Community Ecology Parameter Calculator 1.0
User's Manual

Table of Contents

	A	B	C	D	E	F	G	H	I	J	K
1		Vz1	Vz2	Vz3	Vz4	Vz5	Vz6	Vz7	Vz8	Vz9	Vz10
2	S	21	21	15	28	24	23	15	15	17	27
3	N	89	280	52	191	119	149	44	97	88	134
4	S_E	1	4	3	3	3	1	4	4	4	3
5	S_D	1	0	2	3	1	4	1	3	1	2
6	S_Sd	13	3	1	3	4	5	10	2	5	5
7	S_R	6	3	9	2	6	5	0	6	7	1
8	S_Sr	0	11	0	17	10	8	0	0	0	16
9	N_E	42	233	33	113	74	65	27	65	59	73
10	N_D	6	0	8	40	8	45	3	20	7	23
11	N_Sd	35	22	2	17	15	21	14	6	15	20
12	N_R	6	11	9	4	12	10	0	6	7	2
13	N_Sr	0	14	0	17	10	8	0	0	0	16
14	F_1	6	8	9	17	10	8	6	6	7	16
15	F_2	6	3	1	2	6	5	4	1	2	1
16	F_3	5	1	0	0	1	1	1	0	1	3
17	H'	3.175042	2.658953	3.130016	3.41583	3.333519	3.167536	3.445719	3.17909	3.275997	3.618836
18	E	0.722863	0.605364	0.801153	0.710543	0.727055	0.70023	0.881959	0.813714	0.801474	0.761077
19	E'	0.541067	0.533085	0.619454	0.607734	0.583183	0.584193	0.742803	0.736486	0.696779	0.637396
20	D	0.240752	0.265102	0.159763	0.142622	0.183673	0.219224	0.117769	0.141673	0.143079	0.122076
21	N2	4.153644	3.772132	6.259259	7.011532	5.444444	4.561537	8.491228	7.058515	6.98917	8.191606
22	D_{Ma}	4.455696	3.549378	3.543188	5.140631	4.812598	4.39653	3.699603	3.060303	3.573553	5.308463
23	D_{Me}	2.225996	1.25499	2.080126	2.026009	2.200076	1.884233	2.261335	1.523019	1.812206	2.332445
24	S_{Chao1}	24	31.66667	55.5	100.25	32.33333	29.4	19.5	33	29.25	155
25	Var(S_{Chao1})	10.5	105.4815	2409.75	3910.531	47.68519	35.072	23.0625	558	173.0313	20608

Fig 1: Example of results given by ComEcoPaC for samples (Vz1-Vz10).

1 About the ComEcoPaC program

The ComEcolPaC is an Microsoft Excel 2003 based program (also compatible with version MS Excel 2007 and 2010) calculating common parameters of community ecology samples and various similarity indices.

Copyright and distribution. The ComEcolPaC was created by Pavel Drozd (University of Ostrava, Department of Biology, Chittussiho 10, 710 00 Ostrava, Czech Republic). It is a freeware. Commercial use of the program is possible only with the consent of the author. Any use of the program should be acknowledged. Please report any bugs or problems to the author.

Suggested citation:

Drozd P., 2010: ComEcoPaC – Community Ecology Parameter Calculator. Version 1. Available from: http://prf.osu.cz/kbe/dokumenty/sw/ComEcoPaC/ComEcoPaC.xls.

Author would also appreciate if you could send a reprint of any paper using the program.

2 List of parameters calculated by ComEcoPaC

ComEcolPaC provides following types of calculation:

- Species richness and species diversity (number of species, species richness indices and species diversity indices, species richness estimates).
- Abundance, number of singletons, doubletons and tripletons, basic the Tischler's dominance classes analyses.
- Matrices of similarity between samples (basic qualitative and quantitative indices, distance indices).

Parameters and used abbreviations:

S - number of species (species richness)
N - number of specimens (abundance)
$\mathbf{S_E, S_D, S_{Sd}, S_R, S_{Sr}}$ - number of eudominant, dominant, subdominant, recedent, subrecedent species (Tischler's scale)
$\mathbf{N_E, N_D, N_{Sd}, N_R, N_{Sr}}$ - abundance for eudominant, dominant, subdominant, recedent, subrecedent species (Tischler's scale). Dominance is calculated as a percentage of the individuals of given species in the sample.

$$D_i = \frac{n_i}{N} \cdot 100\,\%$$ n_i - abundance of species i, N - total abundance in sample

Tischler's scale for a species dominance (Tischler 1949):

E	eudominant	$10\,\% \le D_i \le 100\,\%$
D	dominant	$5\,\% \le D_i < 10\,\%$
Sd	subdominant	$2\,\% \le D_i < 5\,\%$
R	recedent	$1\,\% \le D_i < 2\,\%$
Sr	subrecedent	$0\,\% < D_i < 1\,\%$

$\mathbf{F_1, F_2, F_3}$ - number of singletons, doubletons, tripletons (species with 1, 2, 3 individuals).

H' - Shannon-Wiener diversity index

$$H' = \sum_{i=1}^{S} p_i \cdot \log_2 p_i$$ S - species richness (number of species), p_i - proportion of species i

$$p_i = \frac{n_i}{N}$$ n_i - abundance of species i, N - total abundance

E, E' - eveness and corrected eveness.

$$E = \frac{H'}{H_{\max}} \qquad E' = \frac{H' - H'_{\min}}{H'_{\max} - H'_{\min}}$$

$$H'_{\max} = \log_2 S$$

$$H'_{\min} = -\frac{N-S+1}{N}\log_2\frac{N-S+1}{N} + \frac{S-1}{N}\log_2 N$$

D - Simpson's index

$$D = \sum_{i=1}^{s} p_i^2$$

S - species richness, p_i - proportion of species i

N2 - Hill's index (inverted Simpson's index)

$$N_2 = \frac{1}{\sum_{i=1}^{s} p_i^2}$$

S - species richness, p_i - proportion of species i (see Shannon-Wiener index)

D_{Ma} - Margalef index

$$D_{Ma} = \frac{S-1}{\ln N}$$

S - species richness, N - total abundance

D_{Me} - Menhinick index

$$D_{Me} = \frac{S}{\sqrt{N}}$$

S - species richness, N - total abundance

S_{Chao1} - Species richness estimator (Chao 1) and variance of the estimated richness

$$\hat{S}_{Chao1} = S_{obs} + \frac{F_1^2}{2F_2} \qquad \mathrm{var}(S_{Chao1}) = F_2\left(\frac{G^4}{4} + G^3 + \frac{G^2}{2}\right) \qquad G = \frac{F_1}{F_2}$$

S - species richness *observed*, F_1, F_2 - number of singletons, doubletons

Similarity measures

Ja - Jaccard's similarity index

$$Ja = \frac{S_{12}}{S_1 + S_2 - S_{12}}$$

S_{12} - number of species present in both samples (joint occurences)

S_1 (S_2) - number of species present in sample 1 (sample 2).

So - Sörensen's similarity index

$$S\ddot{o} = \frac{2S_{12}}{S_1 + S_2}$$

S_{12} - number of species present in both samples (joint occurences)

S_1 (S_2) - number of species present in sample 1 (sample 2).

S_{sm} - Simple matching coefficent

$$S_{SM} = \frac{S_{12} + S_{-}}{S_1 + S_2 - S_{12} + S_{-}}$$

S_{12} - number of species present in both samples (joint occurences)

S_1 (S_2) - number of species present in sample 1 (sample 2).
S_{-} - number of species absent in both samples

S_b - Baroni-Urbani & Buser index

$$S_B = \frac{S_{12} + \sqrt{S_{12}S_{-}}}{S_1 + S_2 - S_{12} + \sqrt{S_{12}S_{-}}}$$

S_{12} - number of species present in both samples (joint occurences)

S_1 (S_2) - number of species present in sample 1 (sample 2).

S_{-} - number of species absent in both samples

Re - Renkonen index

$$\mathrm{Re} = \sum_{i=1}^{s} \min\left(p_i^j, p_i^k\right)$$

Δ - Eukleidean distance

$$\Delta_{jk} = \sqrt{\sum_{i=1}^{s} \left(n_{ij} - n_{ik}\right)^2}$$

n_{ij} (n_{ik}) - abundance of species i in sample j (sample k)

B - Bray-Curtis Measure

$$B = \frac{\sum_{i=1}^{s} \left|n_{ij} - n_{ik}\right|}{\sum_{i=1}^{s} \left(n_{ij} + n_{ik}\right)}$$

n_{ij} (n_{ik}) - abundance of species i in sample j (sample k)

C - Canberra Metric

$$C = \frac{1}{s}\left[\sum_{i=1}^{s} \frac{\left|n_{ij} - n_{ik}\right|}{n_{ij} + n_{ik}}\right]$$

n_{ij} (n_{ik}) - abundance of species i in sample j (sample k)

C_λ - Morisita's index of similarity

$$C_\lambda = \frac{2\sum_{i=1}^{s} n_{ij} n_{ik}}{(\lambda_1 + \lambda_2) N_j N_k} \quad \lambda_1 = \frac{\sum_{i=1}^{s} \left[n_{ij}\left(n_{ij} - 1\right)\right]}{N_j\left(N_j - 1\right)} \quad \lambda_2 = \frac{\sum_{i=1}^{s} \left[n_{ik}\left(n_{ik} - 1\right)\right]}{N_k\left(N_k - 1\right)}$$

n_{ij} (n_{ik}) - abundance of species i in sample j (k)

N_j (N_k) - total abundance of sample j (k)

3 How to use the ComEcoPaC

Working with ComEcoPac is very simple through the floating toolbar which appears while open the workbook (you have to enable macros in MS Excel otherwise application is not functioning). There are three required worksheets in this workbook and the program automatically creates them when missing.

- **Data** - worksheet for data input in following required format: a) species are in rows, samples in columns; b) all species/samples have a label (name) in first column/row (see Fig below) otherwise data range need not be recognized.
- **Results** - worksheet with parameters calculated.
- **Similarity** - worksheet with similarity matrices calculated.

	A	B	C	D	E	F	G	H	I	J	K	L	M
1		Sam1	Sam2	Sam3	Sam4	Sam5	Sam6	Sam7	Sam8	Sam9	Sam10	Sam11	Sam12
2	Spec1		1				1					2	
3	Spec2	1	4	1									
4	Spec3	3	6	7	1						2		1
5	Spec4	5		16					1	1			
6	Spec5	3						2		2	1		2
7	Spec6	1	19					3	1		1	1	3
8	Spec7	4	4	3	2					1			
9	Spec8		1										
10	Spec9	5		5			1			1			1
11	Spec10	2	1	2									
12	Spec11	17				1							

Fig 2: Required format of entry data.

Toolbar buttons:

- **Calculate Parameters** – At first the program counts a total number of samples and species in Data worksheet and a validation of the counts is required (which means data table range). Possible errors (wrong number of species/samples) arise from missing species/sample labels in first row/column. You can stop the program (click "No" button) and add the missing labels. If the counts are correct then click on "Yes" button and the window for parameters selection will open. Choose parameters required and click OK.
- **Clear All Worksheets** – Clear worksheets (Data, Results, Similarity) for new data input. Results and Similarity worksheets are cleared automatically before you start parameter calculation.
- **Restore Data Example** – Original data will be restored from backup.
- **Go to worksheet** – Jump to selected worksheet.
- **Help** – Open Help document.

Backup of the results:

Worksheets Results and Similarity are automatically cleared. Therefore to backup your previous results, rename both worksheets before you will start new calculation. New worksheets Results and Similarity will be added during calculation procedure.

4 Acknowledgements

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5 Further reading

Krebs Ch., 1998: Ecological Methodology. 2nd edition. Addison Wesley Longman.
Southwood T.R.E. & Henderson P.A., 2000: Ecological Methods. 3rd edition. Blackwell Science.
Tischler W., 1949: Grundzüge der terrestrischen Tierökologie. Braunschweig, Friedrich Vieweg und Sohn.