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Abstract

In a recent paper I presented a sampling formula for species abundances from multiple samples according to the prevailing neutral model of biodiversity, but practical implementation for parameter estimation was only possible when these samples were from local communities that were assumed to be equally dispersal-limited. Here I show how the same sampling formula can also be used to estimate model parameters using maximum likelihood when the samples have different degrees of dispersal limitation. Moreover, it performs better than other, approximate, parameter estimation approaches. I also show how to calculate errors in the parameter estimates, which has so far been largely ignored in the development of and debate on neutral theory.

Introduction

In a recent paper (Etienne 2007) I presented a sampling formula for the joint probability of a data set of species abundances in multiple local samples. This sampling formula assumes the prevailing spatially implicit neutral model of biodiversity (Hubbell 2001, Volkov *et al.* 2003, Etienne 2005) where local communities draw immigrants from a metacommunity that is in a balance between speciation and extinction. In that paper I stated that the formula was only applicable in practice for maximum likelihood estimation of model parameters if all samples are assumed to be equally dispersal limited, that is, that they have the same values of the fundamental dispersal number I_i; I_i is related to the immigration probability m_i by $I_i = \frac{m_i}{1-m_i}(J_i - 1)$, see Etienne & Alonso (2005). I refer to Tomašových (2008) for an application. The reason for this limited applicability was that only under the assumption of equal dispersal limitation the formula, which involved a very large number of sums, simplified to something computationally tractable. Here I show that the formula also simplifies to a computationally tractable (albeit still demanding) form even if the assumption on the fundamental dispersal number I is dropped. This allows simultaneous maximum likelihood estimation of the fundamental biodiversity number θ and each of the fundamental dispersal numbers I_i for each sample i. The utility of the sampling formula is thus substantially extended. Furthermore I demonstrate that the maximum likelihood parameter estimation based on the sampling formula outperforms other, approximate, approaches that have been developed in the meantime. Finally, I note that not only the neutral model parameters themselves can be estimated, but also the errors in the parameters.

Jabot *et al.* (2008) pointed out that m and I actually do not just represent a measure of dispersal, but of recruitment which encompasses both dispersal and establishment. Only if establishment is assumed identical for both immigrant and local individuals, then m and I can be interpreted as measures of dispersal (limitation). From hereon I will assume the broader interpretation in terms of recruitment. Consistency then requires to call I the fundamental recruitment number.

As a final remark in this introduction, I would like to point out that different I-values for samples from different geographic locations is not in contradiction with the neutrality assumption, because individuals of different species are still functionally equivalent. This function is now made dependent on the geographic location, but it is still the same for all species in the same geographic location. In more abstract terms: individuals in the same location are exchangeable, but different locations are not (see also Etienne 2007).

The sampling formula

Suppose that there are N samples from N different local communities, each of which contains J_i individuals ($i = 1...N$), summing to a total of J individuals in all samples together and a total of S different species. The N samples sizes can be summarized by the vector $\overrightarrow{J} = (J_1, ..., J_N)$. The species found in these samples are indicated by an arbitrary order $k = 1...S$ and the data set of all species abundances $\overrightarrow{D}$ can be written as a vector of vectors $\overrightarrow{D} = \left(\overrightarrow{D}_1, .., \overrightarrow{D}_N\right) = ((n_{11}, ..., n_{1S}), ..., (n_{N1}, ..., n_{NS}))$ where n_{ik} represents the number of individuals of species k in sample i. Given θ and $\overrightarrow{I} = (I_1, ..., I_N)$, the sampling formula for such a data set reads (Etienne 2007):

$$P\left[\vec{D}|\vec{I},\theta,\vec{J}\right] = \frac{1}{\prod_{\vec{j}}\Phi_{\vec{j}}!}\left(\prod_{i=1}^{N}\frac{J_i!}{(I_i)_{J_i}\prod_{k=1}^{S}n_{ik}!}\right)\sum_{\{a_{11},...,a_{NS}\}}\left(\prod_{k=1}^{S}\left((a_k-1)!\prod_{i=1}^{N}\overline{s}\left(n_{ik},a_{ik}\right)\right)\prod_{i=1}^{N}I_i^{A_i}\right)\frac{\theta^S}{(\theta)_A} \tag{1}$$

where $\Phi_{\vec{j}}$ is the number of species that have abundance vector $\vec{j}$ across the samples, $\overline{s}(x,y)$ denotes the unsigned Stirling number of the first kind and $(x)_y$ denotes the Pochhammer notation (Etienne 2005, Etienne 2007). Furthermore, I have defined $A_i = \sum_k a_{ik}$ and $a_k = \sum_i a_{ik}$ and $A = \sum_i A_i = \sum_{i,k} a_{ik} = \sum_k a_k$. Equation (1) assumes that species are not labeled, but samples are, the most common use of abundance distributions. Different assumptions on the labeling only affect the prefactor; see Etienne (2007) for more details. The sampling formula can serve as a likelihood in maximum likelihood parameter estimation (Etienne 2007).

Simplification of the sampling formula

The definition of A_i is crucial in the simplification, because with it we can write

$$\begin{aligned} P\left[\vec{D}|\vec{I},\theta,\vec{J}\right] &= \frac{1}{\prod_{\vec{j}}\Phi_{\vec{j}}!}\left(\prod_{i=1}^{N}\frac{J_i!}{(I_i)_{J_i}\prod_{k=1}^{S}n_{ik}!}\right)\sum_{\{a_{11},...,a_{NS}\}}\left(\prod_{k=1}^{S}\left((a_k-1)!\prod_{i=1}^{N}\overline{s}\left(n_{ik},a_{ik}\right)\right)\prod_{i=1}^{N}I_i^{\sum_{k=1}^{S}a_{ik}}\right)\frac{\theta^S}{(\theta)_A} = \\ &= \frac{1}{\prod_{\vec{j}}\Phi_{\vec{j}}!}\left(\prod_{i=1}^{N}\frac{J_i!}{(I_i)_{J_i}\prod_{k=1}^{S}n_{ik}!}\right)\sum_{\{a_{11},...,a_{NS}\}}\left(\prod_{k=1}^{S}\left((a_k-1)!\prod_{i=1}^{N}\overline{s}\left(n_{ik},a_{ik}\right)\right)\prod_{i=1}^{N}\left(\prod_{k=1}^{S}I_i^{a_{ik}}\right)\right)\frac{\theta^S}{(\theta)_A} \end{aligned} \tag{2}$$

where in the first line I have simply substituted this definition and in the second line I have factored out the a_{ik} in the exponent. Note now that we have two products over k after the summation. This can be simplified to a single product:

$$P\left[\vec{D}|\vec{I},\theta,\vec{J}\right]=\frac{1}{\prod_{\vec{j}}\Phi_{\vec{j}}!}\left(\prod_{i=1}^{N}\frac{J_i!}{(I_i)_{J_i}\prod_{k=1}^{S}n_{ik}!}\right)\sum_{\{a_{11},\ldots,a_{NS}\}}\left(\prod_{k=1}^{S}\left((a_k-1)!\prod_{i=1}^{N}\overline{s}\left(n_{ik},a_{ik}\right)I_i^{a_{ik}}\right)\right)\frac{\theta^S}{(\theta)_A} \tag{3}$$

One can write this more compactly as

$$P\left[\vec{D}|\vec{I},\theta,\vec{J}\right]=\frac{1}{\prod_{\vec{j}}\Phi_{\vec{j}}!}\left(\prod_{i=1}^{N}\frac{J_i!}{(I_i)_{J_i}\prod_{k=1}^{S}n_{ik}!}\right)\sum_{A}M\left(\vec{D},A,\vec{I}\right)\frac{\theta^S}{(\theta)_A} \tag{4a}$$

where

$$M\left(\vec{D},A,\vec{I}\right):=\sum_{\{a_{11},\ldots,a_{NS}|\sum_{i,k}a_{ik}=A\}}\prod_{k=1}^{S}\left((a_k-1)!\prod_{i=1}^{N}\overline{s}\left(n_{ik},a_{ik}\right)I_i^{a_{ik}}\right) \tag{4b}$$

Compare this to

$$P\left[\vec{D}|\vec{I},\theta,\vec{J}\right]=\frac{1}{\prod_{\vec{j}}\Phi_{\vec{j}}!}\left(\prod_{i=1}^{N}\frac{J_i!}{\prod_{k=1}^{S}n_{ik}!}\right)\sum_{A}M\left(\vec{D},A\right)\frac{I^A\theta^S}{(I)_J\,(\theta)_A} \tag{5}$$

where

$$M\left(\vec{D},A\right):=\sum_{\{a_{11},\ldots,a_{NS}|\sum_{i,k}a_{ik}=A\}}\prod_{k=1}^{S}\left((a_k-1)!\prod_{i=1}^{N}\overline{s}\left(n_{ik},a_{ik}\right)\right) \tag{6}$$

for the case where all I are equal (Etienne 2007). The main difference is that $I_i^{a_{ik}}$ appears in $M\left(\vec{D},A,\vec{I}\right)$ but this has only a minor additional computational cost: instead of $\overline{s}\left(n_{ik},a_{ik}\right)$ for each value a_{ik} in the sum one needs to compute $\overline{s}\left(n_{ik},a_{ik}\right)I_i^{a_{ik}}$. In maximum likelihood parameter estimation this minor additional computational cost is not negligible because in finding the optimal parameter values $M\left(\vec{D},A,\vec{I}\right)$ needs to be evaluated every time the parameter values change whereas $M\left(\vec{D},A\right)$ only needed to be evaluated once, at the beginning of the optimization procedure. Also, the fact that a_{ik} appears in the exponent of I_i, which is potentially a large number, may incur numerical problems. With the software used (PARI/GP) numerical problems did not occur unless m_i was very close to 1 (I_i very large). The code for maximum likelihood parameter estimation can be found in the online appendix to this paper. It uses the simplex method to find the likelihood optimum. This method is relatively good at finding the global likelihood optimum, but with a high-dimensional parameter space, it is crucial to rerun the optimization algorithm with different initial values to search for the global optimum.

Estimation of the errors in the parameters

The maximum likelihood method also allows for computation of the standard error in the estimates by means of the variance-covariance matrix at the likelihood optimum, The variance-covariance matrix M at the likelihood optimum (where $\frac{\partial \ln P}{\partial \theta}=\frac{\partial \ln P}{\partial I_i}=0$) is the inverse of the observed information matrix I_{o} which in turn is a matrix

of second order derivatives of the loglikelihood evaluated at the optimum: For example, for two samples we have three parameters (θ, I_1 and I_2) and the following variance-covariance matrix:

$$M = I_{\mathrm{o}}^{-1} = \begin{pmatrix} -\frac{\partial^2 \ln P}{\partial \theta_1^2} & -\frac{\partial^2 \ln P}{\partial \theta \partial I_1} & -\frac{\partial^2 \ln P}{\partial \theta \partial I_2} \\ -\frac{\partial^2 \ln P}{\partial I_1 \partial \theta} & -\frac{\partial^2 \ln P}{\partial I_1^2} & -\frac{\partial^2 \ln P}{\partial I_1 \partial I_2} \\ -\frac{\partial^2 \ln P}{\partial I_2 \partial \theta} & -\frac{\partial^2 \ln P}{\partial I_2 \partial I_1} & -\frac{\partial^2 \ln P}{\partial I_2^2} \end{pmatrix}^{-1} \tag{7}$$

Square roots of the diagonal elements (the variances) are the standard errors for the three parameters. The off-diagonal elements (the covariances) provide information on the correlation structure of the estimated parameters. The online material also includes code for estimation of the errors. One can obtain the correlation matrix by dividing each element by the square root of the product of the variances of the two parameters corresponding to that element.

To compute the errors for m_i rather than I_i one needs to perform the following transformation:

$$\frac{\partial^2 \ln P}{\partial \theta \partial m_i} = \frac{\partial^2 \ln P}{\partial \theta \partial I_i} \frac{\partial I_i}{\partial m_i} \tag{8a}$$

$$\frac{\partial^2 \ln P}{\partial m_i \partial m_j} = \frac{\partial^2 \ln P}{\partial I_i \partial I_j} \frac{\partial I_i}{\partial m_i} \frac{\partial I_j}{\partial m_j} \tag{8b}$$

In (8b) there are no first order derivatives because I_i only depends on m_i (not on m_j for $j \neq i$) and $\frac{\partial \ln P}{\partial m_i} = 0$ at the likelihood optimum.

Results

To examine how well the maximum likelihood estimation based on (4a) performs, I first simulated data sets of 3 samples with 1000 individuals each using known parameters (see Etienne 2007 for the algorithm) for various parameter combinations. Then I estimated the parameters using the one-stage (*i.e.* estimating all parameters at once) approach based on (4a) and using the (approximate) two-stage approach (*i.e.* first θ is estimated and then the I_i conditional on θ) of Etienne 2009. The latter is an improved version of the two-stage approach of Munoz *et al*. (2007). Table I has the means and coefficients of variation of the maximum likelihood estimates across the 1000 data sets for each parameter combination. While the mean tells us something about the bias of the estimation method (the larger the difference between this mean and the true parameter value, i.e. the value with which the data were generated, the larger the bias), the coefficient of variation informs us about how far away a parameter estimate for an *individual* data set can be from the true value (the larger the cv, the larger the average individual deviation from the true value); an estimation method can thus be unbiased but still be inaccurate for an individual

data set, or biased yet accurate when corrected for bias. Clearly, the one-stage approach outperforms the two-
98 stage approach, not only because it produces less biased results, but also because the coefficients of variation are substantially smaller.

100 As an example of the estimation of the errors in the parameters I reanalyzed the tropical forest data set also used as an example in Etienne (2007). This data set consists of three Panamanian forest plots (Condit *et al*. 2002):
102 Sherman (5.96 ha of which 5 ha is in the data file), Barro Colorado Island (50 ha) and Cocoli (4 ha). These plots lie along a precipitation gradient (3030 mm/yr, 2616 mm/yr and 1950 mm/yr respectively, Condit *et al*. 2004) which
104 may cause them to have very different degrees of recruitment limitation (Jabot *et al*. 2008). The new methods presented in this paper can help identify whether they indeed have different degrees of recruitment limitation.
106 I find that BCI has less recruitment limitation than Sherman and Cocoli which are equally recruitment-limited, from which one may conclude that two I-values (together with θ) sufficiently describe this data set (Table II).
108 This result is qualitatively consistent with the estimates based on the two-stage approach (Etienne 2009). BCI's central location may explain its higher value of I. The correlation matrix shows that the estimates for the I_i are
110 not correlated with one another, but they are (strongly) correlated with θ as expected (Etienne 2005).

Table II also contains estimates for the three tree communities where instead of the full BCI plot only a 5 ha
112 subplot is taken (see Etienne 2007). This has no substantial effect on the parameter estimates which demonstrates the sample size independence of I in contrast to m.

114 The time to compute the ML parameters with the abovementioned software depends on three types factors. 1. environment-related factors: CPU, platform (Windows, Linux), PARI/GP version, compiled or uncompiled (i.e.
116 interpreted) code 2. likelihood-optimization-related: initial values used in the optimization, tolerance allowed for the function to be optimized and the parameters 3. data-related: number of samples, number of species, number
118 of individuals. As an illustration, the time needed to compute one likelihood value for the tree communities in Panama with the first subsample of BCI was 39 seconds on a 3 GHz Pentium 4 running uncompiled code in PARI
120 /GPversion 2.3.3 under Windows XP, whereas it took fourteen seconds on a single 2 GHz AMD64 node of a cluster running compiled code in PARI/GP version 2.3.4 under Linux.

Discussion

122 I have derived a computationally tractable sampling formula for multiple samples of species abundances, assuming

the most widely used spatially implicit neutral model of biodiversity. It does not need the assumption of Etienne (2007) that all samples are equally recruitment-limited (that is, have the same I-value). Maximum likelihood parameter estimation based on this sampling formula can be done for all parameters simultaneously (*i.e.* it is a one-stage approach in the terminology of Munoz *et al*. 2007) and outperforms the two-stage approach developed by Munoz *et al*. (2007) and Etienne (2009) by having less bias and being more accurate (*i.e.* individual estimates are unlikely to deviate much from the true values).

Because the one-stage approach searches simultaneously for all the parameters that optimize the likelihood, it has another advantage: it potentially recognizes multiple likelihood optima (Etienne *et al*. 2006). As the number of samples increases, it is unlikely that these optima are similar (and thus a clear global optimum exists), because then there is more information in the data on θ (as θ reflects beta diversity). One may find the global likelihood optimum by choosing different sets of starting values of the optimization routine. In contrast, the two-stage approach can only find a single set of parameter estimates which do not necessarily correspond to the global likelihood optimum, although, as stated, the chances that it is far away from the global optimum probably get smaller when the number of samples increase. In any case, the two-stage approach is still useful: it can provide good starting values for the one-stage approach (which otherwise takes long to converge onto the optimum) and, in contrast to the one-stage approach, it remains computationally efficient even when the number of samples becomes large.

Recently, two other approaches to estimating neutral model parameters from species abundances have been put forward. The first approach is by Forster & Warton (2007). They derive a integral likelihood for multiple samples, but this likelihood is less informative because, by being a product over the probabilities for each species' abundance, it conditions on the total number of species as well as on the sample sizes. The sampling formula present in this paper only conditions on the sample sizes and the total number of species is a prediction rather than an assumption. Also, the estimation procedure of Forster & Warton (2007) is, as they state, fraught with numerical problems in evaluating the integral, notwithstanding the fact that they have found clever ways to minimize them. The second approach is by Jabot *et al*. (2008) who dispense with the metacommunity model altogether and only estimate the I_i assuming the aggregated abundances across all samples as a proxy for the metacommunity abundance distribution. When the number of samples is small or when there are many singletons, this assumption is hard to justify. There is a third approach to estimating neutral model parameters (Munoz *et al*. 2008) based on the same spatially implicit model, but this approach uses similarity measures similar to Simpson diversity (see also He 2005) rather than the full abundance vector.

Not only can the sampling formula be used for parameter estimation without the restricting assumption of equal recruitment limitation across all local communities, it is also applicable in the "exact" test of neutrality proposed in Etienne (2007). Furthermore, by being a proper likelihood it enables direct likelihood-based comparisons of the performance of different models of community structure in fitting species abundance data at multiple sites, ranging from model weighting using AIC (Chave *et al*. 2006, Etienne *et al*. 2007) to Bayesian comparisons (Etienne & Olff 2005).

Specifying error estimates will help in interpretation of parameter estimates as in the tropical tree community example. Surprisingly, this has not received much attention in the development of tools in evaluating the neutral theory of biodiversity. In Etienne (2007) I showed that an estimate of the uncertainty in the parameters can also be obtained by parametric bootstrap (which can also be used to test for neutrality): one simulates many data sets with the ML estimates obtained from the real data and then estimates the ML parameters for each of these simulated data sets (Efron & Tibshirani 1993); the distribution of these ML estimates informs one about bias and variance in the ML estimates for the real data (see also Burnham & Anderson 2002). Because this is computationally demanding, the variance-covariance matrix at the likelihood optimum provides a convenient alternative, although it does not give an estimate of the bias. With these two procedures now being available specifying error estimates should become common practice in confrontations of neutral models to diversity data.

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Online Material

ML.zip. A zipfile containing files with source code to compute the maximum likelihood parameter estimates and variance-covariance matrix for a given data set.

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Table captions

Table I. Estimates of θ and m_i in various scenarios of simulated data sets for the two-stage approach of Etienne 2009 and the approach presented here. The values reported are the means and coefficients of variations (c_v) of the parameter estimates over 1000 simulated data sets, each having 3 samples of size 1000. There are no results listed for $\theta = 500$ and $m_1 = 0.001$, $m_2 = 0.002$, $m_3 = 0.004$ because this configuration freqnently results in an abundance data set in which there is no species overlap between samples and thus has an infinite ML estimate for θ.

Table II. Estimates of θ and I_i for the three tropical tree communities in Panama. The first row reports the values for the full three data sets; the ten following rows report the values for each of the ten subplots of BCI (see also Etienne 2007). The last part is the correlation matrix for the full data set.

Tables

Table I:

Scenario	Model parameters					Maximum likelihood parameter estimation													
						Etienne (2008)								This paper					
	J	θ	m_1	m_2	m_3	$\widehat{\theta}$		$\widehat{m}_1$		$\widehat{m}_2$		$\widehat{m}_3$		$\widehat{\theta}$		$\widehat{m}_1$		$\widehat{m}_2$		$\widehat{m}_3$	
						mean	c_v	mean	c_v	mean	c_v	mean	c_v	mean	c_v	mean	c_v	mean	c_v	mean	c_v
1	1000	5	0.1	0.2	0.4	5.8096	0.39	0.2003	1.45	0.2765	1.16	0.3975	0.91	4.9689	0.21	0.1119	0.44	0.2353	0.49	0.4727	0.50
2	1000	50	0.1	0.2	0.4	51.8122	0.19	0.1135	0.69	0.2224	0.56	0.4248	0.50	49.9838	0.097	0.1022	0.16	0.2041	0.16	0.4105	0.18
3	1000	500	0.1	0.2	0.4	507.5497	0.12	0.1005	0.088	0.2009	0.089	0.4026	0.11	501.5142	0.067	0.1005	0.08	0.2009	0.077	0.4007	0.076
4	1000	5	0.01	0.05	0.25	5.8089	0.46	0.0438	3.61	0.1319	1.84	0.3460	1.05	4.8982	0.25	0.0108	0.43	0.0572	0.46	0.3658	0.70
5	1000	50	0.01	0.05	0.25	53.6618	0.29	0.0103	0.23	0.0572	0.76	0.2950	0.70	49.9892	0.12	0.0103	0.21	0.0513	0.16	0.2643	0.25
6	1000	500	0.01	0.05	0.25	577.0717	0.36	0.0100	0.17	0.0505	0.14	0.2615	0.34	504.0792	0.11	0.0101	0.17	0.0504	0.11	0.2521	0.091
7	1000	5	0.009	0.09	0.9	5.9486	0.46	0.0374	3.51	0.1854	1.50	0.5619	0.72	5.1082	0.23	0.0098	0.42	0.1019	0.40	0.7720	0.34
8	1000	50	0.009	0.09	0.9	53.8231	0.28	0.0091	0.22	0.1032	0.75	0.7302	0.38	50.5992	0.10	0.0091	0.20	0.0906	0.15	0.8647	0.16
9	1000	500	0.009	0.09	0.9	555.6823	0.31	0.0091	0.18	0.0907	0.14	0.8181	0.20	503.8535	0.075	0.0090	0.18	0.0901	0.090	0.8975	0.081
10	1000	5	0.001	0.002	0.004	10.5145	1.92	0.0217	5.96	0.0427	4.32	0.0617	3.48	5.0388	0.45	0.0012	0.67	0.0027	1.27	0.0066	4.85
11	1000	50	0.001	0.002	0.004	1533.1730	11.70	0.0010	0.51	0.0039	8.93	0.0105	6.43	56.0378	0.55	0.0010	0.42	0.0020	0.35	0.0042	0.30

Table II:

	Sample sizes and species richness		Maximum likelihood parameter estimation			
	$\overrightarrow{J}$	$\overrightarrow{S}$	$\widehat{\theta}$	$\widehat{I}_{\text{Sherman}}$	$\widehat{I}_{\text{BCI}}$	$\widehat{I}_{\text{Cocoli}}$
Sherman + BCI + Cocoli	$(2860, 21457, 1079)$	$(125, 225, 99)$	235 ± 23	35.7 ± 3.9	65.3 ± 5.9	31.5 ± 3.9
Sherman + BCI_1 + Cocoli	$(2860, 2359, 1079)$	$(125, 152, 99)$	260 ± 29	35.6 ± 3.9	54.2 ± 5.8	30.7 ± 3.7
Sherman + BCI_2 + Cocoli	$(2860, 2151, 1079)$	$(125, 150, 99)$	264 ± 30	35.5 ± 3.9	54.4 ± 5.9	30.9 ± 3.8
Sherman + BCI_3 + Cocoli	$(2860, 2076, 1079)$	$(125, 162, 99)$	265 ± 29	35.0 ± 3.8	63.5 ± 6.7	31.1 ± 3.8
Sherman + BCI_4 + Cocoli	$(2860, 2027, 1079)$	$(125, 171, 99)$	264 ± 29	34.8 ± 3.8	70.5 ± 7.4	31.1 ± 3.8
Sherman + BCI_5 + Cocoli	$(2860, 2000, 1079)$	$(125, 166, 99)$	274 ± 30	34.4 ± 3.7	66.9 ± 7.1	31.3 ± 3.8
Sherman + BCI_6 + Cocoli	$(2860, 2050, 1079)$	$(125, 153, 99)$	286 ± 32	33.9 ± 3.6	56.1 ± 6.0	31.1 ± 3.8
Sherman + BCI_7 + Cocoli	$(2860, 2364, 1079)$	$(125, 147, 99)$	291 ± 33	33.9 ± 3.6	48.2 ± 5.0	30.8 ± 3.8
Sherman + BCI_8 + Cocoli	$(2860, 2225, 1079)$	$(125, 138, 99)$	291 ± 34	34.2 ± 3.7	44.8 ± 4.8	30.8 ± 3.8
Sherman + BCI_9 + Cocoli	$(2860, 2076, 1079)$	$(125, 145, 99)$	292 ± 34	34.3 ± 3.7	50.1 ± 5.3	30.7 ± 3.7
Sherman + BCI_{10} + Cocoli	$(2860, 2129, 1079)$	$(125, 157, 99)$	260 ± 29	35.0 ± 3.8	59.3 ± 6.3	31.3 ± 3.8

Sherman + BCI + Cocoli

Correlation matrix

	$\widehat{\theta}$	$\widehat{I}_{\text{Sherman}}$	$\widehat{I}_{\text{BCI}}$	$\widehat{I}_{\text{Cocoli}}$
$\widehat{\theta}$	1	-0.12	-0.37	-0.052
$\widehat{I}_{\text{Sherman}}$	-0.12	1	0.070	0.0021
$\widehat{I}_{\text{BCI}}$	-0.37	0.070	1	0.031
$\widehat{I}_{\text{Cocoli}}$	-0.052	0.0021	-0.031	1