

AccuCurve 1.0

User's Manual

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	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	Variable	Samples	1	2	3	4	5	6	7	8	9	10	11	12
2	S	Avg(S)	21.78	29.44	38.15	42.26	45.14	48.22	50.87	53.31	55.16	56.78	58.85	60
3		Min(S)	13	19	29	32	37	37	42	46	49	51	55	60
4		Max(S)	33	43	48	52	54	58	59	59	60	60	60	60
5	F1	Avg(F1)	9.83	10.79	12.5	12.94	12.65	12.99	13.6	13.12	13.33	12.86	12.21	12
6		Min(F1)	5	7	6	6	4	5	5	7	8	8	9	12
7		Max(F1)	19	17	18	20	22	21	22	21	20	19	17	12

Fig 1: Example of the results given by AccuCurve. Cummulative species richness and number of singletons (minimum and maximum for each number of subsamples from total of 12 samples)

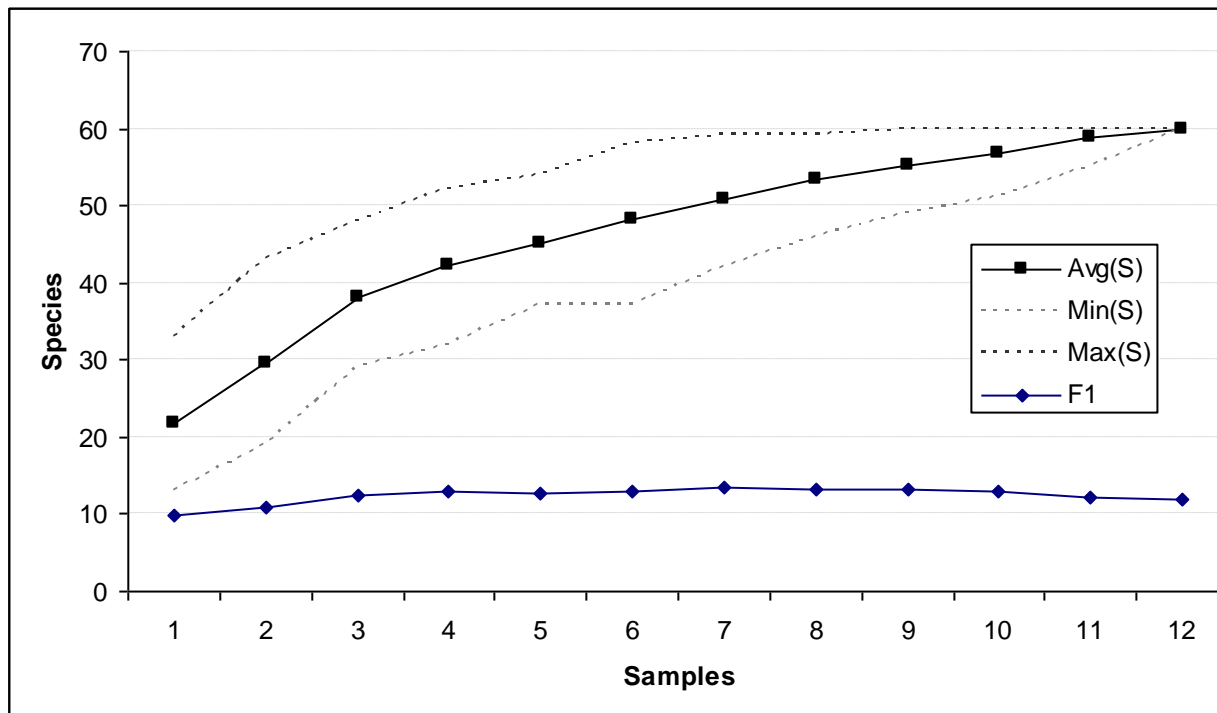


Fig 2: Chart based on results in Fig 1.

1 About the AccuCurve program

The AccuCurve is an Microsoft Excel 2003 based program (compatible with version MS Excel 2007 and 2010) calculating various accumulation curves for a set of samples containing more than one species.

Copyright and distribution. The AccuCurve was created by [Pavel Drozd](#) (University of Ostrava, Department of Biology, Chittussiho 10, 710 00 Ostrava, Czech Republic) and [Vojtech Novotny](#) (Institute of Entomology, Branisovska 31, CZ 370 05 Ceske Budejovice, Czech Republic). It is a freeware. Any commercial use of the program is possible only with the consent of the authors (please see licence agreement attached at the website). Any use of the program should be acknowledged.

Suggested citation:

Drozd P. & Novotny V., 2010: AccuCurve. Version 1. Available from:
<http://prf.osu.cz/kbe/dokumenty/sw/AccuCurve/AccuCurve.xls>.

We would appreciate if you could send a reprint of any paper using the program to authors ([Pavel Drozd](#), [Vojtech Novotny](#))

2 Background of the accumulation curves

The species accumulation curves (SAC) plot a number of species against a measure of sampling effort (e.g. cumulative number of samples). Despite SACs are well known as a method for estimates of species richness and minimal area, they are also very important for an experimental design arrangement, such as a proposal of the most efficient sampling effort for community ecology experiments.

Mathematically, the sampling accumulation means a gradual selection of the subset of k samples from the total of n samples for $k = 1...n$. As the final shape of the curve depends on the order of the samples included successively, randomization process is used to smooth the final accumulation curve. Number of k samples from the "sampling pool" is taken randomly (with or without replacement), then number of species is calculated and the procedure is repeated several times. A number of replications with sample replacement is unlimited while number of replications without replacement is given by formula

$$C(n, k) = \binom{n}{k} = \frac{n!}{k!(n-k)!} \quad \text{where } k \text{ is number of samples taken and } n \text{ is total number of samples.}$$

Besides calculation of the species accumulation (SAC), AccuCurve gives a various community ecology parameters along increasing number of samples and summarize them through several statistics. As the program was formerly written for herbivorous insect research, some of the parameters are useful particularly for host specificity analyses. Here is the overview of the parameters and statistics:

Parameters:

- S – number of species;
- N – abundance (number of individuals);
- F_1 – singletons – number of species with one individual only;
- Q_1 – uniques – number of species occurred only in one sample (number of monophagous species);
- $N(Q_1)$ – abundance of uniques (abundance of the monophagous species);
- Oc – occurrences – number of nonzero cells;
- $Oc(F_1)$ – "singleton" occurrences – number of cells with one individual ;
- Hs – host specificity – $Hs = \frac{Oc - S}{S \cdot (samples - 1)}$, for more details see Novotny & Basset (2005);
- special filter – cells with less than x individuals can be remove from analysis (using filter some parameters based on singleton analysis are disabled).

Statistics

- Avg – average;
- Med – median;
- Mod – mode;
- q_{25} – lower quartile (25% quantile);
- q_{75} – upper quartile (75% quantile);
- range – minimum and maximum;
- Var – sample variance;
- SE – standard error.

Please note that AccuCurve is easy to use and simple application created originally for insect herbivores research. If you are interested in modern sophisticated species richness estimators see [EstimateS](#) (Colwell 2009) which is more suitable for these purposes.

3 How to use the program

Program starts automatically while open the workbook (you have to enable macros in MS Excel otherwise application is not functioning). Using the application is very easy through the floating toolbar which appears while open the workbook (or right click on the worksheet when the toolbar is missing). There is only one required worksheets "Data" in this workbook which the program automatically creates when missing. Input data should be prepared in following format: a) species are listed in rows, samples in columns; b) all species/samples have a label (name) in first column/row (see Fig 2) otherwise data range need not be recognized. A value in the cell "A1" is added by program if missing (see Fig 2).

Other worksheets with complete information on the selected parameters (results for each replication) are created during analysis and all statistics are gathered into a worksheet "Summary". Worksheets are numbered to not rewrite previous analyses.

► ► \Data / S-D / F1-D / N-D / Q1-D / N(Q1)-D / Oc-D / Oc(F1)-D / HS-D / Summary-D / i

Fig 1: Sheet tabs with the results of the analysis. Required sheet "Data" and new sheets with partial results for each selected parameter. Worksheet "Summary" recapitulates all results in one table. Sheets for next analysis will be assign with nuber 1.

	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.

Function of toolbar buttons

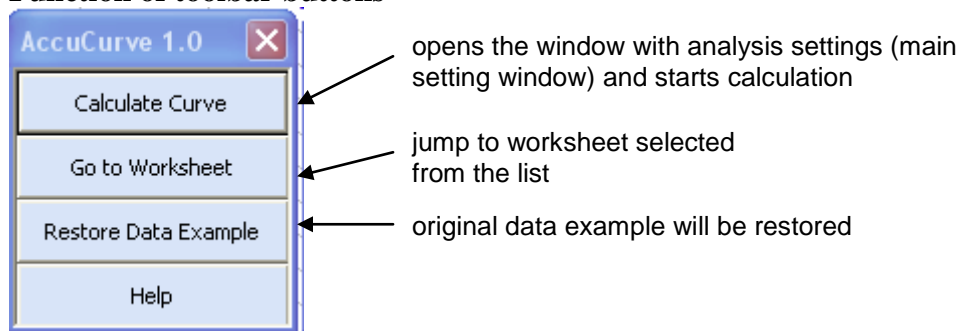


Fig 3: Toolbar buttons.

Settings

No. of combinations: **Run**

Options

☐ All combinations ☒ Random combinations

Type of Results

- ☒ Species (S)
- ☒ Singletons (F1)
- ☒ Abundance (N)
- ☒ Uniques (Q1)
- ☒ Uniques abundance (Nq1)
- ☒ Occurences (Oc)
- ☒ Singletons occurence (OcF1)
- ☒ Host specificity (Hs)

Statistics

- ☒ Average (Avg)
- ☒ Median (Med)
- ☒ Mode (Mod)
- ☒ Quartiles (Q1, Q3)
- ☒ Range (Min, Max)
- ☒ Variance (Var)
- ☒ St. Error (SE)

☐ Eliminate species with less than individuals.

Fig 4: Setting window with optional parameters and statistics.

Main setting window contains textbox for number of replication of k samples (*No. of combinations*) in case of *Random combination* option is selected (see previous chapter). *All combinations* option is enabled for number of samples less or equal 18. Program also allows to eliminate species with abundance less then entered number. However, calculation of singletons is not available in this case.

4 Acknowledgements

This program was created as a part of the long-term research of biodiversity in Papua New Guinea and Czech Republic. We also thank the Fulbright Commission, the National Science Foundation, USA (DEB-97-07928), Grant Agency of Czech Republic (GA ČR 206/07/0811), Grant Agency of the Academy of Science of the CR (GA AV B6187001) and the Institute of Entomology, Czech Academy of Science, for financial support.

5 References and further reading

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