

## 5.0 Introduction

The arguments presented so far have all been "structural", or in the vocabulary of some, "deterministic". In the author's view, "deterministic" is a highly improper description since one need not pretend a system ever followed a rule to study the structure or structures which would allow the rule to function. Indeed, as soon as we discuss anything other than 1-stable minimal systems, the apparent determinism quickly evaporates.

Marriage theory is therefore not a deterministic theory, but neither is it "probabilistic" or "stochastic" as we have so far viewed it. Nonetheless, there are very important problems of empirical interpretation which appear to demand these approaches. In this and the next chapter, I have arbitrarily isolated two sorts of non-deterministic models: those which resemble sampling with a fixed probability (probabilistic models in the present chapter), and those which may have an underlying probabilistic foundation but appear to be more easily modeled by some other technique ("stochastic model", in chapter 6). What we are essentially after in this chapter is a means to estimate with a probability the "viability" of a population with particular population statistics and particular network structure.

## 5.1 Family Sizes

The most important and obvious non-deterministic problem in marriage theory is family size. The minimality condition used so far implies that a population observed over several generations is minimally stable if the size in any later generation is equal to or greater than the size of the first generation, but no bigger than it needs to survive. This allows us to write a simple equation which holds for minimal or nearly minimal surviving sequences (or, for that matter, any surviving sequence).

$$(1) \quad |g_i(t)| \geq |g_i(t-1)|$$

From (1), we can find a new equation. Let  $f_i(t)$  be the frequency of family size occurring in the  $t$ th generation. Since  $\sum_{i=1}^{\infty} f_i(t) = 1$ , then

$$(2a) \quad \sum_{i=1}^{\infty} i f_i(t)$$

is the average family size of the  $t$ th generation and

$$(2b) \quad \sum_{i=1}^{\infty} i f_i(t-1)$$

is the average family size of the  $(t-1)$ th generation.

One may reason that the number of individuals produced in a generation  $n$  is the number of marriages in the previous generation  $|\underline{m}^{(t-1)}|$ , times the proportion of "fertile" marriages  $h_{t-1}$ , times the average family size of that generation. However, if we assume that each generation forms as many marriages as possible, then the number of marriages is simply the population size  $|\underline{G}^{(t-1)}|$  times the minimum of the proportion  $\underline{m}$  of males or  $\underline{f}$  of females ( $\underline{m} + \underline{f} = 1$ ) and we lose no generality by denoting this minimum by  $\underline{m}$ . Therefore, we can write

$$(3) \quad |\underline{G}^{(t)}| = h_{t-1} \underline{m}_{t-1} |\underline{G}^{(t-1)}| \prod_{i=1}^t \text{if}^{(t-1)}.$$

Dividing by  $|\underline{G}^{(t-1)}|$  we get

$$(4) \quad \frac{|\underline{G}^{(t)}|}{|\underline{G}^{(t-1)}|} = h_{t-1} \cdot \underline{m}_{t-1} \cdot \prod_{i=1}^t \text{if}^{(t-1)}.$$

Now, equation (1) implies

$$(5a) \quad \frac{|\underline{G}^{(t)}|}{|\underline{G}^{(t-1)}|} \geq 1$$

holds in turn only if (5b) holds:

$$(5b) \quad \prod_{i=1}^t \text{if}^{(t-1)} \geq \frac{1}{h_{t-1} \cdot \underline{m}_{t-1}}$$

Equation (5b) is interesting for a variety of reasons. First, it is expressed completely in terms of information available on a well done genealogy of a living population at a given time. Second, both sides are independently measurable, so that values may be meaningfully calculated. Third, because it is calculable, it provides a direct means of testing at least one implication: those societies in which equation (5b) does not hold, should also not be minimal, or should be undergoing some transformation (such as migration) which maintains the existing system in spite of the apparent lack of population.

But most important for present purposes, it leads directly to recognition that average family sizes in evolving sequences need not be, and in general are not, the ideal 2 persons per family. Indeed, this only occurs when  $h = 1$ , and  $\underline{m} = 1/2$ , which of course are the conditions of minimal structural stability found in chapter 4. In general,  $h < 1$ , and  $\underline{m} \neq 1/2$ . We wish to study the effects of variations in one or the other of these parameters. (Note that  $h$  may relate in some cases to  $c$  of chapter 1.)

### 5.1 Sex Ratio

One of the main reasons that the average family size is not two persons per family even in an equilibrium condition in that the numbers of males and females in an arbitrary population are not equal. The present section, which was worked out by Mr. Duchamp, provides a means of estimating the increased family size implied.

Let  $n$  be the total number of population pairs in the generation, and  $E(N)$  the expected difference between number of males and females in a population of size  $N$ . Use  $j$  to index possible values of this difference, and  $p$  and  $q$  for the probabilities of males and females respectively. The formula for  $E(N)$  is then given by:

$$E(N) = \sum_{j=0}^N |N - 2j| \binom{N}{j} p^{N-j} q^j$$

In the expression,  $\binom{N}{j}$  is the combinatorial  $\binom{N}{j} = \frac{N!}{j!(N-j)!}$  which may be approximated by the appropriate gamma function

$$\binom{N}{j} = \frac{\Gamma(N+1)}{\Gamma(j+1)\Gamma(N-j+1)}$$

which was used to calculate table 5.1. Because there are small errors as the number of combinations becomes larger, due to approximations in the computer, the values past 80 =  $N$  are not included. Every tenth value is shown only to give an idea of the general behavior of the function, which continues to decline. The table assumes  $\underline{m} = \underline{f} = 1/2$  in calculating expectations.

The average family size in table 5.1 is estimated from

$$\frac{1 - E(N)/N}{2}$$

since  $\frac{E(N)}{N}$  is the proportion lost per generation from an absolute loss of  $E(N)$  in a population of size  $N$ . Entries in the table are the population size  $N$ , expected loss  $E(N)$ , incremental loss  $\Delta E(N)$ , incremental proportion  $\frac{\Delta E(N)}{\Delta N}$ , and the family size needed for equilibrium. Incremental family size is computed as:

$$\frac{\Delta E(N)}{\Delta N} = \frac{E(N) - E(N-2)}{N - (N-2)}$$

Values from table 5.1 will be used again in later chapters.

TABLE 5.1: EQUILIBRIUM FAMILY SIZE FOR SEX RATIO 1/2 IN POPULATIONS OF SIZE N

N	E(N)	LE(N)	$\frac{1 - E(N)/N}{2}$ Equilibrium average family size
2	1.000	1.000	4.000
4	1.500	0.500	1.200
6	1.875	0.375	2.909
8	2.187	0.312	2.752
10	2.460	0.273	2.652
12	2.707	0.246	2.582
14	2.932	0.225	2.529
16	3.142	0.209	2.488
18	3.338	0.196	2.455
20	3.523	0.185	2.427
22	3.700	0.176	2.404
24	3.868	0.168	2.384
26	4.029	0.161	2.366
28	4.184	0.155	2.351
30	4.334	0.149	2.337
32	4.478	0.144	2.325
34	4.618	0.140	2.314
36	4.754	0.135	2.304
38	4.886	0.132	2.295
40	5.014	0.128	2.286
42	5.140	0.125	2.278
44	5.262	0.122	2.271
46	5.382	0.119	2.265
48	5.499	0.117	2.258
50	5.613	0.114	2.253
60	6.154	0.104	2.228
70	6.652	0.096	2.210
80	7.114	0.090	2.195
90	7.547	0.084	2.183
100	7.958	0.082	2.172
110	8.345	0.073	2.164
120	8.720	0.074	2.156
130	9.079	0.070	2.150
140	9.422	0.067	2.144
150	9.755	0.066	2.139
160	10.078	0.066	2.134
170	10.387	0.059	2.130
180	10.690	0.060	2.126
190	10.984	0.058	2.122
200	11.269	0.056	2.119
210	11.548	0.056	2.116
220	11.822	0.053	2.113
230	12.089	0.051	2.111
240	12.345	0.051	2.108
250	12.601	0.047	2.106

## 5.3 Survival Chances I

In this section we will develop a formula specific to circular mating systems. We define  $s$  as the length of a cycle, family size as  $n$ , sex distribution  $p_m + p_f = 1$ , and probability of survival  $p_s$  for a cycle of length  $s$ . We further assume that each distinct family must produce both males and females in order to participate in the mating exchanges. I am aware that this approach ignores many combinatorial difficulties, but hope that those with better skills in the field may improve upon my work.

We proceed as follows. For offspringing family size  $n$ , the probability of all members being males is  $\bar{m}^n$  and of all members being females is  $\bar{f}^n$ . The probability of each of the  $s$  reproducing units being neither all male nor all female is thus

$$(1 - \bar{m}^n - \bar{f}^n)$$

for all  $s$  families to be so,  $p_s$  becomes:

$$p_s = (1 - (\bar{m}^n + \bar{f}^n))^s$$

and for  $\bar{m} = \bar{f} = 1/2$ ,

$$p_s = (1 - 1/2^{n-1})^s$$

Thus for family size  $n = 1$ , the system has no chance of survival, while for large family size, the chances are much higher, depending on the values of  $s$ .

The following are a few examples. With family size 2 and cycle length 3,

$$p_3 = (1 - 1/2)^3 = 1/2^3 = 1/8$$

while with length 5,

$$p_5 = (1 - 1/2)^5 = 1/2^5 = 1/32$$

With family size 3, and cycle length 4, the above formula gives survival probability  $(3/4)^4$ , while with lengths 3 and 5, the probabilities are respectively  $(3/4)^3$  and  $(3/4)^5$ .

A group of this sort may well want to maximize its survival chances. In the present model, there are only two ways to do this: decrease the cycle length, or increase the family size (or both). To allow  $s$  to change for a fixed probability of survival, adjustments in  $n$  are required, and may be found from the following.

With known values of  $p_s$ ,  $n_0$  and  $s_0$ , and a particular new value of  $s_1$ , the formula for  $n$  can be found from:

$$p_{s_0} = (1 - 1/2^{n_0-1})^{s_0} = (1 - 1/2^{n_1-1})^{s_1} = p_{s_1}$$

By taking logs and rearrangement, we get:

$$n = \frac{\log(1 - [1 - 1/2^n] \frac{s}{s_1})}{\log 1/2} + 1$$

for constant probability as structure size changes.

Taking as an example  $n_0 = 2$ ,  $s_0 = 2$ , and  $s_1 = 4$ , this formula gives  $n_1 = 2.74$ . If this data point were graphed, it would be easily seen to lie between the curves for family sizes 2 and 3. The formula generates a whole "family" of related curves, one for each value of average family size, so the particular point is simply in one of the many possible curves.

An analogous expression tells how to change the stability number in order to reduce the family size needed for stability. This time we must presume  $s_0, n_0$  and  $n_1$  are known, and that  $n_1 < n_0$ . We start from the same equality as in the last section, but by very simple taking of logs and division, find:

$$s_1 = \frac{s_0 \log(1 - 1/2^{n_0-1})}{\log(1 - 1/2^{n_1-1})}$$

Reversing the example of the last section, for  $n_0 = 2.74$ ,  $n_1 = 2.0$ , and  $s_0 = 4$ , we find that  $s_1 = 2$  is a suitable solution.

We may thus calculate the chance of survival given values of family size and structural description, and given the values from which these have been adjusted, or to which they will be changed. We can calculate the effect of various changes providing the probability is fixed. We now wish to calculate the needed family size  $n$  to maintain a marriage rate near its structural minimum, for a specified probability of survival. Taking the log of the general formula for  $P_1$  given at the start of the section, we get

$$n = \frac{\log(1 - P_1^{1/s})}{\log(1/2)} + 1$$

As an example, take  $s = 4$ , and the survival chances .5, .75, .9:

$$\begin{array}{ll} \text{for } P_1 = .5, & n = 3.6 \\ P_1 = .75, & n = 4.7 \\ P_1 = .9, & n = 6.3 \end{array}$$

#### 5.4 Survival Chances II

To analyze survival probability, one must ask "survival of what". To answer this, I shall begin with an unproved but provable statement: a very large number of the conceivable marriage systems can be represented by pairs of sibships in "sister exchange". Using  $s$  as the structural number of a given rule, this means that for even numbered structural numbers, one need only analyze the probability that all of the  $s/2 = w$  pairings survive, for 1-stable  $w(M2)$  minimal configurations.

For each of the  $w$  pairs, if the family size is 2, the possible sex distributions are  $(m,m)$ ,  $(m,f)$ ,  $(f,f)$ , which occur if the sex proportions are  $\underline{m} + \underline{f} = 1$ , with frequencies  $\underline{m}^2$ ,  $2\underline{m}\underline{f}$ ,  $\underline{f}^2$ . Construction a table of the possible combinations to calculate frequencies of each type of pairing, it is apparent that only the back diagonal entries are "fully viable" for most systems.

	$\underline{m}^2$	$2\underline{m}\underline{f}$	$\underline{f}^2$
$(m,m)$	$\underline{m}^2$	$2\underline{m}\underline{f}$	$\underline{f}^2$
$(f,m)$	$2\underline{m}\underline{f}$	$2\underline{m}\underline{f}$	$2\underline{m}\underline{f}$
$(f,f)$	$\underline{f}^2$	$2\underline{m}\underline{f}$	$\underline{f}^2$

The entries " $\underline{m}^4$ " and " $\underline{f}^4$ " are clearly not viable in any system, since this pairing of sibships is all of one or the other sex, with the indicated frequency.

Similarly, entries such as  $2\underline{m}\underline{f}^2$  and  $2\underline{m}^2\underline{f}$  show "partially viable" systems, since on the average only one pair of individuals from the four may mate, and two persons of the same sex will be left mateless. (This assumption of monogamy is required by the definitions of chapter 4. However, see section 7.3 for how to relax this assumption.) It is thus apparent that the fully non-viable portion of pairing with average family size  $\bar{n}$  is  $2(\underline{m}\bar{n} + \underline{f}\bar{n})$ , or if  $\underline{m} = \underline{f} = 1/2$ ,

$$(1) \quad v = 2(1/2)\bar{n} = 1/2\bar{n}-1$$

Similarly, there are four "partial-survival" terms in  $v_p$  or where sex ratios are equal

$$(2) \quad v_p = \bar{n}(1/2)\bar{n}-2$$

The corresponding survival probabilities become

$$(3) \quad \begin{array}{l} S_1 = (1 - v)^v \\ S_2 = (1 - v - v_p)^v \end{array}$$

and the equilibrium replacement per individual thus is  $1/S_1$  and  $1/S_2$ , respectively, or  $2/S_1$   $2/S_2$  for replacement family size per successfully mated pair of individuals.

Computation of  $S_1, S_2, 1/S_1, 1/S_2$  for  $w = 1, 2, \dots, 20$  (structural numbers 2, 4, ..., 40) for family sizes 2 through 10 in increments of .2 was carried out by computer. Table 5.2 (see end of this chapter) for  $w = 1, 2, \dots, 10$  shows typical patterns.  $S_1$  starts at low values, but "quickly", usually by  $n \leq 4.0$ , reaches a 90% or higher  $S_1$  survival, and that while  $S_2$  may require astonishingly large replacement per person at small values,  $1/S_2$  also drops to seemingly reasonable levels with smallish  $n$ .

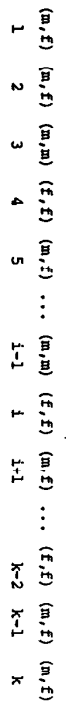
Results of these computations will be summarized in chapter 6. However, note that the results obtained by a Stirling number technique in the next chapter could just as well result from picking a fixed survival probability, and finding the associated family sizes for each.

5.5 Preliminary Probabilities of Cycles

In this section, we will begin to discuss the statistics which need to be developed for a more complete theory of internal population structure (i.e. linkages found in geneological histories). In previous sections, we derived the condition that the average distinct family size in an offspring generation must be greater than or equal to the inverse of the product of the proportion of reproducing matings that survive using a marriage rule if the system has fewer people in it than are required by the structural numbers. Hence, a closely related probability is that of finding a chain large enough to be minimal, or to find the minimal cycle exdstant at a given time, if any. (I point out that material in this section was worked out with the cooperation of Mr. Duchamp.)

The problem discussed here is the probability of being able to have a chain of length  $k$  given:  $k$  = families of 2 siblings each with the probability of male =  $M$ , and the probability of female =  $F$ , subject to condition that male cannot marry male and female cannot marry female. We will use "d.f" to mean "distinct family" (each B-set is a distinct family). Note that we are operating under minimal structural conditions of 1) monogamy; 2) two offspring per family; 3) identifiable and discrete generations; 4) survival to reproduction of all births; 5) marriage within generations but not between them; 6) all available people will marry and reproduce if possible. We seek the probability that the sex distribution of the members of the distinct families will allow marriage which produces a "chain" of length  $k$ .

Label the families: 1, 2, 3, 4, . . . , k. These numbers correspond to segments of the chain. We can represent a particular chain by the following illustration:



By the way, this notation can be easily elaborated "chemical" style by using subscripts for repeated elements, and dots between closed cycles:

$$2(M2) = \{2(mF)_2, 2[(mm)(ff)_2], (mF)_2 \cdot (mm)(ff)\}$$

An admissible chain is one in which: a) the number of links of form (m,m) occurring = the number of links with (f,f) occurring; b) the first part of the first entry (in this example: m) is of opposite sex as the last part of the last entry (in this example: f); c) the second part of  $k$ th entry must be different from the first part of  $(k+1)$ th entry; d) in between any two (m,n) terms must occur an (f,f) term; e) in between any two (f,f) terms must occur an (m,m) term; (note that d and e imply a). Therefore, the placement of the m,m terms and f,f terms completely determine the chain.

Let:  $P_{mm}$  = probability of 2 males in the same family (e.g., sibship),  
 $P_{ff}$  = probability of 2 females in the same family,  
 $P_{mf}$  = probability of a male and a female in the same family.

We can classify all chains according to the number of (m,m) terms or the number of (f,f) terms. A particular chain having  $n(m,m)$  terms has probability

$$P_n^k = (P_{mm}^n)^n (P_{mf}^{1-2n})$$

of occurring.

However, we can argue that the distribution of such elements will not affect the ability to form cycles, since the probability of creating a chain of length  $n$  in a population of  $2n$  is simply the probability of finding  $n$  males and  $n$  females in the population. This follows from the restrictive assumption of 2 people per distinct family, and the need to link distinct families through a male to a female in each marriage pair. Hence the formula giving the probabilities is:

$$P(n) = C_{2n}^n \frac{n^n}{m^n}$$

For the value  $P(n)$  the probability thus calculated is:

$n = 1$	.500
2	.375
3	.312
4	.258
5	.207
6	.163
7	.126
8	.094

This data assumes  $\bar{f} = \bar{m} = 1/2$ .

This shows that cycles of lengths greater than five are relatively unlikely to occur, and that lengths of eight or more are very unlikely, for family size two.

The formula used to calculate this curve is also a special case in another sense, which will be presented now in more general form. The special case presumes that the cycle length  $k$  and number of males in the population are equal. Using  $\bar{p} =$  probability of a male, and  $\bar{q} =$  probability of a female offspring, the distribution of possible offspring pairs is given by the binomial distribution:  $i = (\bar{m} + \bar{f})^{2n}$ , where  $\bar{n}$  is the number of families, each having two offspring per family. In addition,  $|\bar{m}| + |\bar{f}| = 2\bar{n}$ , since there are as many total male plus female offspring as there are families. We can calculate the following probability of being able to get the maximum possible chain of length  $k = P(k)$ , which is:

$$P(k) = \frac{2n-k}{j=k} \binom{2n}{j} \bar{m}^{2n-j} \bar{f}^j$$

providing  $k \leq \bar{n}$ . However, the possibility of a chain of exactly length  $k$  is

$$P_e(k) = \binom{2n}{k} \bar{m}^k \bar{f}^{2n-k} + \binom{2n}{2n-k} \bar{m}^{2n-k} \bar{f}^k$$

Therefore,  $2n - m \leq k$  or  $2n - k \geq m$ , and  $k \leq n \leq 2n - k$  which implies  $k \leq 2n - j \leq 2n - k$ . The formula used above is the special case of this when  $k = \bar{n}$ .

#### 5.6 The Number of First Cousins

One of the more apparently simple questions in an intuitive approach to anthropology is to ask how many first cousins a person can have, given a marriage system. And indeed, the diagrams used so far make the answer appear quite simple. But as one moves from the elementary diagrams, the complexity increases quickly.

The following material gives an example of this, by proceeding from the simple diagrams and the formulas based on them to more involved considerations. The result is a formula for the average expected number of first cousins in a population of an arbitrary composition of cycles and chains of arbitrary length. Such formula leads to notion of equivalence of systems whose structures are vastly different when seen

as geneologies. In particular, it implies that a generation with arbitrary internal structure may in some cases be equivalent to a simple circular system of given length (that is, to one of the configurational elements  $M_i$ ). This emphasizes the potential importance of a theory of cycle structure in future developments.

If we carry out sample calculations on the simple configurational diagrams with two persons per distinct family, as in minimal systems, the average number of first cousins per person in a chain of length  $n$  is  $4 \frac{n-2}{n-1}$ . As can be seen, in an infinite chain, the ratio approaches 4, so that a very long chain and a very long cycle may be equivalent for statistical purposes.

This leads to the interesting observation that we may identify a chain of specified length which is statistically similar to an arbitrary composition of cycles and chains in the population, so long as one knows the average number of first cousins in the system. Where  $z$  is the average number of first cousins,  $z = 4 \frac{n-2}{n-1}$  implies that this equivalent length is  $n = \frac{z+8}{z-4}$ . Both by plotting a few points, the reader can discover that this number grows from  $\bar{n} = 2$  at  $z = 0$ , to  $\bar{n} = 50$  for  $z = 3.99$ , and that as  $z$  approaches 4.0,  $\bar{n}$  very quickly grows into large values! Note that in a cycle, the number of families  $\bar{n}$  is also the length of the cycle.

TABLE 5.2a SURVIVAL PROBABILITIES FOR  $w = 1, \dots, 10; s = 2, 4, \dots, 20$ .

$w = 1$

$n$	$1/S_1$	$S_1$	$1/S_2$	$S_2$
1.0	1.142	0.874	2.666	0.374
1.2	1.104	0.905	2.047	0.488
1.4	1.077	0.928	1.713	0.583
1.6	1.057	0.945	1.509	0.662
1.8	1.043	0.958	1.373	0.727
2.0	1.032	0.968	1.280	0.781
2.2	1.024	0.976	1.212	0.824
2.4	1.018	0.982	1.162	0.860
2.6	1.013	0.986	1.125	0.884
2.8	1.010	0.989	1.097	0.911
3.0	1.010	0.992	1.075	0.929
3.2	1.007	0.994	1.058	0.944
3.4	1.006	0.995	1.046	0.956
3.6	1.004	0.996	1.035	0.965
3.8	1.003	0.997	1.028	0.972
4.0	1.002	0.998	1.022	0.978
4.2	1.002	0.998	1.017	0.983
4.4	1.001	0.998	1.013	0.986
4.6	1.001	0.999	1.010	0.989
4.8	1.000	0.999	1.008	0.991
5.0	1.000	0.999	1.006	0.993
5.2	1.000	0.999		
5.4	1.000			
5.6	1.000			
5.8	1.000			
6.0	1.000			

$w = 2$

2.0	1.306	0.765	7.111	0.140
2.2	1.220	0.819	4.191	0.238
2.4	1.160	0.861	2.936	0.340
2.6	1.118	0.894	2.277	0.439
2.8	1.087	0.919	1.887	0.529
3.0	1.065	0.938	1.638	0.610
3.2	1.049	0.953	1.470	0.680
3.4	1.036	0.964	1.352	0.739
3.6	1.027	0.972	1.266	0.789
3.8	1.020	0.979	1.204	0.830
4.0	1.015	0.984	1.157	0.864
4.2	1.011	0.988	1.121	0.891
4.4	1.009	0.991	1.094	0.913
4.6	1.006	0.993	1.073	0.931
4.8	1.005	0.994	1.057	0.946
5.0	1.003	0.996	1.004	0.957
5.2	1.003	0.997	1.034	0.966
5.4	1.002	0.997	1.027	0.973
5.6	1.001	0.998	1.021	0.979
5.8	1.001	0.998	1.016	0.983
6.0	1.001	0.999	1.012	0.987

$w = 3$

$n$	$1/S_1$	$S_1$	$1/S_2$	$S_2$
2.0	1.492	0.669	18.963	0.052
2.2	1.347	0.741	8.581	0.116
2.4	1.250	0.799	5.031	0.198
2.6	1.182	0.845	3.436	0.290
2.8	1.134	0.881	2.593	0.385
3.0	1.099	0.909	2.097	0.476
3.2	1.074	0.930	1.782	0.560
3.4	1.055	0.947	1.572	0.636
3.6	1.041	0.959	1.425	0.701
3.8	1.031	0.969	1.321	0.756
4.0	1.023	0.976	1.244	0.803
4.2	1.018	0.982	1.187	0.842
4.4	1.013	0.986	1.144	0.873
4.6	1.010	0.989	1.111	0.899
4.8	1.007	0.992	1.086	0.920
5.0	1.005	0.994	1.067	0.936
5.2	1.004	0.995	1.052	0.950
5.4	1.003	0.996	1.040	0.960
5.6	1.002	0.997	1.031	0.969
5.8	1.001	0.998	1.024	0.975
6.0	1.001	0.998	1.019	0.981

$w = 4$

2.0	1.706	0.586	50.567	0.019
2.2	1.489	0.671	17.568	0.056
2.4	1.347	0.742	8.620	0.115
2.6	1.250	0.799	5.186	0.192
2.8	1.183	0.844	3.563	0.280
3.0	1.135	0.880	2.684	0.372
3.2	1.100	0.908	2.161	0.462
3.4	1.075	0.930	1.828	0.547
3.6	1.056	0.946	1.604	0.623
3.8	1.042	0.959	1.449	0.689
4.0	1.031	0.969	1.338	0.747
4.2	1.024	0.976	1.257	0.795
4.4	1.018	0.982	1.197	0.835
4.6	1.013	0.986	1.151	0.868
4.8	1.010	0.989	1.117	0.895
5.0	1.007	0.992	1.090	0.916
5.2	1.005	0.994	1.070	0.934
5.4	1.004	0.995	1.054	0.948
5.6	1.003	0.996	1.042	0.959
5.8	1.002	0.997	1.033	0.967
6.0	1.002	0.998	1.025	0.974

$\bar{n}$	$1/s_1$	$s_1$	$1/s_2$	$s_2$	$\bar{n}$	$1/s_1$	$s_1$	$1/s_2$	$s_2$
$w = 5$									
2.0	1.949	0.512	134.847	0.007	2.0	2.546	0.392	958.917	0.001
2.2	1.644	0.607	35.968	0.027	2.2	2.217	0.451	308.653	0.003
2.4	1.451	0.689	14.771	0.067	2.4	1.814	0.551	74.318	0.013
2.6	1.322	0.755	7.826	0.127	2.6	1.564	0.639	26.894	0.037
2.8	1.234	0.810	4.895	0.204	2.8	1.400	0.714	12.695	0.078
3.0	1.172	0.853	3.436	0.291	3.0	1.289	0.775	7.205	0.138
3.2	1.127	0.887	2.620	0.381	3.2	1.211	0.825	4.671	0.214
3.4	1.094	0.913	2.125	0.470	3.4	1.155	0.865	3.342	0.299
3.6	1.070	0.933	1.806	0.553	3.6	1.115	0.896	2.575	0.388
3.8	1.053	0.949	1.590	0.628	3.8	1.086	0.920	2.101	0.475
4.0	1.040	0.961	1.439	0.694	4.0	1.064	0.939	1.791	0.558
4.2	1.030	0.970	1.331	0.751	4.2	1.048	0.953	1.581	0.632
4.4	1.022	0.977	1.252	0.798	4.4	1.036	0.964	1.433	0.697
4.6	1.017	0.983	1.193	0.838	4.6	1.027	0.973	1.326	0.753
4.8	1.013	0.987	1.148	0.870	4.8	1.020	0.979	1.248	0.801
5.0	1.009	0.990	1.114	0.897	5.0	1.015	0.984	1.189	0.840
5.2	1.007	0.992	1.088	0.918	5.2	1.011	0.988	1.145	0.872
5.4	1.005	0.994	1.068	0.935	5.4	1.009	0.991	1.112	0.898
5.6	1.004	0.995	1.053	0.949	5.6	1.006	0.993	1.087	0.919
5.8	1.003	0.996	1.041	0.960	5.8	1.005	0.994	1.067	0.936
6.0	1.002	0.997	1.032	0.968	6.0	1.003	0.996	1.052	0.950
$w = 6$									
2.0	2.278	9.448	359.594	0.002	2.0	2.910	0.343	2,557.114	0.000
2.2	1.816	9.550	73.638	0.013	2.2	2.217	0.451	308.653	0.003
2.4	1.563	0.639	25.311	0.039	2.4	1.814	0.551	74.318	0.013
2.6	1.398	0.714	11.810	0.084	2.6	1.564	0.639	26.894	0.037
2.8	1.287	0.776	6.725	0.148	2.8	1.400	0.714	12.695	0.078
3.0	1.209	0.826	4.398	0.227	3.0	1.289	0.775	7.205	0.138
3.2	1.154	0.866	3.177	0.314	3.2	1.211	0.825	4.671	0.214
3.4	1.114	0.897	2.471	0.404	3.4	1.155	0.865	3.342	0.299
3.6	1.085	0.921	2.033	0.491	3.6	1.115	0.896	2.575	0.388
3.8	1.064	0.939	1.745	0.572	3.8	1.086	0.920	2.101	0.475
4.0	1.048	0.954	1.548	0.645	4.0	1.064	0.939	1.791	0.558
4.2	1.036	0.964	1.410	0.709	4.2	1.048	0.953	1.581	0.632
4.4	1.027	0.973	1.309	0.763	4.4	1.036	0.964	1.433	0.697
4.6	1.020	0.979	1.235	0.809	4.6	1.027	0.973	1.326	0.753
4.8	1.015	0.984	1.180	0.846	4.8	1.020	0.979	1.248	0.801
5.0	1.011	0.988	1.139	0.877	5.0	1.015	0.984	1.189	0.840
5.2	1.008	0.991	1.107	0.902	5.2	1.011	0.988	1.145	0.872
5.4	1.006	0.993	1.083	0.923	5.4	1.009	0.991	1.112	0.898
5.6	1.005	0.994	1.064	0.939	5.6	1.006	0.993	1.087	0.919
5.8	1.003	0.996	1.050	0.952	5.8	1.005	0.994	1.067	0.936
6.0	1.002	0.997	1.038	0.962	6.0	1.003	0.996	1.052	0.950
$w = 7$									
2.0	1.949	0.512	134.847	0.007	2.0	2.546	0.392	958.917	0.001
2.2	1.644	0.607	35.968	0.027	2.2	2.217	0.451	308.653	0.003
2.4	1.451	0.689	14.771	0.067	2.4	1.814	0.551	74.318	0.013
2.6	1.322	0.755	7.826	0.127	2.6	1.564	0.639	26.894	0.037
2.8	1.234	0.810	4.895	0.204	2.8	1.400	0.714	12.695	0.078
3.0	1.172	0.853	3.436	0.291	3.0	1.289	0.775	7.205	0.138
3.2	1.127	0.887	2.620	0.381	3.2	1.211	0.825	4.671	0.214
3.4	1.094	0.913	2.125	0.470	3.4	1.155	0.865	3.342	0.299
3.6	1.070	0.933	1.806	0.553	3.6	1.115	0.896	2.575	0.388
3.8	1.053	0.949	1.590	0.628	3.8	1.086	0.920	2.101	0.475
4.0	1.040	0.961	1.439	0.694	4.0	1.064	0.939	1.791	0.558
4.2	1.030	0.970	1.331	0.751	4.2	1.048	0.953	1.581	0.632
4.4	1.022	0.977	1.252	0.798	4.4	1.036	0.964	1.433	0.697
4.6	1.017	0.983	1.193	0.838	4.6	1.027	0.973	1.326	0.753
4.8	1.013	0.987	1.148	0.870	4.8	1.020	0.979	1.248	0.801
5.0	1.009	0.990	1.114	0.897	5.0	1.015	0.984	1.189	0.840
5.2	1.007	0.992	1.088	0.918	5.2	1.011	0.988	1.145	0.872
5.4	1.005	0.994	1.068	0.935	5.4	1.009	0.991	1.112	0.898
5.6	1.004	0.995	1.053	0.949	5.6	1.006	0.993	1.087	0.919
5.8	1.003	0.996	1.041	0.960	5.8	1.005	0.994	1.067	0.936
6.0	1.002	0.997	1.032	0.968	6.0	1.003	0.996	1.052	0.950
$w = 8$									
2.0	2.278	9.448	359.594	0.002	2.0	2.910	0.343	2,557.114	0.000
2.2	1.816	9.550	73.638	0.013	2.2	2.217	0.451	308.653	0.003
2.4	1.563	0.639	25.311	0.039	2.4	1.814	0.551	74.318	0.013
2.6	1.398	0.714	11.810	0.084	2.6	1.564	0.639	26.894	0.037
2.8	1.287	0.776	6.725	0.148	2.8	1.400	0.714	12.695	0.078
3.0	1.209	0.826	4.398	0.227	3.0	1.289	0.775	7.205	0.138
3.2	1.154	0.866	3.177	0.314	3.2	1.211	0.825	4.671	0.214
3.4	1.114	0.897	2.471	0.404	3.4	1.155	0.865	3.342	0.299
3.6	1.085	0.921	2.033	0.491	3.6	1.115	0.896	2.575	0.388
3.8	1.064	0.939	1.745	0.572	3.8	1.086	0.920	2.101	0.475
4.0	1.048	0.954	1.548	0.645	4.0	1.064	0.939	1.791	0.558
4.2	1.036	0.964	1.410	0.709	4.2	1.048	0.953	1.581	0.632
4.4	1.027	0.973	1.309	0.763	4.4	1.036	0.964	1.433	0.697
4.6	1.020	0.979	1.235	0.809	4.6	1.027	0.973	1.326	0.753
4.8	1.015	0.984	1.180	0.846	4.8	1.020	0.979	1.248	0.801
5.0	1.011	0.988	1.139	0.877	5.0	1.015	0.984	1.189	0.840
5.2	1.008	0.991	1.107	0.902	5.2	1.011	0.988	1.145	0.872
5.4	1.006	0.993	1.083	0.923	5.4	1.009	0.991	1.112	0.898
5.6	1.005	0.994	1.064	0.939	5.6	1.006	0.993	1.087	0.919
5.8	1.003	0.996	1.050	0.952	5.8	1.005	0.994	1.067	0.936
6.0	1.002	0.997	1.038	0.962	6.0	1.003	0.996	1.052	0.950



