Socioeconomic inequalities in health: Measurement, computation, and statistical inference

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Abstract

This paper clarifies the relationship between two widely used indices of health inequality and explains why these are superior to others indices used in the literature. It also develops asymptotic estimators for their variances and clarifies the role that demographic standardization plays in the analysis of socioeconomic inequalities in health. Empirical illustrations are presented for Dutch health survey data.

Key words: Socioeconomic inequality; Concentration index; Standard errors
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1. Introduction

This paper clarifies the relationship between two widely used indices of health inequality, namely the relative index of inequality (RII) and the concentration index (CI). It explains why these are superior to other indices used in the empirical literature. The paper also clarifies the role that demographic standardization plays in the analysis of socioeconomic inequities in health.

Since the indices of health inequality are generally estimated from sample observations, it is useful to be able to test whether any observed differences in

their values are statistically significant. This paper develops accurate distribution-free asymptotic estimators of the standard errors of both the RII and CI. There is, of course, an extensive literature on the sampling properties of the Gini index to which the CI is related (Nygord and Sanstöm, 1981; Kakwani, 1990; Cowell, 1989). These sampling distributions are derived by applying Hoeffding's (1948) theorem on order statistics. This methodology cannot be applied to derive the sampling distribution of CIs because they can be both negative and positive and, therefore, cannot be written in the form of order statistics. Thus, the derivations of the standard error formulae of this paper (presented in the Appendix) are new, providing more general results. The formulae in the current paper reduce to the standard formulae for the Gini index when ranking by ill-health coincides with socioeconomic ranking (see Appendix B).

2. Two indices of socioeconomic inequality in health

The illness concentration curve plots the cumulative proportion of the population – ranked by socioeconomic status (SES), beginning with the least advantaged – against the cumulative proportion of illness.[1] If $L(s)$ lies above (below) the diagonal, inequalities in illness favour the more (less) advantaged members of society. Health inequality can be measured by the CI, denoted below by C, defined as twice the area between $L(s)$ and the diagonal:

$$C = 1 - 2\int_0^1 L(s)\,ds.$$ (1)

C takes a value of zero when $L(s)$ coincides with the diagonal and is negative (positive) when $L(s)$ lies above (below) the diagonal.[2]

On individual-level data C can be computed straightforwardly. Let x_i ($i = 1, \ldots, n$) be the ill-health score of the ith individual. Each of the n individuals are then ranked according to their SES, beginning with the most disadvantaged. C can then be calculated as

$$C = \frac{2}{n \cdot \mu} \sum_{i=1}^{n} x_i R_i - 1,$$ (2)

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[1] Cf. Wagstaff et al. (1989). On concentration curves and indices more generally, see Kakwani (1977, 1980) and Lambert (1993).

[2] The minimum and maximum values of C using individual-level data are -1 and $+1$ respectively; these occur when all the population's ill-health is concentrated in the hands of the most disadvantages person and the least disadvantages person respectively.

where $\mu = (1/n)\sum_{i=1}^{n} x_i$ is the mean level of ill-health and R_i is the relative rank of the ith person. Eq. (2) makes clear the dependence of C on the socioeconomic dimension to the distribution of ill-health. Suppose that person i's ill-health falls by an amount Δ, whilst person j's rises by the same amount. The effect on C is given by

$$\Delta C = \frac{2}{n \cdot \mu} \Delta(R_i - R_j),$$

which is clearly positive (negative) if i is more (less) disadvantaged than j. This sensitivity to the socioeconomic dimension to inequalities in health is not a feature of several other indices used in the literature.[3] Eq. (2) also makes clear that C depends on the ill-health of *all* members of society.

Inequalities in health are frequently investigated using grouped data, the groups comprising socioeconomic groups (SEGs), social classes, groups of persons with similar levels of educational attainment, or income groups.[4] Let μ_t ($t = 1, \ldots, T$) be the morbidity rate of the tth SEG and f_t its population share. Rank the T SEGs according to their SES, beginning with the most disadvantaged. If $L(s)$ is assumed to be piecewise linear, C can be calculated as

$$C = \frac{2}{\mu} \sum_{t=1}^{T} f_t \mu_t R_t - 1,$$ (3)

$\sum_{t=1}^{T} f_t \mu_t$ being the mean morbidity rate, and R_t is the relative rank of the tth SEG, defined as

$$R_t = \sum_{\gamma=1}^{t-1} f_\gamma + \tfrac{1}{2} f_t,$$ (4)

and indicating the cumulative proportion of the population up to the midpoint of each group interval.[5]

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[3] It is not true of the Gini coefficient (cf., e.g., Illsley and Le Grand, 1986), the index of dissimilarity (cf., e.g., Preston et al., 1981), or the index of inequality (cf. Pappas et al., 1993). On this point cf. Wagstaff et al. (1991).

[4] In cross-country comparisons in particular, the scope for meaningfull comparison is often limited by difference in the way groups are defined. Some researchers have succeeded, however, in achieving a higher degree of comparability with existing surveys (see, e.g., Vagerö and Lundberg, 1989; Kunst and Mackenbach, 1994). In any case the problem is likely to become smaller over time, since various international organisations have launched initiatives aimed at harmonizing survey questions relevant to this area of research.

[5] Eq. (3) makes clear the fact that, where grouped data are used, C depends on the relative sizes of the SEGs, a property not shared by the range.

The RII, which has invariably been used in the context of grouped data, is the slope of a regression of a group's relative morbidity, μ_t/μ, on its relative rank, R_t. The grouped nature of the data calls for Weighted Least Squares (WLS), the WLS estimate of the RII being easily obtained by running OLS on

$$[\mu_t/\mu]\sqrt{f_t} = \alpha \cdot \sqrt{f_t} + \beta \cdot R_t\sqrt{f_t} + u_t, \tag{5}$$

the estimator of $\hat{\beta}$, of which is equal to the RII. The RII and the CI are, in fact, related to one another by (cf. Wagstaff et al., 1991)

$$\hat{\beta} = C/2\sigma_R^2, \tag{6}$$

where $\sigma_R^2 = \sum_{t=1}^{T} f_t(R_t - \frac{1}{2})$.

3. Demographic factors and avoidable inequality

So far we have said nothing about the role demographic factors in generating health inequality – illness rates have been assumed to be *crude* illness rates. Comparing $L(s)$ with the diagonal, or the RII with zero, presupposes that all socioeconomic inequalities in illness are avoidable. This is unrealistic, since there are biological influences on health that are to a large degree unalterable. It is clearly unreasonable, for example, to suppose that a person of 85 could be made as healthy as a 20-year old. The diagonal is thus an unsuitable benchmark against which to compare $L(s)$ and zero is an unsuitable benchmark against which to compare the RII if crude morbidity rates are used in its calculation.

One approach is to use the direct method of standardization. This requires that grouped data be used and involves applying the age–sex-specific average illness rates of each SEG to the age and gender structure of the population (cf., e.g., Rothman, 1986)]. The standardized illness rate for SEG t is equal to

$$\mu_t^+ = \sum_d n_d \mu_{dt}/n, \tag{7}$$

where n_d is the number of persons in the dth demographic group in the population as a whole. μ_{dt} is the morbidity rate amongst persons in the dth demographic group in SEG t. If age–sex-specific morbidity rates are equal to the population rates in each age–sex group (i.e., $\mu_{dt} = \mu_d \; \forall d$), the standardized rates will not vary across SEGs (i.e., $\mu_t^+ = \mu \; \forall t$). The extent of avoidable inequality could be assessed by means of the RII with the directly standardized rates (i.e., the μ_t^+) being used instead of the unstandardized rates (i.e., the μ_t). Alternatively a directly standardized concentration curve can be constructed, denoted by $L^+(s)$, based on the each of the T SEGs' shares of standardized illness:

$$S_t^+ = f_t \sum_d n_d \mu_{dt} \Big/ \sum_d n_d \mu_d; \tag{8}$$

these are equal to f_t if $\mu_{dt} = \mu_d$ $\forall d$. If $L^+(s)$ lies above the diagonal, the less advantages SEGs experience higher age–sex-specific illness rates than the population as a whole, whilst the opposite is true if $L^+(s)$ lies below the diagonal. Thus an alternative measure of avoidable inequalities in health is thus twice the area between $L^+(s)$ and the diagonal:

$$C^+ = 1 - 2\int_0^1 L^+(s)\,ds, \tag{9}$$

which is negative (positive) if avoidable inequalities favour the more (less) advantages SEGs and zero if there are no avoidable inequalities in health.

The fact that the direct standardization requires the use of grouped data is a disadvantage, since the number of SEGs used will affect the numerical values of C and C^+. An alternative is to use the indirect method of standardization, which can also be used on individual-level data. This involves replacing person i's degree of illness by the degree of illness suffered *on average* by persons of the same age and gender as person i (cf., e.g., Rothman, *op. cit.*). Let $L^*(s)$ be the corresponding concentration curve. If the more disadvantages members of society are in the demographic groups that are most prone to illness, $L^*(s)$ will lie above the diagonal, indicating that it is unreasonable to suppose that $L(s)$ could ever be brought down as far as the diagonal. If, by contrast, the more disadvantaged members of society are in those demographic groups that are *least* prone to illness, $L^*(s)$ will lie below the diagonal, indicating that it would be feasible to bring $L(s)$ *below* the diagonal. An alternative measure of avoidable inequalities in health is thus twice the area between $L(s)$ and $L^*(s)$:

$$I^* = 2\int_0^1 [L^*(s) - L(s)]\,ds = C - C^*, \tag{10}$$

which is negative (positive) if there are avoidable inequalities favouring the more (less) advantaged members of society. C^* can be computed straightforwardly using Eq. (2) but replacing the actual illness score with the indirectly standardized score.

4. Statistical inference

Consider first the case of grouped data. Application of OLS to Eq. (5) automatically provides a standard error for the RII.[6] A standard error for C can

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[6] This is, in effect, the method used by Kunst and Mackenbach (1994).

easily be obtained from the following convenient regression:

$$2\sigma_R^2[\mu_t/\mu]\sqrt{n_t} = \alpha_1 \cdot \sqrt{n_t} + \beta_1 \cdot R_t\sqrt{n_t} + u_t. \tag{11}$$

The OLS etimator β_1 is equal to

$$\hat{\beta}_1 = \frac{2}{\mu} \sum_{t=1}^{T} f_t(\mu_t - \mu)(R_t - \tfrac{1}{2}), \tag{12}$$

which, from Eq. (3), shows that $\hat{\beta}_1$ is equal to C. These standard errors are not, however, wholly accurate, since the observations in each regression equation are not independent of one another. In the Appendix we develop the following estimators which take into account the serial correlation in the data:

$$\text{var}(\hat{\beta}) = \frac{1}{n\sigma_R^4}\left[\sum_{t=1}^{T} e_t^2 f_t - \left(\sum_{t=1}^{T} e_t f_t\right)^2 + \frac{1}{\mu^2}\sum_{t=1}^{T} \sigma_t^2(R_t - \tfrac{1}{2} - \tfrac{1}{2}C)^2\right], \tag{13}$$

$$\text{var}(\hat{C}) = \frac{1}{n}\left[\sum_{t-1}^{T} f_t a_t^2 - (1 + C)^2\right] + \frac{1}{n\mu^2}\sum_{t-1}^{T} f_t\sigma_t^2(2R_t - 1 - C)^2, \tag{14}$$

where σ_t^2 is the variance ill-health score in the tth SEG,

$$e_t = \tfrac{1}{2}a_t - \hat{\beta}[1 + R_t^2 - (s_t + s_{t-1})], \tag{15}$$

$$a_t = \frac{\mu_t}{\mu}(2R_t - 1 - C) + 2 - q_{t-1} - q_t, \tag{16}$$

$$q_t = \frac{1}{\mu} \sum_{j=1}^{t} \mu_j f_j, \tag{17}$$

being the ordinate of $L(s)$, $q_0 = 0$, and

$$s_t = \sum_{j=1}^{t} f_j R_j, \tag{18}$$

with $s_0 = 0$. If one or other of the standardization methods is being used, one clearly needs to replace μ by the standardized value. If the direct method of standardization is being used, σ_t^2 is, by definition, equal to zero for all T SEGs and n in the denominator has to be replaced by T, the reason being that μ_t^+ is defined only at the level of the SEG, not at the level of the individual, and hence there are only T independent observations.[7]

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[7] The estimation of a statistic from grouped data always give larger standard errors because of loss of degrees of freedom. If σ_t^2 was not equal to zero, then there are n degrees of freedom. But if we assume zero variation within groups, the degrees of freedom are reduced to T, the number of groups. Thus, the effective sample size is T not n.

On ungrouped data, the simplest way to obtain a standard error for C is to run OLS on the following equation:

$$2\sigma_R^2[x_i/\mu] = \alpha_2 + \beta_2 \cdot R_i + u_i. \tag{19}$$

The estimator of β_2 is equal to

$$\hat{\beta}_2 = \frac{2}{n \cdot \mu} \sum_{i-1}^{n} (x_t - \mu)(R_i - \tfrac{1}{2}), \tag{20}$$

which, from Eq. (2), shows that $\hat{\beta}_2$ is equal to C. From Eq. (14) one can obtain a standard error for C. Using the same method, one can obtain a standard error for C^*, but a standard error for I^* is not easily obtained because the sample estimates of C and C^* are not independently distributed. We can, however, estimate a standard error for I^* by means of the following convenient regression:

$$2\sigma_R^2\left[\frac{x_i}{\mu} - \frac{x_i^*}{\mu^*}\right] = \alpha_3 + \beta_3 \cdot R_i + u_i, \tag{21}$$

where x_i^* is the indirectly standardized value of x_i and μ^* is the mean of x_i^*. The OLS estimate of β_3 in Eq. (21) will be equal to I^* and from this regression we also obtain a standard error for I^*. As in the case of grouped data, the standard errors obtained using these convenient regressions are not entirely accurate. More accurate standard errors are obtained by taking into account the serially correlated nature of the error structure. Bearing in mind that with individual-level data the analogue of σ_i^2 is zero, the variance of $\hat{C}$ can be calculated as[8]

$$\mathrm{var}(\hat{C}) = \frac{1}{n}\left[\frac{1}{n}\sum_{i=1}^{n} a_i^2 - (1 + C)^2\right], \tag{22}$$

where a_i is defined along the lines of a_t. The variance of $\hat{I}^*$, by contrast, can be computed as

$$\mathrm{var}(\hat{I}^*) = \frac{1}{n}\left[\frac{1}{n}\sum_{i-1}^{n} (a_i - a_i^*)^2 - I^{*2}\right], \tag{23}$$

where a_i^* is defined analogously to a_i except that indirectly standardized values are used in its calculation instead of actual values.

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[8] See Appendix B for the derivation of the result given in (22)

5. Empirical illustrations

In this section we report some empirical illustrations using data from the combined 1980 and 1981 Dutch *Health Interview Surveys* (*HIS*). The sample size, after deletion of cases with missing information, is 10,232 persons. Our stratifying variable is pre-tax household income per equivalent adult.[9] We use two widely available indicators of ill-health – chronic illness (a dummy variable indicating the presence or absence of any chronic illness) and self-assessed health (the *HIS* question being 'How is your health in general?', to which respondents could reply 'good', 'fair', 'varies', and 'poor').[10] In the case of the former, we simply used the actual values of the variable. In the case of the latter, we have assumed that underlying the categorical self-assessed health variable is a continuous latent ill-health variable with a standard lognormal distribution (cf. Wagstaff and van Doorslaer, 1994a).[11]

For the purpose of illustrating the methods for grouped data, we have divided the sample into income deciles. In general, the lower deciles suffer somewhat higher levels of ill-health than the higher deciles (Table 1). With the exception of the bottom decile, the effect of the standardization is to reduce the mean ill-health levels of the lower income groups and raise those of the upper income groups. The negative values of C, C^+, β, and β^+ in Table 2 imply that even after taking into account the demographic structure of the sample, inequalities in health favour the better-off. The values suggest that inequality is more pronounced if health is measured by self-assessed health than if it is measured by chronic illness.[12] The standardized variants of C and β (C^+ and β^+) are smaller than the unstandardized variants (C and β), implying that some of the inequality in crude morbidity rates is unavoidable and due simply to the age structure of the sample. The standard errors for C^+ and β^+ are a good deal smaller than those of C and β – this presumably reflects the fact that the direct standardization reduces the variation in illness rates. The standard errors obtained using the two methods differ somewhat, but not apparently in any predictable way. It

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[9] The equivalence scale used is that used by the Dutch Central Bureau of Statistics (cf. Schiepers, 1988). The scale takes into account the number of adults and children in the household, as well as the age of the eldest child.

[10] Our methods could, of course, be applied with health measures other than our chosen indicators; see for instance Bhargava (1994).

[11] In effect, we obtain the values for each of the four categories by dividing up the area under the standard lognormal distribution according to sample proportions falling into each of the four categories.

[12] This conclusion is consistent with other research where both self-assessed health and chronic illness are measured by dichotomous variables (cf. Kunst et al., 1992; van Doorslaer, Wagstaff, and Rutten, 1993). The reason is probably that the chronic illness dichotomous variable insufficiently captures the underlying differences in the severity of chronic illness (O'Donnell and Propper, 1991).

Table 1
Means for grouped data

Decile	Chronic unstandardized	Chronic standardized	SAH unstandardized	SAH standardized
1	0.2808	0.2885	1.6317	1.6837
2	0.3629	0.3125	1.9946	1.7684
3	0.3405	0.3061	1.7503	1.6549
4	0.2985	0.2844	1.6329	1.5769
5	0.2965	0.2972	1.4760	1.4980
6	0.2805	0.2944	1.3817	1.4341
7	0.2622	0.2755	1.2733	1.3279
8	0.2811	0.2967	1.3310	1.4285
9	0.2600	0.2791	1.2468	1.2939
10	0.2766	0.2870	1.2062	1.2544
Total	0.2940	0.2921	1.4925	1.4927

Standardizations are direct standardizations and obtained using Eq. (8), with two gender groups and five age groups (18–34, 35–44, 55–64, 65–74, 75 +).

Table 2
Concentration indices and standard errors for grouped data

	Chronic illness[a]	Chronic illness[b]	SAH[a]	SAH[b]
C	− 0.0402	− 0.0402	− 0.0827	− 0.0827
se(C)	0.0165	0.0164	0.0153	0.0139
t-test: C	− 2.4332	− 2.4512	− 5.4164	− 5.9496
C^+	− 0.0111	− 0.0111	− 0.0609	− 0.0609
se(C^+)	0.2965	0.2972	0.0067	0.0085
t-test: C^+	− 1.6912	− 1.6838	− 9.0509	− 7.1824
β	− 0.2435	− 0.2435	− 0.5010	− 0.5010
se(β)	0.1001	0.0994	0.0925	0.0845
t-test: β	− 2.4332	− 2.4478	− 5.4164	− 5.9297
β^+	− 0.0672	− 0.0672	− 0.3690	− 0.3690
se(β^+)	0.0397	0.0352	0.0408	0.0513
t-test: β^+	− 1.6912	− 1.9079	− 9.0509	− 7.1903

$\sigma_R^2 = 0.0825$ in our sample.

[a] Obtained using convenient regressions (11) and (5).
[b] Obtained using formulae in Eqs. (3), (13), and (14).

is not possible to conclude, for example, either from the empirical illustrations or from the relevant formulae whether the method that corrects for serial correlation is likely to produce smaller or larger standard errors than the method that

Table 3
Concentration indices and standard errors for individual-level data

	Chronic illness[a]	Chronic illness[b]	SAII[a]	SAII[b]
C	− 0.0404	− 0.0403	− 0.0837	− 0.0836
se(C)	0.0088	0.0096	0.0071	0.0086
t-test: C	− 4.5764	− 4.2064	− 11.7778	− 9.6848
C*	− 0.0306	− 0.0305	− 0.0263	− 0.0262
se(C*)	0.0023	0.0055	0.0018	0.0057
t-test: C*	− 13.2148	− 5.5027	− 14.3930	− 4.6306
I*	− 0.0098	− 0.0099	− 0.0572	− 0.0574
se(I*)	0.0085	0.0086	0.0069	0.0068
t-test: I*	− 1.1554	− 1.1480	− 8.3298	− 8.4962

The t-ratios presented in the table were calculated from the coefficients and the standard errors to seven decimal places rather than the four in the table - hence the fact that calculating the t-ratios from the figures in the table give slightly different numbers.

[a] Obtained using convenient regressions regressions (19) and (21).
[b] Obtained using formulae in (2), (10), (22), and (23).

does not. In Table 2 the differences are fairly small and the t-values are such that using either method leads to the same conclusions concerning the existence of otherwise of significant inequalities in health.[13]

The indirect standardizations in Table 3 used in computing C* were obtained using regression analysis along the lines set out in van Vliet and van de Ven (1985) and Wagstaff and van Doorslaer (1994b). A logit model was used in the case of chronic illness, and OLS in the case of the self-assessed health variable, having first replaced the four ordinal scores with the latent ill-health variable scores. The standardized values, x_i^*, are then simply the predicted values retained from these regressions. The values of C for chronic illness and self-assessed health in Table 3 are slightly smaller (i.e., larger in absolute size) than those obtained using the grouped data in Table 2. The standard errors of C in Table 3, obtained using individual-level data, are substantially smaller (40–50%) than those in Table 2, obtained using grouped data. The standard errors of I*, by contrast, are not markedly different from those of I^+ (i.e., C^+) reported in Table 2 – this reflects the reduction in sample variation caused by the standardizations. The t-tests testing the significance of I* from zero suggest that there are

[13] The insignificance of inequalities in standardized chronic illness rates may be due to the fact the chronic illness questions in the HIS are posed in such a way as to encourage the reporting of even fairly 'minor' chronic conditions such as excema and migraine, which tend to be commonest among the higher income groups in the Netherlands (cf., e.g., van Doorslaer, Wagstaff, and Janssen, 1993).

no significant avoidable inequalities in the presence of chronic illness but that there are significant avoidable inequalities in self-assessed health. These are the same conclusions that were reached with the grouped data in Section 4, though the t-values for chronic illness are a good deal smaller in the case of I^* and I^+.

6. Conclusions

We have shown that the RII and CI are closely related to one another and that it is possible to construct a variant of the CI to allow inequalities in health to be measured on individual-level data even with age–sex standardization. This allows the extra precision allowed for by individual-level data to be retained but at the same time allows one to net out of one's calculations the unavoidable component of health inequality attributable to the demographic structure of the sample. We have also derived asymptotic distribution-free standard errors for both the RII and the CI. Finally, the empirical illustrations in the paper suggest that there may, in practice, only be small differences between the standard errors obtained using the method which does not take into account serial correlation and those obtained using the method proposed in this paper which does take it into account. Surprisingly, the results also suggest that in this context the gain in precision associated with the use of individual-level data may not always be that large.

Appendix A: Derivation of standard errors based on groupe data

Suppose there are T socioeconomic groups and f_t is the population relative frequency of the tth group, then $\sum_{t=1}^{T} f_t = 1$. It is reasonable to assume that the sample absolute frequencies $(n_1, n_2, \ldots, n_T)$ based on a sample of n individuals follow a multinomial distribution so that the means, variances, and covariances of the sample estimates of the relative frequencies are given by

$$\mathrm{E}(\hat{f}_t) = f_t, \quad \mathrm{var}(\hat{f}_t) = \frac{1}{n} f_t(1 - f_t), \quad \mathrm{cov}(\hat{f}_t, \hat{f}_{t'}) = -\frac{1}{n} f_t f_{t'}, \quad \text{if} \quad t \neq t',$$

where $t = 1, 2, \ldots, T$. Then one can always write

$$\hat{f} = f + \varepsilon, \tag{A.1}$$

where $f' = (f_1, f_2, \ldots, f_T)$, $\hat{f} = (\hat{f}_1, \hat{f}_2, \ldots, \hat{f}_T)$, and $\varepsilon' = (\varepsilon_1, \varepsilon_2, \ldots, \varepsilon_T)$, ε being the error vector such that

$$\mathrm{E}(\varepsilon) = 0 \quad \text{and} \quad \mathrm{E}(\varepsilon\varepsilon') = \frac{1}{n} \Sigma, \tag{A.2}$$

Σ being the $T \times T$ matrix given by

$$\Sigma = \mathrm{diag}(f) - ff'. \tag{A.3}$$

Let $m' = (\mu_1, \mu_2, \ldots, \mu_T)$, μ_t being the average morbidity of the tth SEG, then the mean morbidity of the society is given by

$$\mu = m'f. \tag{A.4}$$

Let $\hat{\mu}_t$ be the sample estimate of μ_t, then one can always write

$$\hat{\mu}_t = \mu_t + \delta_t,$$

where δ_t is the error term such that

$$\mathrm{E}(\delta_t) = 0 \quad \text{and} \quad \mathrm{E}(\delta_t^2) = \sigma_t^2/n_t.$$

If $\hat{m}' = (\hat{\mu}_1, \hat{\mu}_2, \ldots, \hat{\mu}_T)$ and $\delta' = (\delta_1, \delta_2, \ldots, \delta_T)$, then one can write

$$\hat{m} = m + \delta, \tag{A.5}$$

such that $\mathrm{E}(\delta) = 0$ and $\mathrm{E}(\delta\delta') = (1/n)\Omega$, where $\Omega = \mathrm{diag}(\sigma^2)[\mathrm{diag}(f)]^{-1}$, σ^2 being the $T \times 1$ vector with the tth element equal to σ_t^2.

A sample estimate of the mean morbidity rate of the society is given by

$$\hat{\mu} = \hat{m}'f,$$

which in view of (A.1) and (A.5) can be written as

$$\hat{\mu} = \mu + m'\varepsilon + f'\delta, \tag{A.6}$$

which on assuming that ε and δ are independent gives the result: $\sqrt{n}(\hat{\mu} - \mu)$ follows normal distribution with mean zero and variance $(m'\Sigma m + f'\Omega f)$. This gives the variance of $\hat{\mu}$ as

$$\mathrm{var}(\hat{\mu}) = \frac{1}{n}\left[\sum_{t=1}^{T} f_t(\mu_t - \mu)^2 + \sum_{i=1}^{T} f_t\sigma_t^2 \right]. \tag{A.7}$$

Let us now introduce a $T \times T$ matrix

$$A = \begin{bmatrix} \frac{1}{2} & 0 & 0 & \ldots & 0 \\ 1 & \frac{1}{2} & 0 & \ldots & 0 \\ 1 & 1 & \frac{1}{2} & \ldots & 0 \\ 1 & 1 & 1 & \ldots & \frac{1}{2} \end{bmatrix},$$

which has the property that

$$A + A' = \iota\iota',$$

where $\iota' = (1, 1, \ldots, 1)$ is the row vector of T elements, each of which being equal to 1.

Let $R' = (R_1, R_2, \ldots, R_T)$, R_t being the relative rank of the tth SEG (defined in (4)); then $R = Af$. A sample estimate of R will then be given by $\hat{R} = A\hat{f}$ which from (A.1) gives

$$\hat{R} = R + A\varepsilon. \tag{A.8}$$

We may now write the sample estimate of the concentration measure C as

$$\hat{C} = \frac{2}{\hat{\mu}} \hat{m}'[\mathrm{diag}(\hat{f})]\hat{R} - 1. \tag{A.9}$$

Substituting (A.1), (A.5), and (A.8) into (A.9) and applying Taylor's expansion gives

$$\hat{C} = C + a'\varepsilon + b'\delta + O_p\left(\frac{1}{n}\right), \tag{A.10}$$

where

$$a = \frac{1}{\mu}[2\,\mathrm{diag}(R)m + 2A'\,\mathrm{diag}(f)m - (1 + C)m],$$

$$b = \frac{1}{\mu}[2\,\mathrm{diag}(f)R - (1 + C)f],$$

and $O_p(1/n)$ includes all the remainder terms that are of order $1/n$ or less in probability. Eq. (A.10) immediately gives the result: $\sqrt{n}(\hat{C} - C)$ follows an asymptotic normal distribution with zero mean and variance $(a'\Sigma a + b'\Omega b)$ which gives

$$\mathrm{var}(\hat{C}) = \frac{1}{n}\left[\sum_{t=1}^{T} f_t a_t^2 - (1 + C)^2\right] + \frac{1}{n\mu^2}\sum_{t=1}^{T} f_t \sigma_t^2(2R_t - 1 - C)^2, \tag{A.11}$$

where

$$a_t = \frac{\mu_t}{\mu}(2R_t - 1 - C) + 2 - q_{t-1} - q_t \quad \text{and} \quad q_t = \frac{1}{\mu}\sum_{r=1}^{t} \mu_r f_r, \tag{A.12}$$

being the ordinate of the concentration curve.

The relative index of inequality RII, which we denote by β, is related to the concentration as $\beta = C/2\sigma_R^2$, where $\sigma_R^2 = \sum_{t=1}^{T} f_t(R_t - \frac{1}{2})^2$ (Eq. (6)). A sample estimate of β is given by

$$\hat{\beta} = \hat{C}/2\hat{\sigma}_R^2, \tag{A.13}$$

where

$$\hat{\sigma}_R^2 = \sum_{t=1}^{T} \hat{f}_t(\hat{R}_t - \tfrac{1}{2})^2.$$

Utilizing (A.8) and (A.10) into (A.13) and Taylor's expansion gave

$$\text{var}(\hat{\beta}) = \frac{1}{n\sigma_R^4}\left[\sum_{t=1}^{T} f_t e_t^2 - \left(\sum_{t=1}^{T} f_t e_t \right)^2 + \frac{1}{\mu^2} \sum_{t=1}^{T} \sigma_t^2 \left(R_t - \tfrac{1}{2} - \frac{C}{2} \right)^2 \right], \tag{A.14}$$

where

$$e_t = \frac{a_t}{2} - \hat{\beta}[1 + R_t^2 - s_t - s_{t-1}], \quad s_t = \sum_{r=1}^{t} f_r R_r, \quad s_0 = 0.$$

If we assume that the groups are homogeneous (which is the case when individual observations are available), σ_t^2 will be zero in each group. The formulae of $\text{var}(\hat{C})$ and $\text{var}(\hat{\beta})$ will simplify considerably. In this situation, $\hat{C}$ given in (A.10) will be given by

$$\hat{C} = C + a'\varepsilon + O_p\left(\frac{1}{n}\right). \tag{A.15}$$

Similarly, if the sample estimate of standardized C^* can be written as

$$\hat{C}^* = C^* + a'^*\varepsilon + O_p\left(\frac{1}{n}\right), \tag{A.16}$$

where the tth element of a^* is given by

$$a_t^* = \frac{\mu_t^+}{\mu^+}(2R_t - 1 - C^*) + 2 - q_t^* - q_{t-1}^*, \tag{A.17}$$

where μ_t^+ and μ^+ are the standardized morbidity means and $q_t^* = (1/\mu^+)\sum_{r=1}^{t} \mu_r^+ f_r$ is the ordinate of the concentration curve $L^*(s)$.

A sample estimate of I^* will then be given by

$$\hat{I}^* = \hat{C} - \hat{C}^*, \tag{A.18}$$

which in view of (A.15) and (A.16) becomes

$$\hat{I}^* = I^* + (a - a^*)'\varepsilon + O_p\left(\frac{1}{n}\right).$$

This immediately lead to the result that $\sqrt{n}(\hat{I}^* - I^*)$ follows an asymptotic normal distribution with variance equal to $(a - a^*)\Sigma(a - a^*)$, which gives

$$\text{var}(\hat{I}^*) = \frac{1}{n}\left[\sum_{t=1}^{T}(a_t - a_t^*)f_t - I^{*2}\right]. \tag{A.19}$$

Appendix B: Derivation of standard errors based on individual observations

Eq. (A.11) provides the standard errors of $\hat{C}$ computed on the basis of grouped data. We may now give an alternative derivation of the variance of $\tilde{C}$ estimated on the basis of individual observations. $\tilde{C}$ can be written as

$$\tilde{C} = \frac{2}{n\hat{\mu}}\sum_{i=1}^{n}x_i\tilde{R}_i - 1, \tag{B.1}$$

where x_i is the ill-health score of the ith individual and $\tilde{R}_i = (2i - 1)/2n$, where i is the ith rank when individuals in the sample are arranged in ascending order of x_i. It will be useful to write (B.1) as

$$\tilde{C} = \hat{d}/2\hat{\mu}, \tag{B.2}$$

where

$$\hat{d} = \frac{1}{n}\sum_{i=1}^{n}\hat{d}_i,$$

$$\hat{d}_i = 2x_i\tilde{R}_i - \hat{\mu}(\hat{q}_i + \hat{q}_{i-1}) - (x_i - \hat{\mu}),$$

$$\hat{q}_i = \sum_{j=1}^{i}x_j \Big/ \sum_{j=1}^{n}x_j.$$

Then following Fraser (1957), we obtain

$$n\,\text{var}(\hat{\mu}) = \frac{1}{n}\sum_{i=1}^{n}(x_i - \hat{\mu})^2,$$

$$n\,\text{var}(\hat{d}) = \frac{4}{n}\sum_{i=1}^{n}(\hat{d}_i - \hat{d})^2,$$

$$n\,\text{cov}(\hat{d}, \hat{\mu}) = \frac{2}{n}\sum_{i=1}^{n}(x_i - \hat{\mu})(\hat{d}_i - \hat{d}).$$

Then applying the δ method given in Rao (1965, p. 321) the estimated variance of $\tilde{C}$ from (B.2) is obtained as

$$\text{vâr}(\tilde{C}) = \frac{1}{4n\hat{\mu}}[\text{vâr}(\hat{d}) + 4\tilde{C}^2\,\text{vâr}(\hat{\mu}) - 4\tilde{C}\,\text{côv}(\hat{d},\hat{\mu})]$$

$$= \frac{1}{4\hat{\mu}^2 n}\sum_{i=1}^{n}(\hat{d}_i - \hat{d} - \tilde{C}x_i + \tilde{C}x_i + \tilde{C}\hat{\mu})^2. \tag{B.3}$$

Note that one can also derive $\text{vâr}(\tilde{C})$ from Eq. (A.11) by substituting $\sigma_t^2 = 0$ which gives

$$\text{vâr}(\tilde{C}) = \frac{1}{n}\sum_{i=1}^{n}(a_i - 1 - \tilde{C}), \tag{B.4}$$

where

$$\hat{a}_i = \frac{x_i}{\hat{\mu}}(2\hat{R}_i - 1 - \tilde{C}) + 2 - \hat{q}_i - \hat{q}_{i-1}.$$

Comparing (B.3) and (B.4) we note that the two expressions are identical. Thus, the two alternative derivation of the standard errors give identical results.

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