

# How nearly random mutations to sentences affect their acceptabilities: Preliminary quantitative analyses based on ARDJ data

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## Abstract

ARDJ s2u data consists of 300 sentences paired with acceptability ratings. Out of them, 36 are “originals” that were human-made and other 264 are their “mutations” that were generated either by nearly random replacement of a nominal, a verbal or a positional (e.g., case-marker) or by random swapping a pair of phrases (i.e., *bunsetu*) inside. This allows us to analyze effects of mutation systematically. With DBSCAN of the originals, layered analysis of mutation effects was carried out. Findings are: i) No mutations improve low acceptabilities; ii) The order of systematicity is:  $p < v < n < s$ ; iii) The order of effect size is:  $p < v, n, s$ , so that *n*-, *s*-mutations often cause as large effects as *v*-mutation, or even larger; iv) No simple dichotomy is possible between “acceptable” and “unacceptable” sentences. Rather, their distinction is continuous and graded, so that (logistic) regression is a better modeling of the distinction.

## 1 Introduction

Linguistics is concerned with acceptabilities of sentences, if not exclusively. But acceptability is an elusive notion [1, 2, 3, 4, 5, 6]. Any group of linguists rarely agree on its theoretical definition, meaning that it is a highly theory-laden notion [7]. If its theoretical definition is somehow shared, its operative definition is virtually missing. The situation is still worse. Even if presume its definition is fine, we are still far from knowing what acceptabilities really are. No unbiased, large-scale collection of the required data has ever been done. In particular, we are far from fully understanding what modifications to a sentence bring about what effect, and to what degree, because data-driven study into this problem has never been done. What linguists know about acceptability suffers from “confirmation-bias” [8, 9, 10, 11, 12, 13]. This is the issue that dictates this research based on *Acceptability Rating Data for Japanese* (ARDJ for short) [14, 15, 16, 17, 18, 19].

ARDJ is a project of empirically-oriented language science, rather than mere linguistics, that attempts to implement the framework of randomized control trials in the field of linguistics, with sympathy for *Evidence-based Medicine*

(*EBM*) [20, 21]. A crucial conviction that paved the way for ARDJ is that intuitions by experts (e.g., acceptability judgments by linguists) are valuable with no doubt, but they are too weak “evidence” to be treated as “facts”; rather, they are more or less reliable “guides.”

The stimuli used in the ARDJ surveys comprise two kinds of sentences: 36 “originals” hand-crafted by humans and their “variants” generated by applying nearly random mutations on the originals. Mutations are only nearly random rather than fully random, because they have target sites, and values for replacement are chosen based on word2vec distributional similarities. See [16] for relevant details. Appendix A.1 gives a brief summary. Effects of mutation can be systematically analyzed by comparing responses to the originals and their mutations.

## 2 Analysis and results

To make our analysis effective, we use PCA, tSNE with DBSCAN clustering, overplot, and KL-divergence-based heatmap/clustering. In §2.3.1–§2.3.4, analysis of effects of mutation is implemented as a layered analysis in which Clusters 1, 2, 3 and 4, are taken as four separate groups of data. Discarding the originals in Clusters 2, 3 and 4, KL-divergence-based analysis is performed on mutations to the originals in Cluster 1 in §2.4. Lastly, effects are analyzed by exploring properties of mutation-wise KL-divergence heatmaps in §2.5.

### 2.1 36 originals and their attributes

ARDJ s2u data [17] has 36 “originals” presented in Figure 1, o01, o02, ..., o36, with relevant attributes. Details are presented in §2.1. How this data was prepared is described in Appendix A. The originals are sorted decreasingly by r01, r12 values, and increasingly by r23, r3x values. Only 32 originals have more than 2 mutations. So, the number of effective originals is 32 rather than 36, as Figure 1 shows. The effective ones have (8.31 - 1) mutations/variants on average, with a maximum of 16 and minimum of 4.

o.id	S.TEXT	s.id	r01	r12	r23	r3x	count
o05	男性がステージンで角砂糖を紙袋に入れた。	s109	0.73	0.06	0.02	0.01	8
o08	長身は口で指のしほりをした。	s227	0.76	0.06	0.02	0.02	9
o27	先生が机の下のひびきを聞いた。	s246	0.76	0.06	0.02	0.02	6
o20	息子が親の机で手紙を隠して人を見た。	s100	0.81	0.10	0.02	0.01	6
o06	担当者が携帯電話で出張先から電話を入れた。	s199	0.86	0.11	0.01	0.02	8
o34	先輩が先輩で先輩から先輩を見た。	s179	0.82	0.11	0.03	0.03	8
o22	通り魔が歩道の歩道で先輩を見た。	s196	0.79	0.14	0.05	0.03	7
o03	目がキーンと早くラジオを聞いた。	s279	0.78	0.16	0.05	0.01	7
o31	弟が家で練習を聞いた。	s021	0.78	0.16	0.04	0.02	7
o17	医師が手術で先輩と先輩を見た。	s267	0.78	0.15	0.02	0.05	8
o06	職員が先輩で先輩で先輩を見た。	s245	0.79	0.16	0.05	0.02	7
o25	脚本家が話し合いで毎日に行われた。	s096	0.74	0.20	0.04	0.02	10
o23	先輩が先輩で先輩で先輩を見た。	s231	0.74	0.16	0.07	0.03	7
o29	先輩が先輩で先輩で先輩を見た。	s169	0.71	0.18	0.07	0.04	9
o09	先輩が先輩で先輩で先輩を見た。	s168	0.69	0.23	0.05	0.03	8
o02	先輩が先輩で先輩で先輩を見た。	s161	0.66	0.27	0.05	0.02	7
o21	先輩が先輩で先輩で先輩を見た。	s158	0.59	0.32	0.05	0.03	9
o16	人が先輩で先輩で先輩を見た。	s206	0.56	0.34	0.07	0.03	9
o04	先輩が先輩で先輩で先輩を見た。	s191	0.46	0.07	0.00	0.00	9
o11	先輩が先輩で先輩で先輩を見た。	s079	0.44	0.09	0.03	0.04	9
o01	先輩が先輩で先輩で先輩を見た。	s051	0.41	0.34	0.20	0.05	9
o02	先輩が先輩で先輩で先輩を見た。	s144	0.41	0.38	0.12	0.10	5
o07	先輩が先輩で先輩で先輩を見た。	s103	0.38	0.31	0.19	0.12	1
o04	先輩が先輩で先輩で先輩を見た。	s099	0.27	0.42	0.21	0.10	1
o05	先輩が先輩で先輩で先輩を見た。	s205	0.20	0.38	0.28	0.13	1
o28	先輩が先輩で先輩で先輩を見た。	s101	0.19	0.51	0.21	0.08	9
o06	先輩が先輩で先輩で先輩を見た。	s275	0.17	0.48	0.15	0.20	1
o13	先輩が先輩で先輩で先輩を見た。	s157	0.10	0.42	0.29	0.20	8
o33	先輩が先輩で先輩で先輩を見た。	s153	0.09	0.41	0.30	0.20	9
o30	先輩が先輩で先輩で先輩を見た。	s258	0.06	0.42	0.25	0.26	8
o19	先輩が先輩で先輩で先輩を見た。	s052	0.05	0.38	0.25	0.32	9
o14	先輩が先輩で先輩で先輩を見た。	s204	0.04	0.41	0.29	0.25	9
o15	先輩が先輩で先輩で先輩を見た。	s054	0.04	0.21	0.39	0.36	8
o10	先輩が先輩で先輩で先輩を見た。	s190	0.04	0.29	0.31	0.36	17
o12	先輩が先輩で先輩で先輩を見た。	s178	0.04	0.37	0.27	0.32	8
o18	先輩が先輩で先輩で先輩を見た。	s047	0.02	0.39	0.35	0.24	9
sum			17	9	5	5	270
count			36	36	36	36	36
average			0.48	0.26	0.13	0.13	7.50
max			0.92	0.51	0.39	0.46	17.00
min			0.02	0.06	0.00	0.01	1.00
stdev			0.32	0.14	0.12	0.14	2.96

Figure 1: 36 originals with attributes

The originals were clustered using DBSCAN, giving us 4 clusters. §2.2 deals with this result. The resulting clustering is laid out over a PC1-PC2 plane of PCA rotation and a Dim1-Dim2 plane of tSNE transformation. This gives us how the sentences are associated to each other.

## 2.2 Clustering of originals and all stimuli

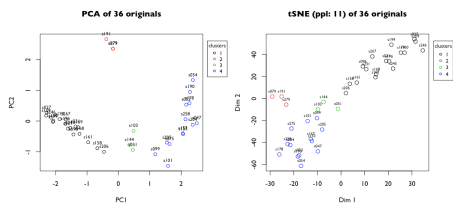


Figure 2: PCA and tSNE of 36 originals

### 2.2.1 Clustering originals only

DBSCAN was used to cluster the 36 originals to identify 4 clusters, which are shown in PCA and tSNE plots in Figure 2. tSNE in Figure 2 suggests the existence of a unified dimension along which acceptability can be measured. The deviance of Cluster 2 from it can be accounted for its special nature described below.

### 2.2.2 Clustering all 270 stimuli

For comparison, we present clustering of all stimuli including the 36 originals described above. Figure 3 gives PCA and tSNE plots of DBSCAN clustering. Note that the setting for eps and minPts parameters here is independent from those for the parameters for the DBSCAN clustering of the 36 originals.

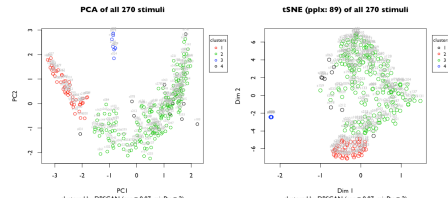


Figure 3: PCA and tSNE of all 270 stimuli

## 2.3 Layered Analysis

This clustering result seems natural in that clusterwise overplots in Figure 4 seem to capture both the similarities and dissimilarities quite well. Each cluster consists of instances with surprising similarities.

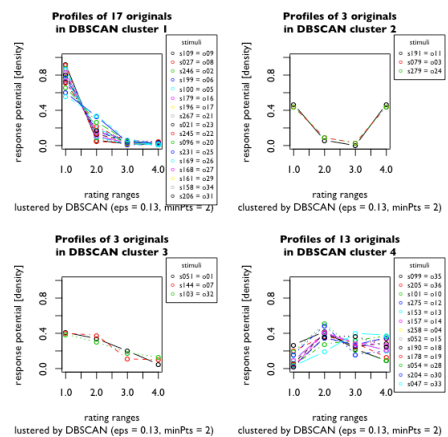


Figure 4: Clusterwise overplots of originals

Comparing with the data in Figure 1, we can safely conclude the following:

- (1) a. Cluster 1 identifies the group of “acceptable” stimuli, Cluster 4 the one of “unacceptable” stimuli, and Clusters 2 and 3 the ones of “ambiguous” stimuli, with different qualities.
- b. Cluster 3 consists of 3 instances, o03, o11 and o24, that have a “split” decision, in that raters are split into two groups of those who accept them fully and those who reject them fully.
- c. Cluster 4 consists of 3 instances, o01, o07 and o32, that have a nearly “uniform” distribution of (un)acceptability along the range, though with a slight inclination toward acceptability.

With these distinctions among the originals, we can now turn to effectively analyzing the effects of mutation to answer the research question: how random mutations to sentences affect their acceptabilities, and to what extent.

### 2.3.1 Analysis 1a: Mutations to originals in Cluster 4

We start our analysis with the one of the mutations to the originals to Cluster 4, a relatively large cluster, having 13

members which can be labelled as “unacceptable” stimuli. This is because the effects are simple and can be characterized most easily.

Effects of mutation are analyzed in three visualizations, as shown in Figure 5: i) overplot of response profiles (in the leftmost column); ii) proportional distribution of range values after reordering; and iii) layout of DBSCAN clusters in a rotated geometry  $G$ .

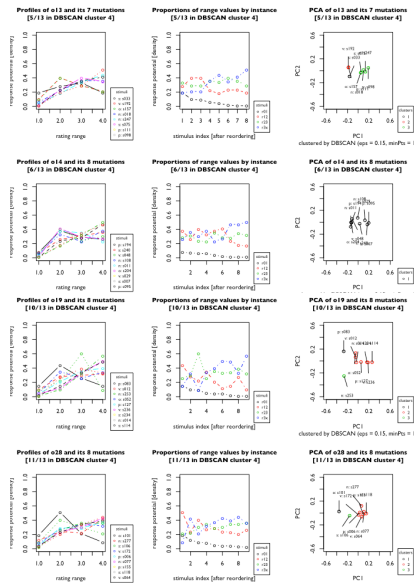


Figure 5: Mutations to originals to Cluster 4 [4 samples]

In each analysis, stimuli are ordered by their range values. So, their positions relative to o in the legend roughly indicate if mutations increase or decrease acceptabilities.

As suggested by the plots in Figure 5, virtually no mutations improve the original acceptabilities. In addition, the response profiles, i.e., shapes of distribution, stay unchanged for most cases. So, there seems to be a rule like “once (made) deviant, always deviant.” This finding is not truly surprising, let alone unexpected; yet, it deserves a mention because this is the first empirical confirmation of a truism on a large scale that has long awaited testing.

### 2.3.2 Analysis 1b: Mutations to originals in Cluster 3

Effects of mutations to cases in Cluster 3 are similar to the ones to stimuli in Cluster 4. Stimuli in Cluster 3 almost are almost never improved by any mutation, though, admittedly, we can hardly state generalizations safely because we have too few affected cases.

### 2.3.3 Analysis 1c: Mutations to originals in Cluster 2

Effects of mutations to cases in Cluster 2 are somewhat different from the ones to stimuli in Cluster 3. Unlike stimuli in Cluster 3, stimuli in Cluster 2 sometimes improve, though, again, we can hardly state generalizations safely

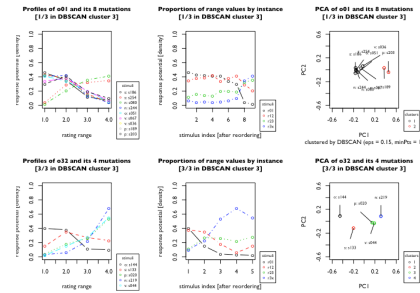


Figure 6: Mutations to originals to Cluster 3 [One case was dropped due to insufficient cases.]

due to having too few affected cases. It is interesting that o11 and o24 get more acceptable through certain mutations, though o03 does not possess such properties.

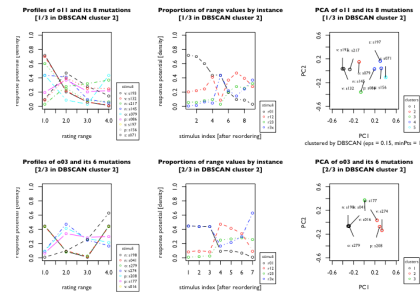


Figure 7: Mutations to originals to Cluster 2 [2 samples]

### 2.3.4 Analysis 1d: Mutations to originals in Cluster 1

Mutations to the originals in Clusters 2, 3 and 4 tell us virtually nothing interesting about how mutations affect acceptability, because we can hardly identify meaningful differences between mutations and their originals. This is not true of mutations to the originals in Cluster 1.

Mutation effects are different case by case, but generally speaking, we can observe the following:

- (2) a. Lexical changes (i.e., mutations to either n(ominals), v(erbals), or p(ositionals)) nearly always drop acceptability, while non-lexical changes (i.e., swapping) do not. Swapping often keeps the acceptability.
- b. It is not true, at least not observed, that n-changes reduce acceptability more than v- and p-changes, as far as degree of deviance is measured.
- c. Changes to p introduce only a slight amount of deviance, though it is unignorable.
- d. Effects of mutation are diverse, in that the number of clusters recognized is greater than the ones in other clusters, Clusters 2, 3 and 4.
- e. Mutations do not simply make sentences unacceptable, in that resulting profiles do not always look like those in the originals in Cluster

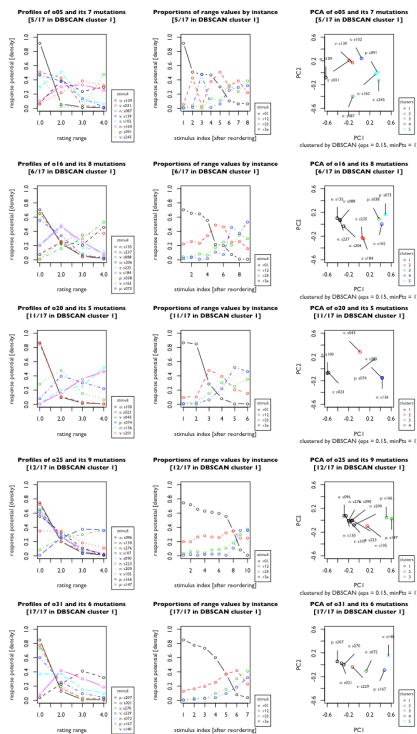


Figure 8: Mutations to originals to Cluster 1 [5 samples]

4. Rather, they look more like the originals in Cluster 3 or 2. So, the effects of mutation are more subtle than researchers have guessed.

With their relative importance, cases in Cluster 1 deserve further exploration. We do it by analyzing them with KL-divergence cross-table.

## 2.4 Analysis 2: KL-divergence for originals to Cluster 1

The diagrams in Figure 9 are heatmaps of the 9 samples, taken in Figure 8, allowing us to make the following observations:

- (3) a. p- and v-mutations tend to cluster together, but not always.
- b. swapping and n-mutations tend to lack systematic effects, though they often cause drastic deterioration.

## 2.5 Analysis 3: KL-divergence cross-table by mutation

Different types of mutation, i.e., p, v, n and s, have different magnitudes of effects. To estimate them, we can use KL-divergence heatmaps, as shown in Figure 10.

If the contrasts between “hot” and “cool” areas are sharp, the magnitude of effects can be judged to be large. If the

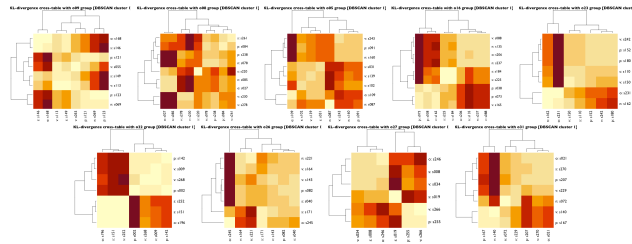


Figure 9: KL-div. heatmaps for Cluster 1 cases [o09, o08, o05, o16, o23, o22, o26, o27, o31]

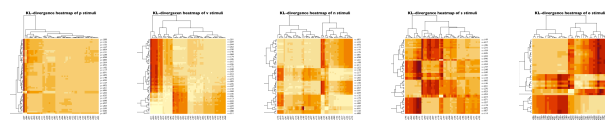


Figure 10: KL-div. heatmaps for mutation types [p, v, n, s, o]

degree contrasts are spread, effects are unsystematic. With this criterion, we can conclude that i) the effect of p mutations is least contrastive and most systematic; ii) that of v mutations is second least contrastive and rather systematic; iii) that of n mutations is second most contrastive and rather unsystematic; and iv) that of s mutations is most contrastive and most systematic. Note that the 36 originals are contrastive only because they are largely designed so.

## 3 Discussion and Conclusion

So, what are causes of reduced acceptabilities? With the results so far, we can now decide if we are able to answer this question. The most sincere answer to this would be: there is no simple answer to this question. What does this mean, then?

Simple dichotomy between “acceptable” and “unacceptable” kinds of sentences is too simple and unrealistic, though it is widely accepted and practiced in many areas of linguistics. What really matters about acceptabilities are response profiles (distributional pattern of responses) rather than categorical judgments, on the one hand, and regression to response profiles rather than binary classification (e.g., dichotomy = categorical judgment), on the other. This is a conclusion compatible with the results in [15].

What do linguists need to do with this reality, then? We would suggest that the goals of linguistics should be redefined. Redefined goals include the **construction of a mapping from sentences in textual form (e.g., values in *s.text* in Table 1) to response profiles (e.g., arrays of values [r01, r12, r23, r3x] in the table in Figure 1), yielding overplots in Figures 4.** This can never be attained until large-scaled, bias-free databases like ARDJ are built for as many languages as possible. Until then, linguistics would never make itself an empirical science.

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All statistic analyses were done on R version 3.6.3, a free statistical software developed by R Core Team (<https://www.r-project.org>).

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## A Data preparation

### A.1 Construction of stimuli

To make the outcomes of ARDJ truly empirical and useful, we need to employ as unbiased stimuli as possible. The best way to implement it is to employ automatic generation rather than relying too much on human intuitions. Random mutation in DNA sequences serves as a model. The basic idea is the following:

#### (4) Steps of randomized generation with targets

- Step 1. Construct sentences, called “originals,”  $O = \{o_1, o_2, \dots, o_n\}$  with or without deviance.
- Step 2. Introduce random mutations to instances of  $O$ . Let  $M$  denote the result.
- Step 3. Mix  $O$  and  $M$  and use its subsets for acceptability rating tasks.

More details of Step 2 are given in the following:

- (5) A) Random replacement of a lexical item under POS-identity (edit type: l(exical)); B) Random replacement of a postpositional case-marker (P) with another (edit type: p(ositional)); C) Random positional exchange of a given pair of NPs (or PPs) (edit type: s(wapping)).

provided that items for replacement are selected on a pre-defined measure such as distributional similarity.

The first and second authors developed Python scripts to implement mutations of A-, B- and C-classes. They are provided at <https://github.com/kow-k/Japanese-sentence-mutators>.

### A.2 Surveys

By 2019, ARDJ completed two experiments. The first one, called “Survey 1,” was carried out in 2017. It was intended to be a pilot study with only a limited variety of responders (roughly 200 college students only) on 200 sentences for stimuli. Kuroda et al. [16] reported on this survey. The second experiment, called “Survey 2,” was carried out in 2018. This was the main study, with the stimulus set expanded to 300 with some overlap with Survey 1.

Survey 2 had two phases, Phases 1 and 2, and collected responses from 1,880 participants in total. Phase 1 was a small scale, paper-based survey, to which 201 participants (mostly all college or university students) contributed responses. This was comparable to the pilot study done in 2017. Phase 2 was a large scale web survey to which 1,679 participants contributed responses. They were significantly more varied in their attributes and we would safely state responses obtained were randomized enough. Survey 2 unified (s2u) data consists of unification of responses from Phase 1 and Phase 2. These data are freely available at <https://kow-k.github.io/Acceptability-Rating-Data-of-Japanese/>, but you need to register to use them.

### A.3 Collection of ratings/responses

On acceptability rating, participants were asked to choose one of the four choices in (6).

- (6) **0.** 違和感がなく自然に理解できる文 [natural and easy to understand]; **1.** 違和感を感じるが理解可能な文 [more or less deviant but comprehensible]; **2.** 違和感を感じて理解困難な文 [deviant and difficult to understand]; **3.** 不自然な理解不能な文 [quite unnatural and incomprehensible]

Prefixes 0, 1, 2 and 3 are added to indicate the degrees of deviance, though they need not be on a single scale.

Outlier responders were filtered out using standard deviation ( $0.6 < sd < 1.5$ ) and Mahalanobis distance ( $< 0.95$ ). See Kuroda et al [17] for relevant details.

### A.4 Standardizing responses

Note that gr0, ..., gr9 are different data sets, and cannot be directly compared. Comparison of them requires standardization. All groups were collapsed and responses were counted for each of the four rating ranges  $r[0, 1)$ ,  $r[1, 2)$ ,  $r[2, 3)$ , and  $r[3, \infty)$ .

Table 1 shows 10 samples of this process. These raw counts were then converted into proportions to item-wise sums. This gave us density array,  $P = (p[0, 1), p[1, 2), p[2, 3), p[3, \infty))$ , as exemplified in Table 2. Note that allowed response values were 0, 1, 2, and 3. These numbers are reinterpreted as ranges  $r[0, 1)$ ,  $r[1, 2)$ ,  $r[2, 3)$ , and  $r[3, \infty)$ , respectively, where  $r[i, j)$  means a sum of response counts between  $i$  and  $j$  with  $i$  included and  $j$  excluded. The converted arrays of ranged response probabilities in this format are to be called “response potentials.” They are commensurable among groups with different sets of responders, and were used as effective encodings of the responses in a variety of analyses.

s.id	$r[0, 1)$	$r[1, 2)$	$r[2, 3)$	$r[3, \infty)$	sum
s021	128	25	5	2	160
s064	3	42	53	53	151
s128	5	50	32	60	147
s188	1	12	36	98	147
s231	119	27	10	4	160
s282.4	27	77	32	15	151

Table 1: Frequency table by ranges (6 samples)

s.id	$p[0, 1)$	$p[1, 2)$	$p[2, 3)$	$p[3, \infty)$	sum
s021	0.800	0.156	0.031	0.013	1.00
s064	0.020	0.278	0.351	0.351	1.00
s128	0.034	0.340	0.218	0.408	1.00
s188	0.007	0.082	0.245	0.667	1.00
s231	0.744	0.169	0.063	0.025	1.00
s282.4	0.179	0.510	0.212	0.099	1.00

Table 2: Density table by ranges (6 samples)