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A Statistical Analysis of Human Random Number Generators

Yukito IBA and Mieko TANAKA-YAMAWAKI

The Institute of Statistical Mathematics
106 Minatoku Minami-Azabu 4-6-7, Tokyo, Japan
TEL 03-5421-8759, E-mail iba@ism.ac.jp

Department of Social Sciences, Sugiyama Jogakuen University
Chikusa-ku, Nagoya 464 Japan
TEL 052-781-1186 ex.632, FAX 052-783-6732
E-mail mieko@ss.sugiyama-u.ac.jp

Abstract:
We study a random number generation test where subjects are requested to write sequences of digits as random as possible. The results of our experiments are reported and a model-based approach is proposed for the analysis of the sequences from the test.

Key Words:
Human Random Number Generator, Random Number Generation Test,
Statistical Model, Markov Chain

1 Introduction

1.1 Can We Behave as a Random Number Generator ?

Let us consider a psychological test: "Write a sequence of numbers as random as possible". The remarkable feature of this kind of tests (called the *random number generation tests*) is that the subject is provided neither prescribed list of answers nor deterministic rule to follow. The seemingly simple demand "being random" is in fact a very difficult task. As might be expected, most people cannot behave as a good random number generator. A Human Random Number Generator (HURG, hereafter) is often far from the ideal one.

What are the underlying mechanisms of HURGs? A HURG seems to take two steps in producing a response. At the first stage, we generate several candidates for the response. Very often these candidates are the fragments of patterns generated from our memory. At the next stage we compare these candidates with the sequence already produced, then choose one. This feedback mechanism is employed many times when we are allowed to have enough concentration, while it is cut after a few times when the concentration is limited.

This picture of HURGs suggests that the random number generation test can be regarded as a probe to the patterns embedded in our mind. Examples of such patterns are the sequence of numbers in the natural order 0-1-2-3- and the sequence of even numbers 2-4-6-8-. More complex patterns may exist. Some patterns might be specific to a culture or an individual subconsciousness.

Random number generation is also useful for the study of the mechanism of divergent thinking, which cannot be explored with tests in which the subjects are requested to follow deterministic rules. For this purpose, the use of numbers {0,1,2,..,9} limits too much diversity of possible patterns at the first stage and makes us possible to obtain more clear-cut information on the flexibility of our thinking.

The random number (or sequence, in general) generation test has a long history. Works from 1949 to 1971 are reviewed in Wagenaar (1972). For later works, we refer to Spatt and Goldenberg (1993) and references therein. In Japan, random sequence generation tests were introduced by Teraoka (1963) and Murakami (see, Matsuda (1973)). While Teraoka's paper seems better known in foreign literatures, Murakami's work activated explorations in Japan mainly in the area of psychiatry and clinical psychology (Matsuda (1973)). We are also introduced to this area by the paper, Murakami et al. (1973).

1.2 The Scope of the Present Paper

In this paper we are mainly concerned with the analysis of the patterns in sequences from HURGs. We also try to give a basis to the study of HURGs by means of statistical modelings. A systematic use of statistical models is useful for clarifying the relationship between assumptions on the regularity of sequences from HURGs.

This paper is organized as follows. We summarize our experiments on HURGs in Sec.2 and discuss basic properties of HURGs in Sec.3 using our data. In Sec.4 statistical models for HURGs are introduced. In Sec.5 remarks on the future studies of HURGs are given.

This work is in part (Sec.2 and 3) based on two senior theses written by Chika Hiraoka and by Mikako Kani under the supervision of one of the authors (M. T.), which have been submitted to Sugiyama Jogakuen University in January 1996. Parts of this paper was read at the meetings of the Physical Society of Japan (September 1995, Osaka and April 1996, Kanazawa) and at the 4th Workshop on Complex Systems (December 1995, Kyoto).

2 Experiments

We investigate a "{0..9} random number generation test", where we request a sequence of integer $\{S_i\}$ $(0 \leq S_i \leq 9)$. We call this version of HURG as the "{0..9} HURGs". Our data are taken according to the procedure in Murakami et al. (1973). That is, subjects are requested to write as many numbers as possible in a prescribed time interval (1, 2 or 3 minutes). The typical sequences are made of $50 \sim 200$ responses.

We have two sets of data A and B which consist of the data provided by 20 students of Sugiyama Jogakuen University and by 35 students of Seiwa Junior High School. In A and B each subject contributes once.

We also have sets Ha and Hb that contain the data taken from an individual. The experiment corresponds to the set Hb is carried out several months after the experiment for Ha with the feedback of the results of the earlier experiments. The sets Ha and Hb are taken by limiting the time to be two minutes and contain 30 and 19 sequences respectively.

Although we have some other sets of data, we do

not analyze them in this paper. At this stage of the work we do not try any rigorous control of the conditions of the experiments and the sets Ha, Hb are generated by the subject who had some prior knowledge on HURGs.

3 Basic Properties of HURGs

Here we briefly discuss the basic properties of HURGs using our data.

First we consider the frequencies of numbers in the sets of sequences (Fig.1a - 1d). Fig.1a and Fig.1b show the results corresponding to the sets A and B. These sets consist of data from many subjects. Although some inhomogeneities of the frequencies are found in Fig.1b corresponding to the set B, it is hard to establish common trends in the sets A and B. On the other hand, Fig.1c and Fig.1d, which correspond to the same subject, show that some of the typical patterns of the deviations are repeated even after several months.

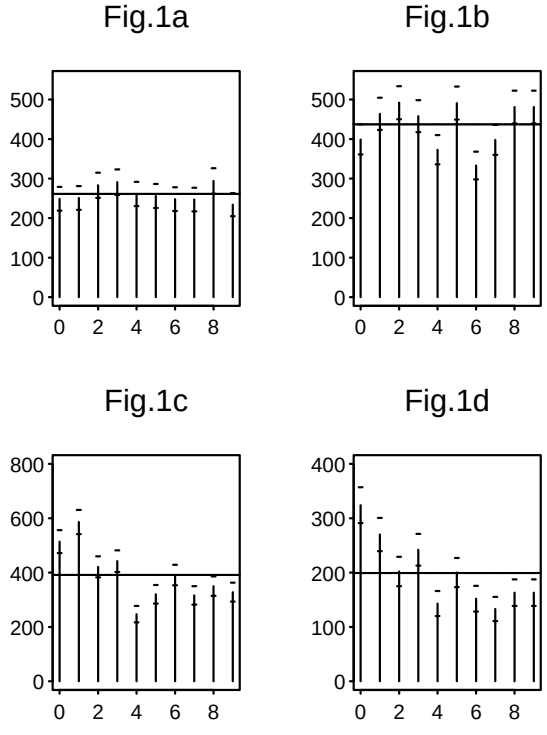


Fig.1.
The observed frequencies of the numbers $0, 1, .., 9$. Fig.1a, 1b, 1c and 1d correspond to the sets A, B, Ha and Hb respectively. The horizontal line corresponds to the frequencies expected in the case of the ideal random number generator. Error bars show ± 2 standard deviations with the assumption of independence of each response. Note that the error bars in Fig.1a and 1b do not contain the effect of individual differences.

Next we examine the correlations between neighboring pairs. As many authors have suggested, the statistics of neighboring pairs in the sequences $\{S_i\}$ from HURGs seriously deviate from the ideal one. By writing the difference between neighbors as $d_i = S_{i+1} - S_i$, we summarize the characteristic features of deviations observed in the sets A and B as follows:

- Pairs with $|d_i| = 0$ are rarely produced. This property of HURGs seems well known in the literature.

- Pairs with small $|d_i|$'s, typically $|d_i| = 1$ or 2, are more frequent than expected in the case of the ideal random number generator.

  This can be understood as the effect of the natural ordering of the numbers.

- Pairs with medium $|d_i|$'s are less frequent than expected in the case of the ideal random number generator.

- Pairs with large negative d_i's, typically $d_i = -9$, are more frequent than expected in the case of the ideal random number generator.

  This will be explained by the assumption that when subjects find themselves near the end 9 of the available region, they tend to jump to the other end of the available region.

Rath (1966) also reported the statistics of differences between neighboring pairs in $\{0..9\}$ HURGs. His results show a preference for the pairs with $|d_i| = 1, 9$ and an avoidance for pairs with $|d_i| = 0, 3 \sim 8$.

These characteristics are described in Fig.2a - 2d, in which the numbers of the pairs in the sets A, B, Ha and Hb are plotted against differences between pairs. Apparent differences between Fig.2c and Fig.2d corresponding to the same subject may be explained by the effect of the feedback of the the results of the earlier experiment. In the set B, while the pairs with $|d_i| = 2$ are frequent, the pairs with $|d_i| = 1$ are not so distinguished as in the set A. The reason of this difference is not clear.

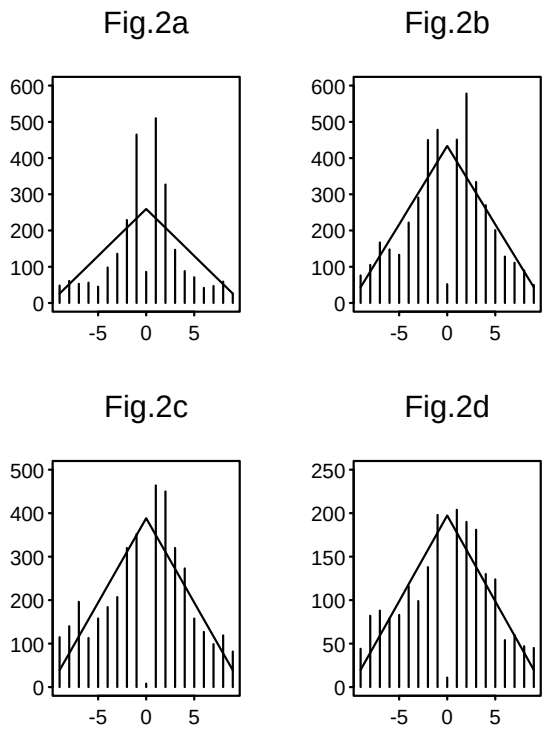


Fig.2.
The number of the ordered pairs S_iS_{i+1} in a set of sequences with the difference $d = S_{i+1} - S_i$ is plotted against d (vertical lines). The results corresponding to the set A, B, Ha and Hb are shown in Fig.2a, 2b, 2c and 2d respectively. The solid line corresponds to the expected frequencies in the case of the ideal random number generator.

4 Models for HURGs

4.1 Motivation

In this section we will introduce statistical models for HURGs and discuss the maximum likelihood estimation (MLE) for these models. They provide convenient tools for the analysis of the sequences from HURGs.

Although many authors suggest the relevance of Markov chain models in the study of HURGs, most of them consider only generic Markov chain models, which do not have constraints between transitional probabilities (except for the trivial constraints corresponding to the restriction of the order of Markov chains). Teraoka (1963) tried to describe the assumptions on HURGs as non-trivial constraints among transition probabilities. However, he treated very simple constraints and did not refer to MLE.

The model-based approach is useful to remove ambiguities from the assumptions on the regularities of the sequences. Consider the following statement "The preference on S_{i+1} is determined only through the difference $d = S_{i+1} - S_i$". To give a proper meaning to the statement, we should assign the probability zero to impossible cases, say $d = 8$ for $S_i = 5$, and renormalize transition probabilities to ensure the normalization. Clearly such a procedure is better described by an explicit formula of the transition probabilities. See the equation (1) in Sec.4.2 and the equation (3) in Sec.4.3 as examples.

Our approach is also relevant for checking observed frequencies with a given assumption on regularities. For example even when there are significantly many subsequences 2-4 in a sequence, it may be explained by the excess of 2 or 4 or the assumption that "The pairs with $|d_i| = 1\, or\, 2$ are more frequent than expected". After we fit statistical models to data, we can measure the deviations from an assumption as deviations from the expectations with the corresponding model. An illustrative example is given in Fig.3 in Sec.4.2.

The necessity for separating "lower level" correlations from "higher order" one is known in the studies of HURGs (for example, Weiss (1964), Rath (1966), Wagenaar (1970)). Our approach reduces to these earlier attempts when we restrict our models to the generic Markov models. However, it has an advantage for assumptions corresponding to models with arbitrary constraints among transition probabilities.

4.2 A Model for HURGs

Here we present an example of models of HURGs with a parameterization of the first order Markov chain model. Let us consider the following parameterization of the transition probabilities $P(\beta \mid \alpha)$ from a response α to the next response β,

$$P(\beta \mid \alpha) = \frac{\exp(h_\beta + g_{\beta-\alpha})}{\sum_{\beta=0}^{9} \exp(h_\beta + g_{\beta-\alpha})}. \qquad (1)$$

Here $\{h_\beta,\, \beta = 0,..,9\}$ and $\{g_\delta,\, \delta = -9,-8,..,8,9\}$ are the parameters of the model, which satisfy the relations $\sum_{\beta=0}^{9} h_\beta = 0$, $\sum_{\delta=-9}^{9} g_\delta = 0$ and $\sum_{\delta=-9}^{9} \delta g_\delta = 0$. The set of parameters are not unique for given $\{P(\beta \mid \alpha)\}$ without these relations.

When we define $n_{\alpha\beta}$ as the number of the ordered pairs $\alpha\beta$ in a set $\{\{S_i\}\}$ of sequences $\{S_i\}^{(1)}, \{S_i\}^{(2)}, ..$

, the log-likelihood of our model is

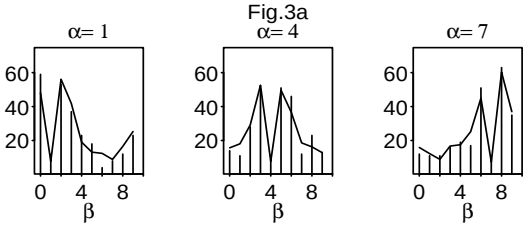
$$\log L(\{\{S_i\}\} \mid \{h_\gamma\}, \{g_\delta\}) = \sum_{\alpha=0}^{9} \sum_{\beta=0}^{9} n_{\alpha\beta} \log P(\beta \mid \alpha). \tag{2}$$

When a set $\{\{S_i\}\}$ of sequences is given, we estimate these parameters by maximizing the log-likelihood function (2) through a gradient ascent method. It takes less than 10 seconds for each calculation on a SUN Sparc 5 workstation.

In this model we assume the term $g_{\beta-\alpha}$ that is responsible for the correlations between a neighboring pair $\alpha\beta$ depends only on the difference $\beta - \alpha$ between them. This assumption gives constraints among transition probabilities and the number of free parameters reduce from 90 in the generic first order Markov chain model to $26 = 10 + 19 - 3$ in the model.

This model is the minimal one that reproduce the inhomogeneity in the probabilities of the numbers (Fig.1) and the distributions of the difference between neighboring pairs (Fig.2). That is, this model corresponds to the assumption that "The preference on S_{i+1} is determined by the preference on each number and the difference $d = S_{i+1} - S_i$ from the previous response".

Once the model is fitted to data, we can study the deviations of the observations from the expectations with the model. Here we define the predicted frequencies $\widetilde{n}_{\alpha\beta}$ of neighboring pairs as one-step ahead predictions by the model $\widetilde{n}_{\alpha\beta} = n_{\alpha\cdot} \cdot P(\beta \mid \alpha)$, where $n_{\alpha\cdot} = \sum_{\beta'} n_{\alpha\beta'}$ is the frequencies of the number α in a set of sequences. In Fig.3a - 3d the differences between the predicted frequencies $\widetilde{n}_{\alpha\beta}$ and the observed frequencies $n_{\alpha\beta}$ of neighboring pairs are shown for the sets A, B, Ha and Hb. A large differences in the frequencies represented by solid lines and by vertical lines indicate deviations of data from the prediction of the model.



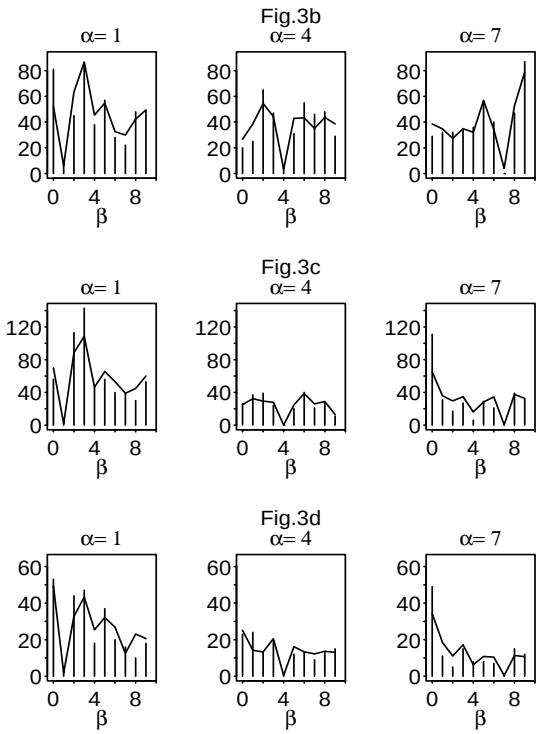


Fig.3.
Comparisons between the predicted frequencies $\widetilde{n}_{\alpha\beta}$ and the observed frequencies $n_{\alpha\beta}$ of neighboring pairs. Fig.3a, 3b, 3c and 3d correspond to the sets A, B, Ha and Hb respectively. The results for $\alpha = 1, 4, 7$ are shown. Solid lines show the predicted frequencies $\widetilde{n}_{\alpha\beta}$ of neighboring pairs with the model and vertical lines show the frequencies $n_{\alpha\beta}$ of neighboring pairs in the original data (e.g., the observed frequency of the pair 7-0 is shown by the first vertical line in each of the right panels).

Fig.3 shows the model (1) fits fairly well to the frequencies of neighboring pairs in these sets of data. There are, however, notable deviations from the model. For example, Fig.3c indicate the excess of the pair 7-0 in the set Ha against the model (1). Although the excess of the pair 7-0 is also seen in Fig.3d corresponding to the set Hb taken from the same subject, it is not so distinguished as in the set Ha.

4.3 Extensions of the Model

There are general properties of HURGs that cannot be described by the models based on the first order Markov chain. For example triplets like 6-5-6 and 3-4-3 are hardly seen in the sequences from HURGs. Such

"recessive" correlations also exists for the pairs with several responses between them. Wagenaar (1970) argued that Markov models with at least sixth order is required to explain the repulsion between same numbers in some of his data.

Another correlation that cannot be perfectly described by the first order Markov chain model is the excess of the "counting sequences" like 1-2-3 or 6-4-2. Although such correlations are partially explained by the excess of neighboring pairs with small differences, say 1-2 or 2-3, we can assume the further excess of the "counting sequences", which cannot explained by the first order Markov chain model.

We can easily extend our models for HURGs to include these effects. For example the excess of the "counting sequences" and the deficiency of the triplets of "$\alpha\beta\alpha$" type are represented by the following parametrization of the second order Markov chain models.

$$P(\gamma \mid \alpha,\beta) = \frac{\exp(h_\gamma + g_{\gamma-\beta} + f_{\gamma-2\beta+\alpha} + e_{\gamma-\alpha})}{\sum_{\gamma=0}^{9} \exp(h_\gamma + g_{\gamma-\beta} + f_{\gamma-2\beta+\alpha} + e_{\gamma-\alpha})}. \tag{3}$$

Here the transition probability $P(\gamma \mid \alpha,\beta)$ of the second order Markov chain model is the conditional probability that the response γ is generated after an ordered pair of responses $\alpha\beta$. The terms $f_{\gamma-2\beta+\alpha}$ and $e_{\gamma-\alpha}$ are defined as

$$f_{\gamma-2\beta+\alpha} = \widehat{f} \quad if \quad \gamma-2\beta+\alpha = 0 \tag{4}$$
$$= 0 \quad else \tag{5}$$
$$e_{\gamma-\alpha} = \widehat{e} \quad if \quad \gamma-\alpha = 0 \tag{6}$$
$$= 0 \quad else. \tag{7}$$

When we define $n_{\alpha\beta\gamma}$ as the number of the ordered triplets $\alpha\beta\gamma$ in a set $\{\{S_i\}\}$ of sequences, the log-likelihood $\log L(\{\{S_i\}\} \mid \{h_\eta\},\{g_\delta\},\widehat{f},\widehat{e})$ of our model is

$$\log L = \sum_{\alpha=0}^{9}\sum_{\beta=0}^{9}\sum_{\gamma=0}^{9} n_{\alpha\beta\gamma} \log P(\gamma \mid \alpha,\beta). \tag{8}$$

We can fit the model to the data by maximizing the log-likelihood just as we have done for the model (1).

A description with larger number of adjustable parameters is not necessarily better. Then we must be careful to choose the description for a set of sequences. Fortunately, there are several ways to choose representations of adequate complexity for a given set of sequences. Model selection procedures with the minimization of AIC (Sakamoto et al. (1986)) or with the minimization of MDL (Rissanen (1989)) are examples of them. Systematic application of the likelihood ratio test is also useful for the purpose.

We study HURGs with a set of models, which includes the model described by the Eq.(3) as a special case. Our preliminary results show that the term $e_{\gamma-\alpha}$ is relevant even for subsets of data with small number of sequences. On the other hand, the significance of the term $f_{\gamma-2\beta+\alpha}$, which is responsible for "counting sequences", seems considerably dependent on data.

5 Discussions

It is desirable to take more data under controlled conditions. For example, the notion of "random" is to be given to the subject to some extent, such as "throwing dice every time in your mind", etc. However we cannot set the condition too strong in order to preserve the creativity in the thinking of the subject.

In Sec.4.2 we propose a method based on the analysis of the residuals. Another interesting strategy for the study of patterns in HURGs is to introduce a number of models each of which represents characteristic patterns in the sequences. Then the detection of characteristic patterns reduce to the selection among these models. An example of this strategy is found in the program CATDAP (Sakamoto (1991)), which analyze contingency tables through model selection with AIC. Another example is computation of complexity of strings with FSMX models (Rissanen (1986)). This strategy will be useful for the study of HURGs.

Acknowledgments

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