

Distribution of Korean family names

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Abstract

The family name distribution in Korea is investigated in comparison with previous studies in other countries. In Korea, both the family name and its birthplace, where the ancestor of the family originated, are commonly used to distinguish one family name from the others. The family name distributions with and without the information of the regional origins are analyzed by using different data sets of various sizes, and compared with previous studies performed in other countries. The growth rate of the family is empirically obtained. Contrary to commonly used assumptions, the growth rate is found to be higher for the smaller family. © 2004 Elsevier B.V. All rights reserved.

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1. Introduction

Different from other countries, Korea is known to have relatively small number of family names. For example, the nationwide survey in 2000 has shown that the population of the family name Kim is about 10 million, which means that about one among five Koreans is Kim. In general, the family names have been devised to distinguish one family from the other. Accordingly, if the number of family names is too small, or family sizes are too big, the distinction with other families becomes very

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inefficient. From this reasoning, it is natural that Koreans have developed an additional way to give a kind of sub-system by using the information of the birthplace of the family name, i.e., where the ancestor of the family came from. For example, one of the authors of the present paper has the family name Kim from Gimhae, a region in southern Korea. The family name Kim in the 2000 survey has been found to have 348 different regional origins. Almost all Koreans know the regional origins of their family names from their birth and the state keeps this information in the population register.

In Korean culture, having an unfamiliar family name is not common at all, and most people hesitate to invent new names. For 15 years from 1985 to 2000 (Table 1), the number N_f of family names in Korea increased only by 11 ($11/277 \approx 4\%$ increase). In contrast, the number N_r of the family names with regional origins (e.g., Kim from Gimhae is taken to be different from Kim from Gyeongju), is increased in the same period by 829 ($829/3359 = 25\%$ increase) (see Table 1). Consequently, this shows that most Koreans consider inventing new family names as taboo, while branching out by using new regional origins (but with the same family name) is totally acceptable in Korean culture.

In this work, we study the distributions of the Korean family names with and without regional origins. From the above observations, one expects that the distributions look very different with and without the regional origins, and that the former distribution is similar to other countries, where having new family names is not a taboo as in Korea.

The data sets analyzed in this work are as follows (Table 1): Korea85 and Korea00 are for the total population of Korea in the years 1985 and 2000, which were downloaded from Korean National Statistical Office [1]. The set Ajou03 is from the list of registered students in Ajou University in 2003, and the other sets Seongnam98, Osan04, and Hwaseong04 are extracted from telephone books published in the corresponding cities at years 1998, 2004, and 2004, respectively. We have information of the regional origins only in Korea85 and Korea00. Throughout the paper, N is the size of populations, N_r and N_f are the numbers of family names with and without regional origins, respectively.

Table 1

Data set	N	N_f	N_r
Korea00	45,985,289	288	4,188
Korea85	40,419,652	277	3,359
Seongnam98	248,460	161	—
Osan04	19,632	114	—
Ajou03	9,802	109	—
Hwaseong04	3,952	87	—

Date sets: Korea00 and Korea85 are for the total populations in Korea in the years 2000 and 1985 [1]. Seongnam98, Osan04, and Hwaseong04 are extracted from telephone books, and Ajou03 is obtained from the list of registered students in Ajou University. N_r and N_f are numbers of family names with and without the regional origins, and N is the population.

For the k th family name (when the family name is arranged from the biggest family to smallest one in descending order), $f(k)$ is the number of people who have that name, leading to $\sum_{k=1}^{N_f} f(k) = N$. We also use the integrated probability distribution function $P_{\text{int}}(n)$, which measures the proportion of the families with size greater than n .

The paper is organized as follows: In Section 2, which contains the main results of the present work, we study various aspects of family name distributions without regional origins. The relationships among the three basic quantities, $N_f(N)$, $f(k)$, and $P_{\text{int}}(n)$ are analytically found and compared with empirical results. The distributions for various sizes of populations in Table 1 are compared with previous results in other countries. The empirically obtained growth rate as a function of the family size is also discussed. In Section 3, we perform analysis on the distributions of family names with regional origin (e.g., Kims from different regional origins are considered to be different names). Finally, Section 4 is devoted to discussions and conclusions.

2. Family name distribution

2.1. Relations: $N_f(N)$, $f(k)$, and $P_{\text{int}}(n)$

We first present in Fig. 1 the number N_f of family names versus the population. As the population is increased, the number of family names is shown to increase logarithmically. This observation is in sharp contrast to Ref. [2], where $N_f \sim N^{0.65}$ has been observed in Japan, instead of $N_f \sim \ln N$. Due to the lack of information, we are not able to study N_r versus N .

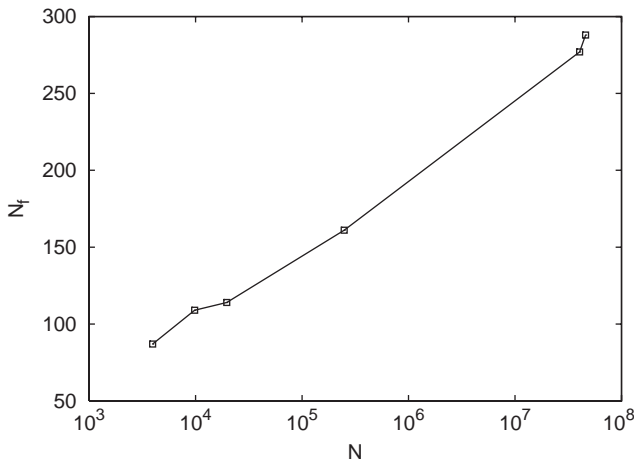


Fig. 1. The number N_f of family names without regional origins versus the population N . As the population is increased, N_f is shown to increase logarithmically. Note that only the horizontal axis is in log scale. Data are from Table 1 and the line is only a guide to the eyes.

In Fig. 2(a), the integrated distribution function $P_{\text{int}}(n)$, measuring the proportion of the family names with populations greater than or equal to n is displayed. Since every family has at least one person as its member, one gets $P_{\text{int}}(n=1) = 1$. As n is increased, $P_{\text{int}}(n)$ is a monotonically decreasing function of n until $P_{\text{int}} = 0$ is reached for $n > \max_k f(k) = f(1)$. The logarithmic decay form in Fig. 2(a) is again very different from the corresponding results for other countries, where the power-law form $P_{\text{int}}(n) \sim n^{1-\gamma}$ has been observed with $\gamma \approx 2$ for USA and Brazil [3], and $\gamma \approx 1.75$ for Japan [2]. The probability distribution function $P(n)$, which is simply the normalized histogram, is easily obtained from the derivative of P_{int} with respect to n from $P_{\text{int}}(n) = \int_n^\infty P(n') dn'$, i.e., $P(n) = -dP_{\text{int}}/dn$. In a practical point of view, $P_{\text{int}}(n)$ is more convenient than $P(n)$, since some practical issues like the bin size in $P(n)$ need not be taken care of. As will be clearly shown below the same logarithmic form in Figs. 1 and 2(a) is not accidental.

Another convenient and frequently used way of showing the distribution is the so-called Zipf's plot [4], where the population $f(k)$ of the family name is plotted in terms of the rank k . Fig. 2(b) is the Zipf's plot of $f(k)$ obtained from the data set Korea00 (see Table 1). It is clearly exhibited that $f(k)$ decays exponentially with k , again in contrast to Ref. [2] where the power-law decay has been observed.

The Zipf's plot of $f(k)$ in Fig. 2(b) and $P_{\text{int}}(n)$ are easily related since $P_{\text{int}}(n)$ is simply the number of family names of the size greater than n : Draw the horizontal line at the vertical position n in Fig. 2(b) and the value of k at the crossing point is simply $P_{\text{int}}(n)$ multiplied by N_f . In other words, once the functional form $f(k)$ is

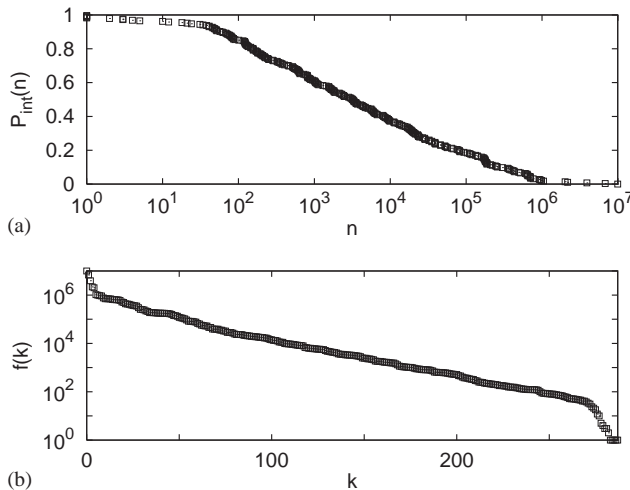


Fig. 2. (a) Integrated probability function $P_{\text{int}}(n)$ versus the family size n . $P_{\text{int}}(n)$ measures the ratio of the number of families of the sizes not less than n to the total number of family names. In a broad range of n , P_{int} is described very well by $P_{\text{int}}(n) \sim -\ln n$. (b) The population $f(k)$ as a function of the rank k of the family (Zipf's plot). The biggest family, Kim in this case, has the rank $k = 1$. In a broad range, $f(k)$ shows exponential decay. Both (a) and (b) are obtained from the data set Korea00 (see Table 1).

given, we obtain the relation

$$P_{\text{int}}(n) = f^{-1}(n)/N_f, \quad (1)$$

connecting the Zipf's plot and the integrated probability function.¹ The function $f(k)$ is always a monotonically decreasing function of k by definition, which confirms the existence of the inverse function $f^{-1}(n)$. Via Eq. (1) the logarithmic form of $P_{\text{int}}(n)$ in Fig. 2(a) implies the exponential form of $f(k)$ in Fig. 2(b) and vice versa.

We next establish the simple mathematical relation between $P_{\text{int}}(n)$ obtained for the total population N_{tot} and $N_f(N)$ obtained for various sizes N of population. The only assumption we make is that the set of $N (= xN_{\text{tot}}$ with $0 < x < 1$) individuals is taken at random without any bias.² In other words, the family with the rank k has $f(k)$ members in total, and thus in the subset of the size xN_{tot} , there are $xf(k)$ members by the same name. Consequently, once $f(k)$ for the total population is given, N_f for the subset of the size xN_{tot} is simply the number of family names that has more than one individual, $[xf(k) > 1]$, which leads to

$$N_f(xN_{\text{tot}}) = \sum_k \Theta(f(k) - 1/x), \quad (2)$$

where $\Theta(y)$ is the Heaviside step function with $\Theta(y) = 1$ for $y > 0$ and $\Theta(y) = 0$ otherwise. From the definition of $f(k)$, the right-hand side of Eq. (2) equals the value of k at the crossing point of the two curves $f(k)$ and $1/x$, yielding

$$N_f(N) = f^{-1}(N_{\text{tot}}/N) = N_f(N_{\text{tot}})P_{\text{int}}(N_{\text{tot}}/N), \quad (3)$$

where $N = xN_{\text{tot}}$ and the identity in Eq. (1) have been used. It should be noted that the relation between the Zipf's plot of $f(k)$ and the family name distribution function in Eq. (1) should hold in any case, while the relation between $N_f(N)$ and P_{int} holds only when the assumption of unbiased random sampling of population is valid. As a specific example, for the power-law form $P_{\text{int}}(n) \sim n^{-a}$, $N_f(N) \sim N^a$ is expected. It is not clear whether or not this relation has been violated in Ref. [2], where somehow self-contradictory results $P_{\text{int}}(n) \sim n^{-0.75}$ and $N_f(N) \sim N^{0.58}$ have been concluded from the same unbiased random sampling of population. However, if the proper size of errorbars are taken, we strongly believe that the discrepancy should vanish.

In Fig. 3(a), $N_f(N)$ from P_{int} for Korea00 and Korea85 are displayed together with the values in Table 1. Although all curves show the logarithmic dependence, i.e., $N_f \sim \ln N$, $N_f(N)$ from P_{int} computed by using Eq. (3) shows a systematic difference that it lies higher than the empirical results at any N . This makes us conclude that the assumption of unbiased random sampling of population is not entirely valid for data sets in Table 1. Nevertheless, the logarithmic dependence persists for all three different curves in Fig. 3(a), which appears to justify the unbiased sampling assumption as a reasonable approximation. The substantial difference in Fig. 3(a) can be interpreted as follows: Significant number of families exist in localized areas.

¹Similar result when both $f(k)$ and $P_{\text{int}}(n)$ are of the power-law form has been discussed in Ref. [2].

²The assumption appears to be very reasonable in modern societies or in big cities, while it may not be valid for small rural towns where the family name distribution is far from the one for the whole country.

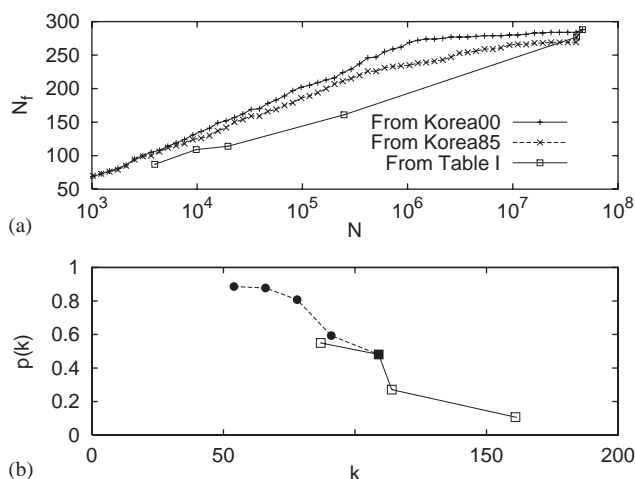


Fig. 3. (a) The number N_f of family names versus the population N , computed from P_{int} for Korea00 and Korea85 via Eq. (3). For comparison, data points in Fig. 1 are included. (b) The probability $\Pi(k)$ that an individual of the family name at the rank k is selected by the random sampling of the population. $\Pi(k)$ is a monotonically decreasing function of k , implying that people with rare names are difficult to be found in urban cities. The points are obtained by using Eq. (4) and values in Table 1 for Seongnam98, Osan04, Ajou03, and Hwaseong04. The data point marked by filled square is for Ajou03 and is somehow special since it is not based on the residential location but from the list of students in a university. Points denoted by the filled circles are obtained from random sampling within Ajou03.

For example, in some villages in rural areas, most people in the community have the same family name. Another possibility is that new names originate from foreigners who just became Koreans with new Korean names. The latter case can probably be found only in the biggest city, Seoul. Such non-uniformly distributed names in a geographic sense are captured in nationwide surveys but one cannot find them in the telephone book in cities we are investigating in this work. Accordingly, actual values of $N_f(N)$ can be different and lie lower than the expected values from Eq. (3) based on the assumption of the unbiased random sampling.

We then elaborate the above explanation further by introducing the probability $\Pi(k)$ that the name of the k th rank is chosen. The unbiased random sampling corresponds to $\Pi(k) = 1$. The extension of the above derivation of $N_f(N)$ is straightforward: The number of people with the name k in the subset of the population is now given by $x\Pi(k)f(k)$ and the $N_f(N)$ is the number of family names satisfying $x\Pi(k)f(k) > 1$. From the same reasoning as before, $N_f(N)$ with $g(k) \equiv \Pi(k)f(k)$ now reads $N_f(N) = g^{-1}(N_{\text{tot}}/N)$. Consequently, one gets the expression of the probability that the name at the rank N_f is chosen as

$$\Pi(N_f) = \frac{1}{f(N_f)} \frac{N_{\text{tot}}}{N}. \quad (4)$$

We then use the values N_f and N from the empirical values in Table 1 and then take $f(N_f)$ from the Zipf's plot for Korea00 to compute $\Pi(k)$ in Fig. 3(b), where

Seongnam98, Osan04, Ajou03, Hwaseong04 have been used. The data point (marked as filled square) for Ajou03 is somehow special since Ajou03 is not based on the residential location of individuals (Table 1). It is interesting to note that $\Pi(k)$ is a decreasing function of k , suggesting that a randomly chosen individual in urban cities is more probable to have top rank names than for the whole nation. This appears to be consistent with the expectation that rare names (with lower ranks) are not distributed uniformly across the whole country. We also sampled randomly N individuals ($N = 500, 1000, 2000, 4000$) from Ajou03 and count how many names (N_f) are found in the set. We then compute $\Pi(N_f)$ in the same way [filled circles in Fig. 3(b)].

2.2. Zipf's plots of $f(k)$

In this section, we investigate the distributions of family names for various data sets in Table 1. In Fig. 4, all data sets in Table 1 are shown to have qualitatively the same distribution: Zipf's plots of $f(k)$ for all data sets show exponential decay form, implying that the integrated probability distribution follows the logarithmic form (see discussions in Section 2.1). The unanimously found logarithmic form for $P_{\text{int}}(n)$ then suggests that the probability distribution $P(n)$, which measures how many family names have the size n , follows the following form:

$$P(n) \sim n^{-\gamma}, \quad (5)$$

with $\gamma \approx 1$ in Korea, in a sharp contrast to other countries where $\gamma > 1.5$ has been concluded. This somehow unique family name distribution in Korea can be understood from the birth–death model in Ref. [3], where it has been shown that

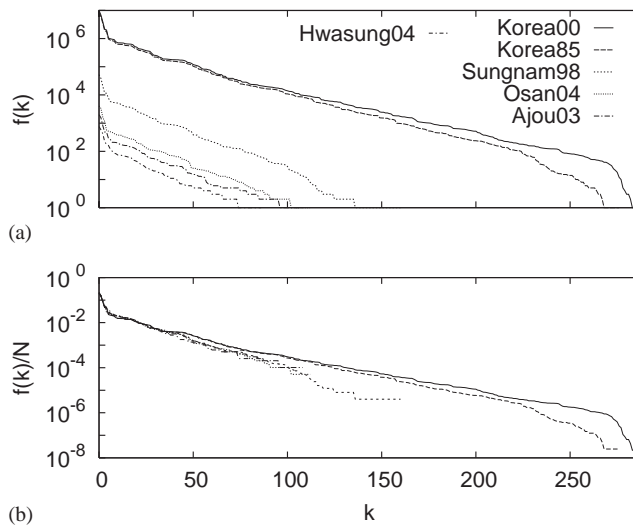


Fig. 4. (a) The population $f(k)$ as a function of the rank k of the family (Zipf's plot) for all data sets (see Table 1). (b) $f(k)/N$ versus k for the same data as in (a).

$P(n) \sim n^{-1}$ occurs in a stationary state if the total population does not grow (or the death rate $\mu = 1$) and the rate α of new name generation is very small. The latter condition appears to be fulfilled in Korea since only a very small number of new names were generated between 1985 and 2000 (see Table 1). Furthermore, the family names in Korea have been introduced to Korean societies a very long time ago (at least one thousand years ago), and therefore, one can assume that the Korean family name distribution is very close to the one at stationary state although the population is still growing. Although new name generation is also very rare in Japan like in Korea, family names in Japan, on the contrary, have a short history (most names were created about 120 years ago [2]). The qualitatively different family name distribution in Japan appears to imply that the distribution is still far from its stationary state as pointed out in Ref. [2]. From this perspective, it is very plausible that as time proceeds the family name distributions in other countries also should approach $P(n) \sim n^{-1}$ eventually, in the condition that the rate of new name generation becomes sufficiently small.

2.3. Growth rate of family size

When the family name was introduced in human history, it is expected that the larger the family, the more probable the family's survival, since the size of the family was the measure of its strength in many respects such as labor power and the number of warriors. In other words, the population growth rate of a family must have been an increasing function of the size of the family a long time ago. However, in a modern society, the population growth rate is not necessarily an increasing function of the family size since the size is no longer a matter of life and death.

We use two data sets Korea85 and Korea00 to compute the growth rate of the family size for each family name in 15 years. The growth rate of the total population is 0.1377 during this period as shown in Table 1. It is found that no name actually disappeared between 1985 and 2000, but 11 new names were created. In Fig. 5, we plot the growth rate r as a function of (a) the rank k and (b) the size n of the families. There are several very interesting features. The growth rate of some families is huge. For example, one family at a very low rank had only one individual as its member in 1985 while the family size became 462 in 2000, with a growth rate of 461 in 15 years. This can never be explained from any biological viewpoint (no one can have several hundreds of children in 15 years), but rather must be a reflection of some sociological or psychological forces. Relatively high growth rates are mostly observed in families at lower ranks, and $r(k)$ in Fig. 5(a) is roughly an increasing function of k . Such a nonuniform growth rate can be explained from the assumption that (1) the family name with a high growth rate was recently invented and that (2) the family of a smaller size tries harder to increase the number of its members by e.g., recruiting new members from relatives who still keep the old name. The above assumptions look reasonable since most people, especially who have small family sizes, probably want to see their names flourishing, not disappearing in the future.

In Fig. 5(b), we display the growth rate $r(n)$ as a function of the family size n . As expected from Fig. 5(a), $r(n)$ is a roughly decreasing function of n , saturating towards

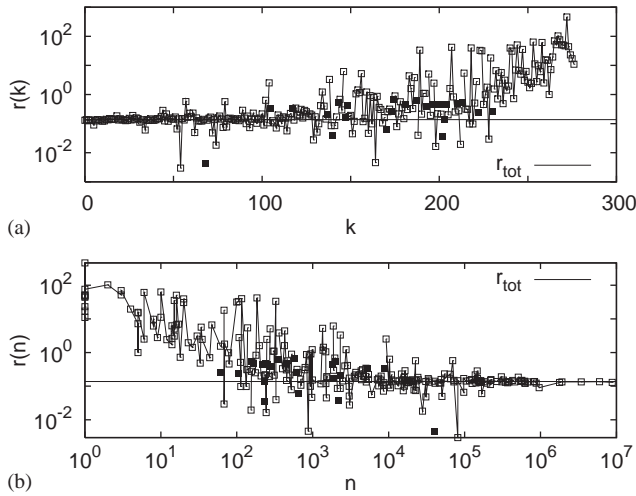


Fig. 5. The population growth rate r as a function of (a) the rank k of the family and (b) the size n of the family. r is obtained from Korea85 and Korea00 from $r = [f(k)^{2000} - f(k)^{1985}] / f(k)^{1985}$ with $f(k)^{\text{year}}$ being the size of the family of the rank k at a given year. The sizes of a number of families are found to decrease giving negative values of r . In this case, we plot $-r$ instead and denote those families as filled squares. The growth rate of total population $r_{\text{tot}} = 0.1377$ is shown (full line) for comparison.

the total growth rate r_{tot} . It is interesting to see that $r(n)$ is significantly higher than r_{tot} when $n \lesssim n_c = 10^3$. The size n_c can be interpreted as the size scale beyond which the nonbiological growth is dominated by the biological growth. One can also associate n_c with a psychological turning point in people's mind separating small and big families.

3. Family name with regional origin

As an additional way to distinguish families in Korea, the regional origins of families are simultaneously used in Korea. In this section, we regard the family name with different regional origins as distinct names, e.g., Kim from Gimhae and Kim from Gyeongju are considered to be different names, and study various aspects of the distribution.

Fig. 6 shows the integrated probability function $P_{\text{int}}(n)$ measuring the proportion of families which have more than n family members. The distribution in Fig. 6, with the broad intermediate range described by the power-law behavior, is very different from the corresponding plot in Fig. 2. In other words, the family name distributions are completely different with and without the regional origins. Furthermore, although the distribution of the family names without information of regional origins in Korea is very different from other countries, if the regional origins are used to distinguish one family from others the distribution shows the qualitatively similar behavior to that in other countries. More specifically, the power-law behavior $P(n) \sim n^{-\gamma}$ [i.e., $P_{\text{int}}(n) \sim n^{1-\gamma}$] is observed in a broad range of n .

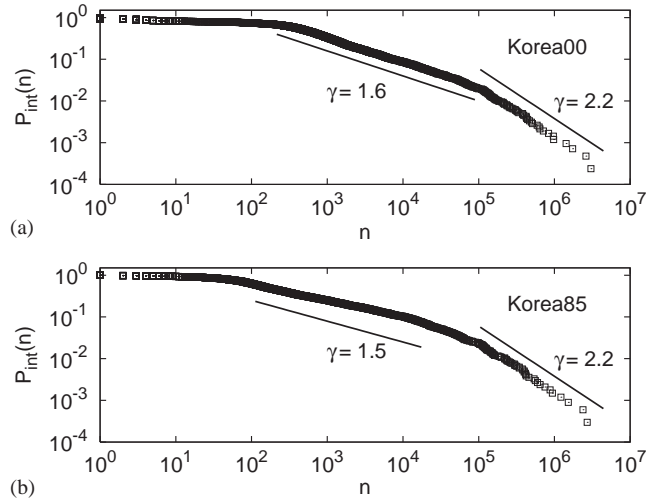


Fig. 6. Integrated probability function $P_{\text{int}}(n)$ versus the family size when the name with different regional origins is taken as different for data sets (a) Korea00 and (b) Korea85.

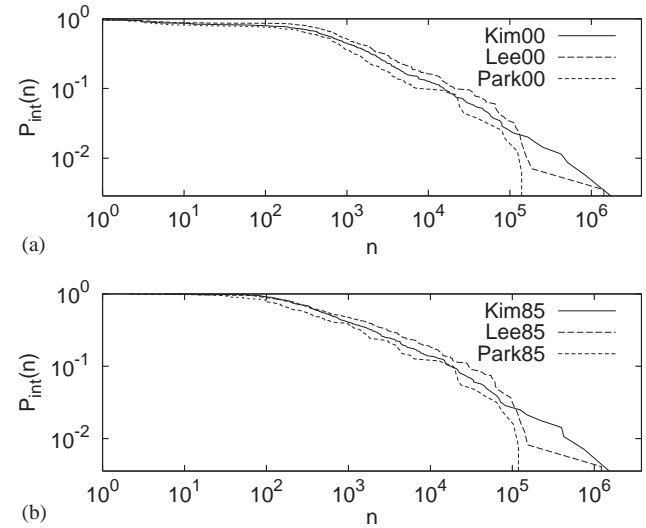


Fig. 7. $P_{\text{int}}(n)$ for subsets with the family name Kim, Lee, and Park subtracted from (a) Korea00 and (b) Korea85. Kim's with different regional origins are considered to be different. The power-law decay behavior of $P_{\text{int}}(n)$ are ubiquitously seen.

Fig. 7 is for the subsets of (a) Korea00 and (b) Korea85. For example, Kim00 is a subset of Korea00 that contains only the name Kim but from different regional origins. The three biggest families Kim, Lee, and Park have 348, 283, and 159 different regional origins in Korea00, and 281, 244, and 127 in Korea85, implying

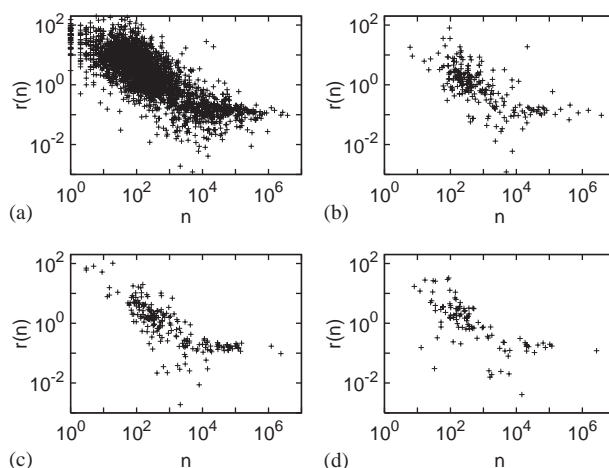


Fig. 8. Growth rate $r(n)$ as a function of family size n for (a) Korea, (b) Kim, (c) Lee, (d) Park. Identical family names but with different regional origins are considered as different.

that new regional origins have been branching out quite rapidly within a family. All curves in Fig. 7 have similar power-law decay behaviors as in Fig. 6.

We finally investigate in Fig. 8 the growth rate $r(n)$ for the family name with regional origin as a function of the family size n for (a) the whole data set Korea, and for three major family names (b) Kim, (c) Lee, and (d) Park; All show qualitatively the same behaviors as in Fig. 5 in Section 2.3, i.e., very high growth rate for small families, and saturation to average growth rate beyond around $n = 10^3$. It is interesting to note that as long as the growth rate $r(n)$ is concerned, the behavior does not depend much on whether the regional origins are taken into account or not. This implies that a family with a very common family name but with a very rare regional origin still considers itself as small and thus makes tremendous nonbiological efforts to increase its members.

4. Conclusion

We, in this paper, have studied the distributions of Korean family names extracted from various sources: from nationwide surveys in 1985 and 2000, from telephone books published in three cities, and from the list of registered students in a university. Family name with and without regional origins have been found to show quite different distributions: Integrated probability distribution is logarithmic without regional origins (Kim from Gimhae and Kim for Gyeongju are regarded as the same name), while it is power-law behavior with regional origins (Kim from Gimhae is considered to be a different name than Kim from Gyeongju). The difference is also reflected in the Zipf's plot of family size $f(k)$ with the family rank k : exponential versus power-law.

Relation between $P_{\text{int}}(n)$ and $f(k)$ have been established, and $N_f(N)$ (how many family names are found in population N) has been shown to have a simple relation with $f(k)$ (and thus with $P_{\text{int}}(n)$) by using the assumption of random unbiased sampling. The empirical observations show systematic deviations from the expected values, which were then used to compute the probability $\Pi(k)$ that the family at the rank k is selected if we pick one individual at random. Interestingly, $\Pi(k)$ has been found to be decreasing function of k , implying that small family names are hard to find in general.

Growth rate $r(n)$ for family of size n has been computed from empirical data (with and without regional origins). All show very interesting behaviors: Huge growth rate [$O(10^2)$ in 15 years] for small families implying nonbiological growth, and saturation towards average growth rate starting from around $n_c \approx 10^3$, which has been interpreted as the sociological/psychological separation point of big and small families.

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