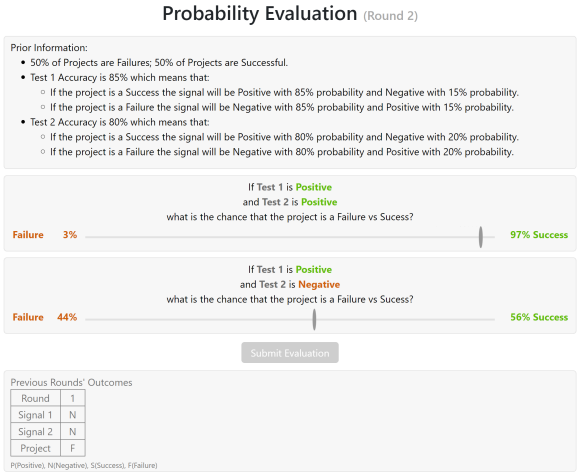
- As clarified in the instructions, when asked *"If the test is Positive/Negative, what is the chance that the project is a Failure vs. Success?"* there is initially no indicator on the slider. We made this decision to prevent participants from being anchored. Only after they click somewhere on the slider does the indicator and the accompanying probabilities show up. For a concrete example, compare the top right and middle left screenshots in Figure 7.
- After clicking the "Submit Evaluation" button, participants were informed about the particular realized value of the signal and whether the project was a Failure or Success. See the middle right screenshot above.
- The realized signals and project outcomes from previous rounds are summarized in a table at the bottom of the interface. See bottom left for an example in Round 2 and bottom right for an example in Round 17. We keep track of past outcomes to shut down possible effects that imperfect recall may have.

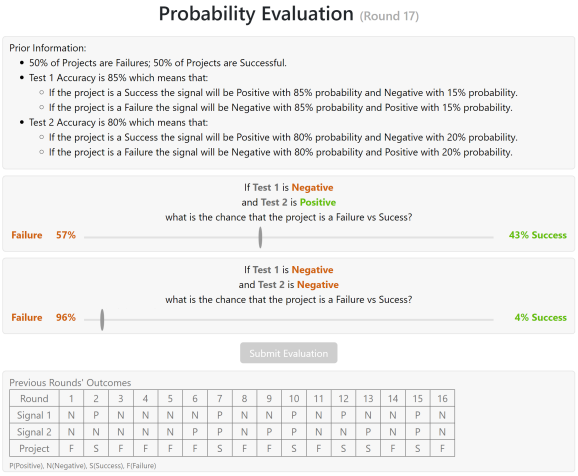
2.2 Simultaneous Treatment Interface





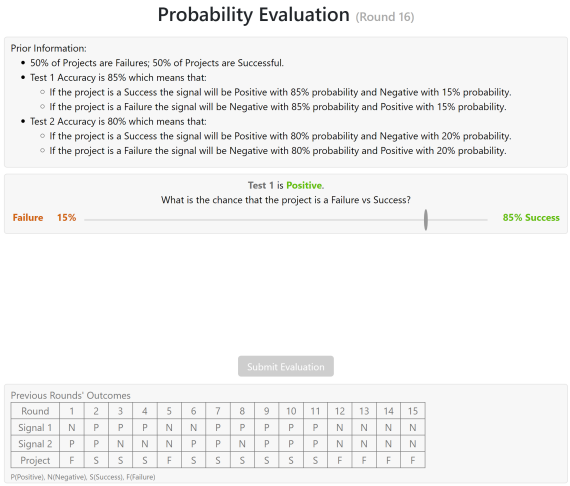


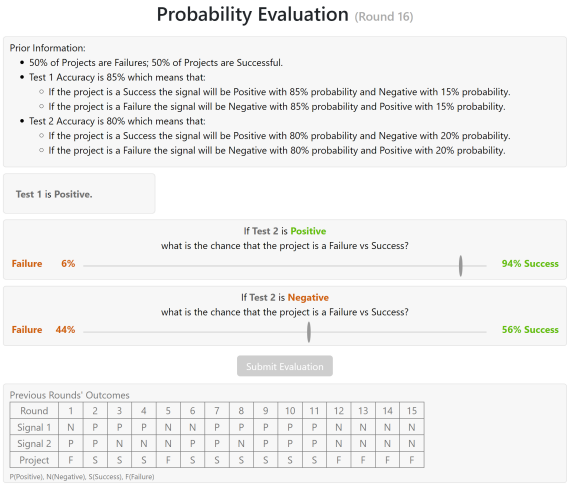




- Most of the design choices are unchanged from the Baseline treatment. However, in the simultaneous treatment, participants received both signals at the same time.

2.3 Sequential Treatment Interface





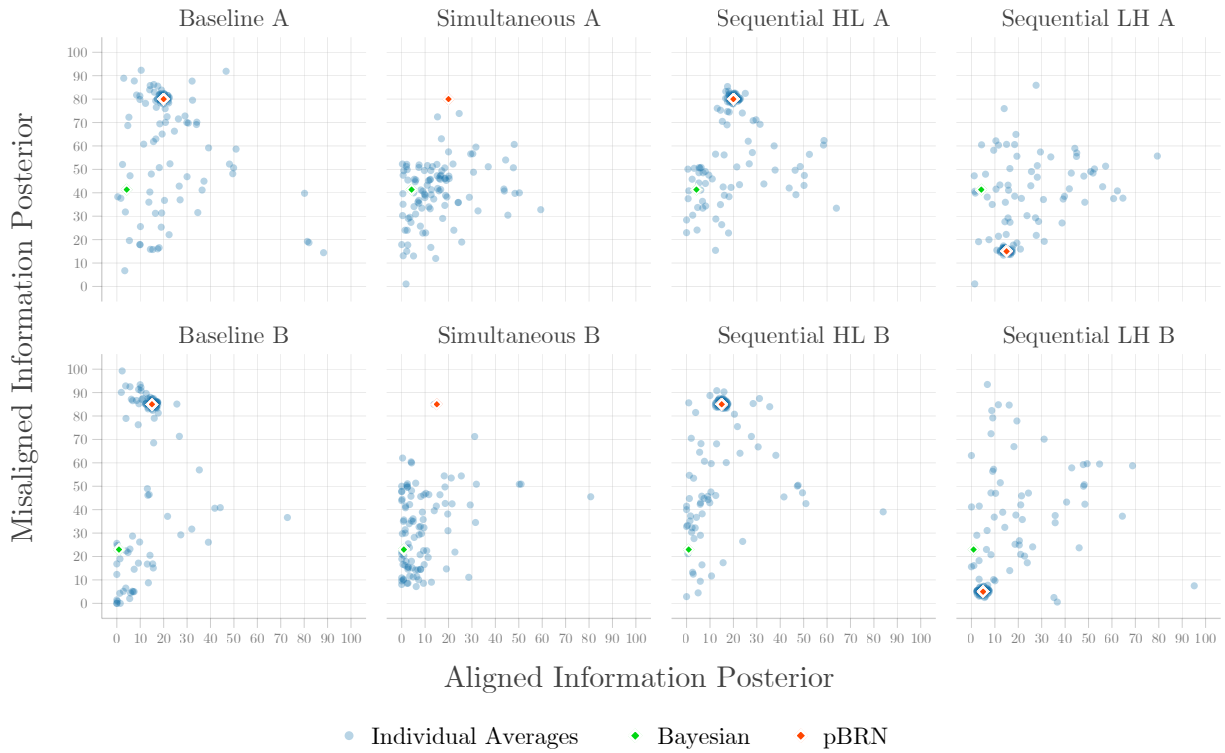
- Once more, most of the design choices are unchanged from the previous treatments. However, in the sequential treatment, participants received signals sequentially. Upon receiving the first signal, their posterior probability was elicited. Afterward, participants stated their posteriors conditional on the realized value of the second signal.
- The interface displays the outcome of the first signal when participants make choices conditional on the outcome of the second signal.

3 Related Data Analysis

3.1 Individual Level Analysis

Figure 8 displays the counterpart of **Figure 9** in the main text, utilizing data from the last five rounds only.

Figure 8: Average Individual Choices: Last Five Rounds

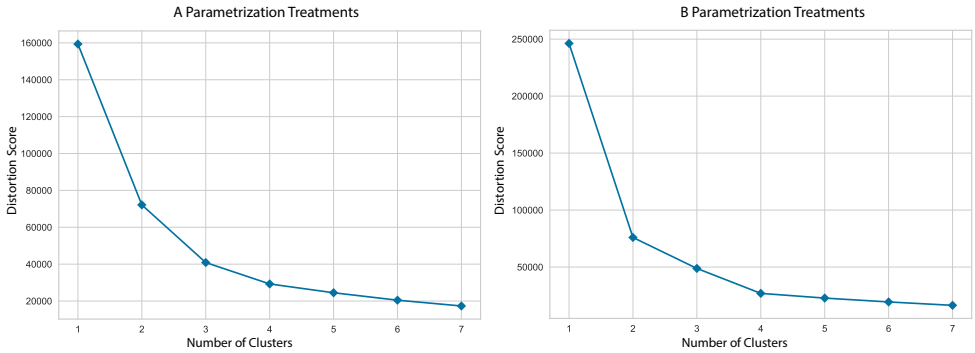


Notes: To help distinguish the large amount of data bundled on the pBRN level, we apply a jitter of 1.5 magnitude. This jittering perturbs the datapoint no further than a distance of 1.5 from the initial value. The top(bottom) row displays data across treatments under parametrization A(B).

3.2 Classifying Types

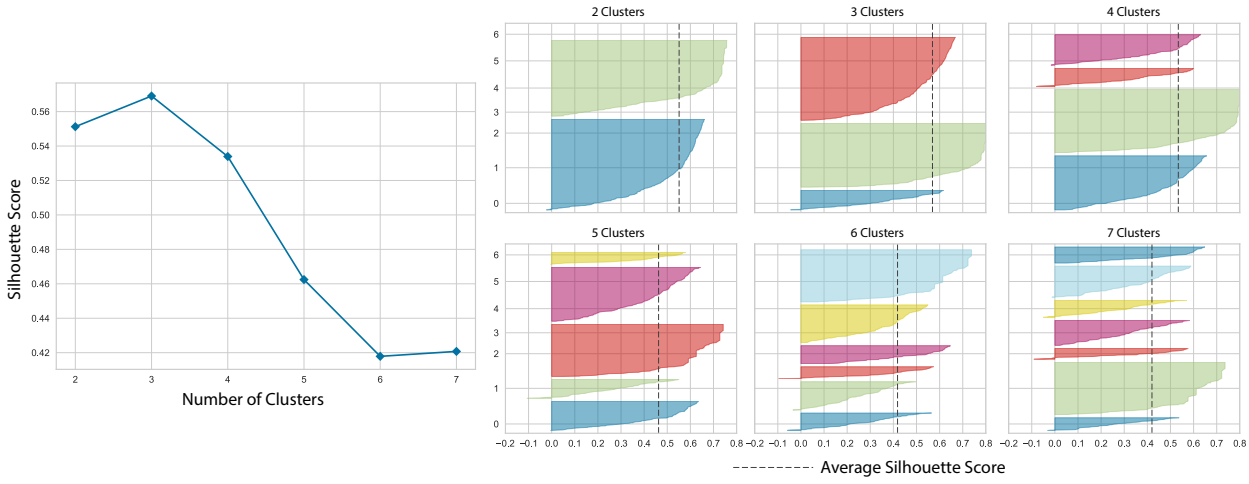
The elbow method is a way to determine the optimal number of clusters in a dataset for k-means clustering. It works by plotting the sum of squared distances between each point and the centroid of its cluster against the number of clusters used. The plot looks like an arm, and the elbow point on the arm represents the best number of clusters to use. This is because the elbow point is where adding more clusters does not significantly improve the clustering results. The elbow method helps to select an appropriate number of clusters for k-means clustering, avoiding underfitting or overfitting the data. The graphs shown in Figure 9 reveal that the elbow method recommends three clusters for parametrization A, while for parametrization B, the score is somewhat ambiguous between two, three, and four clusters. We supplement our calculations by determining the optimal number of clusters via the silhouette method.

Figure 9: Distortion Score Elbow for K-Means Clustering



The silhouette method is a way to evaluate the quality of clustering results in a dataset. It works by measuring how similar an observation is to its own cluster compared to other clusters. The silhouette score ranges from -1 to 1, with higher values indicating better clustering results. A score of 1 indicates that the observation is well-matched to its own cluster and poorly-matched to other clusters. A score of -1 indicates the opposite, while a score of 0 indicates that the observation is equally similar to its own cluster and other clusters. The silhouette method calculates the average silhouette score of all observations in the dataset and uses this as a measure of how well the data is clustered. The method can be used to compare different clustering methods or to select the best number of clusters to use in a k-means clustering analysis. By selecting the number of clusters that maximizes the silhouette score, the method can help improve the accuracy and reliability of the clustering results. The graphs shown in Figure 10 reveal that the silhouette score is maximized under three clusters.

Figure 10: Silhouette Scores For K-Means Clustering



We thus decide to proceed with the clustering exercise with three clusters.

4 Pilot Data

4.1 Estimated Means

We ran two pilot studies under parametrization A for the Baseline and Simultaneous treatment. In Table 1, we compare the estimated mean from Baseline A and Simultaneous A with the estimated means in their corresponding pilot treatments. The variable *Constant* captures the estimated mean in the regular session, whereas the variable *Pilot* captures the difference of the estimated mean from this value in the pilot treatment. As can be seen, regardless of the error clustering level, the difference is never statistically significant.

Table 1: Estimated Means

	Baseline A			Simultaneous A		
	No C	Ind C	Ind C + Last 5	No C	Ind C	Ind C + Last 5
Constant	63.79***	63.79***	60.43***	41.65***	41.65***	40.29***
	(0.595)	(1.971)	(2.428)	(0.384)	(0.987)	(1.295)
Pilot	0.434	0.434	5.911	1.001	1.001	1.483
	(1.041)	(3.680)	(4.285)	(0.667)	(1.740)	(2.382)
N	3000	3000	750	3020	3020	755

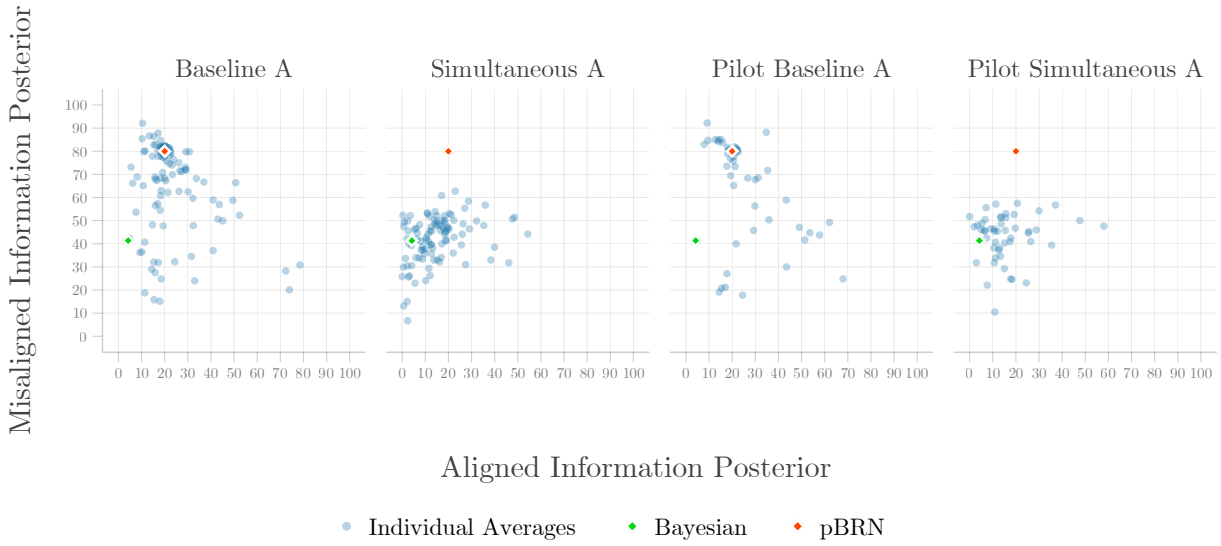
Standard errors in parentheses

* $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$

4.2 Individual Level Analysis

In Figure 11, we plot the individual level data for Baseline A and Simultaneous A, as well as their corresponding pilot treatments.

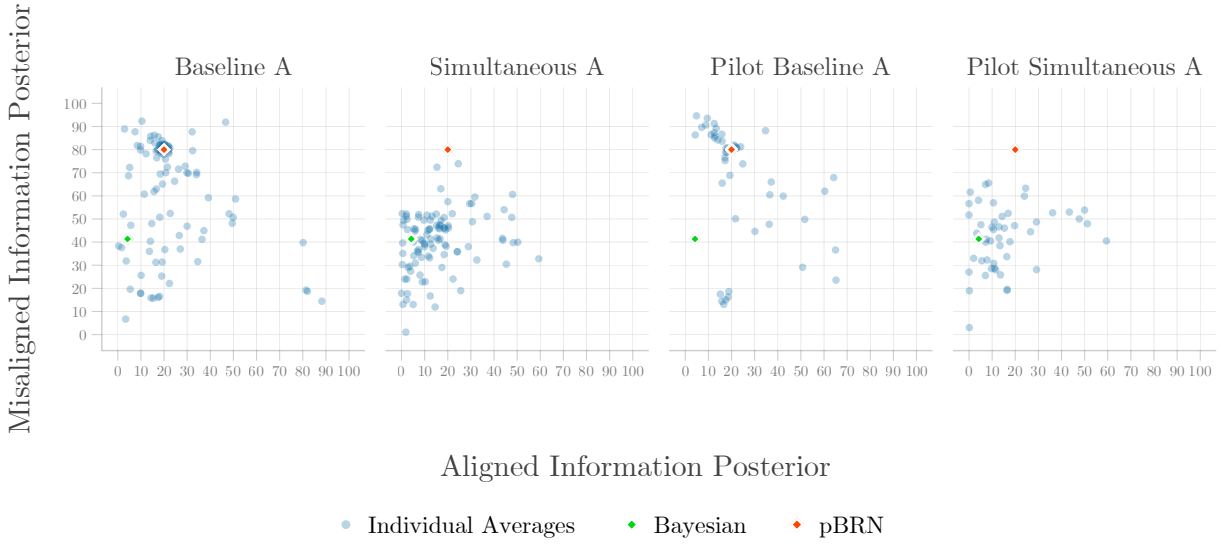
Figure 11: Average Individual Choices



Notes: To help distinguish the large amount of data bundled on the pBRN level, we apply a jitter of 1.5 magnitude. This jittering perturbs the datapoint no further than a distance of 1.5 from the initial value.

In Figure 12, we do the same utilizing data from the last five rounds only.

Figure 12: Average Individual Choices: Last Five Rounds



Notes: To help distinguish the large amount of data bundled on the pBRN level, we apply a jitter of 1.5 magnitude. This jittering perturbs the datapoint no further than a distance of 1.5 from the initial value.