# Sampling Strategies for the Assessment of Ecological Diversity

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## • ECOLOGICAL DIVERSITY QUANTIFICATION



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## • ESTIMATION OF DIVERSITY INDEXES

# ECOLOGICAL DIVERSITY QUANTIFICATION

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• traditionally ED relies on the apportionment of abundance (or related quantities such as biomass or coverage) into the animal or plant species forming the ecological community under study (Patil and Taille, 1982)

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e.g.

ecological diversity of the snakes in a delineated tropical area ecological diversity of the trees in a nature reserve

## **QUANTIFICATION OF DIVERSITY BY INDEXES**

(evenness, dominance and rarity of species)

huge literature

detailed reviews : Dennis *et al*, 1979, Magurran, 1988, Frosini, 2003

a relevant contribution

Patil and Taille (1979, 1982) - average rarity diversity indexes

#### NOTATIONS

- A size of the study area
- **N** number of individuals in the community (total abundance)
- *k* number of species in the community (species richness)
- $N_l$  number of individuals (abundance) of species l (l = 1, ..., k)

 $p_l = N_l / N$  relative abundance of species l (l = 1, ..., k)

 $\mathbf{N} = [N_1, \dots, N_k]^{\mathrm{T}}$  abundance vector

 $\mathbf{p} = [p_1, \dots, p_k]^T = \mathbf{N}/(\mathbf{1}^T \mathbf{N})$  relative abundance vector

#### **AVERAGE RARITY DIVERSITY INDEXES**

• a community is diverse when there is a large number of rare species (Patil and Taille, 1979,1982)

R(p) rarity of a species depending on its relative abundance

$$\Delta = \sum_{l=1}^{k} p_l R(p_l)$$

 $R(p) = -\ln p$  (Shannon index)

R(p)=1-p (Simpson index)

# ESTIMATION OF DIVERSITY INDEXES

#### **ABUNDANCE ESTIMATION**

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N is unknown and must be estimated to estimate  $\Delta$ 

 $\hat{\Delta} = \Delta(\hat{\mathbf{N}})$ 

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- *n* **number of independent drawings**
- $x_l$  number of sampled individuals of species l

$$\mathbf{x} = [x_1, \dots, x_k]^{\mathrm{T}}$$

 $\hat{\mathbf{p}} = \mathbf{x} / n$  best estimator for  $\mathbf{p}$ 

Good (1953), Blyth (1958), Basharin (1959), ..., Baczkowsky et al (2000), Chao and Shen (2003)

## ANIMALS, PLANTS CANNOT BE SELECTED FROM COMMUNITIES JUST LIKE BALLS FROM AN URN !!!

- Pielou (1966)
- Heyer and Berven (1973)
- Zahl (1977)
- Heltshe and Bitz (1979)
- Heltshe and Forrester (1983)
- Gove et al (1994)

#### more recently ....

• Sterbaa (2008), Motza, Sterbaa e Pommereningb (2010), Ramezani, Holm, Allard e Ståhl (2010)

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• no assumptions about the population under study

• "Design-based inference is objective, nobody can challenge that the sample was really selected according to the given sampling design. The probability distribution associated with the design is real, not modelled or assumed" Sarndal et al (1992)

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- owing to the lack of frame, the most effective schemes for sampling ecological populations differ from the traditional ones
- their choice is mainly determined by practical considerations on the nature of the community to be sampled

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De Vries (1986), Thompson (1992), Schreuder *et al.* (1993), Overton and Stehman (1995)

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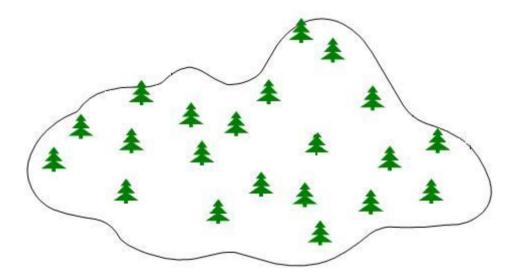
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• the encounter schemes must be strictly ruled to determine (directly or by field measurements) the first-order inclusion probabilities at least for the selected units (computation of the Horvitz-Thompson estimate)

## **PLOT SAMPLING**

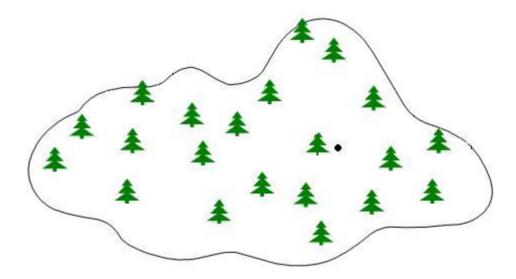
a point is randomly thrown onto the study area and the selected units are those included in a circular or square plot of a pre-fixed size a centered at the sample point



- all the inner units have first-order inclusion probability  $\pi_j = a/A$ • edge effects can be removed by suitable modifications of the
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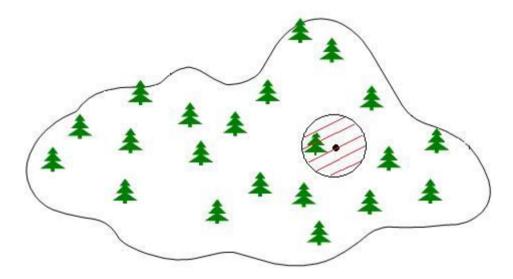
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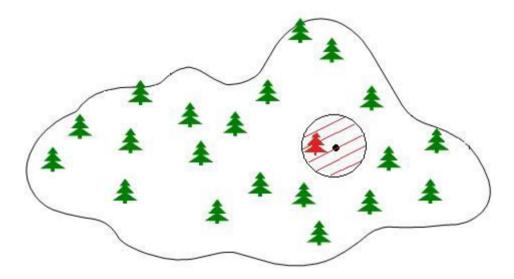
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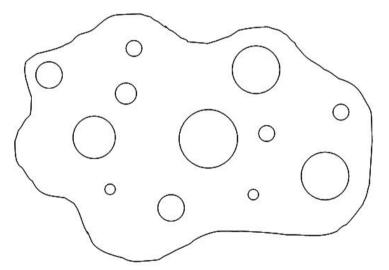
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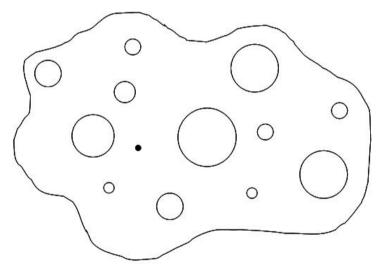
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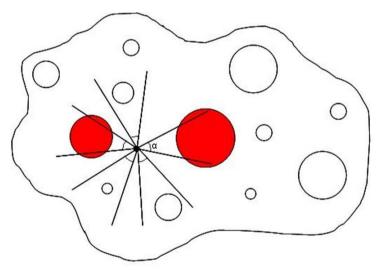
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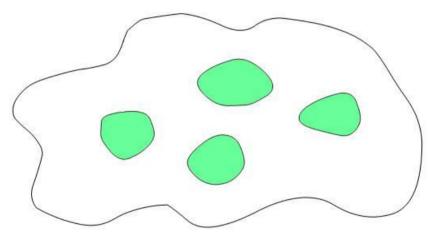
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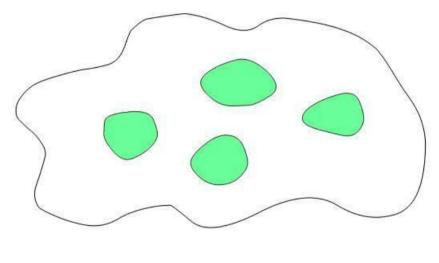


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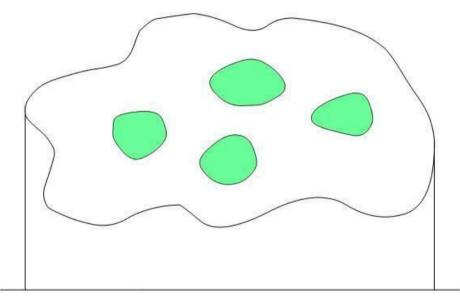
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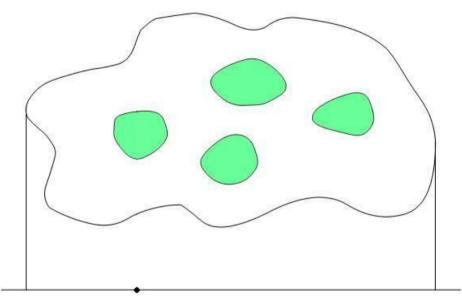
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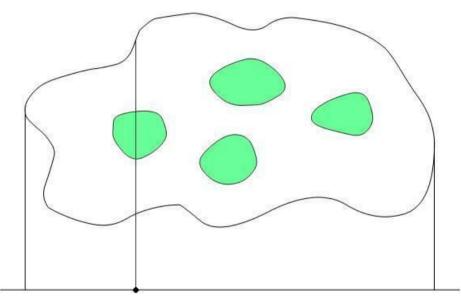
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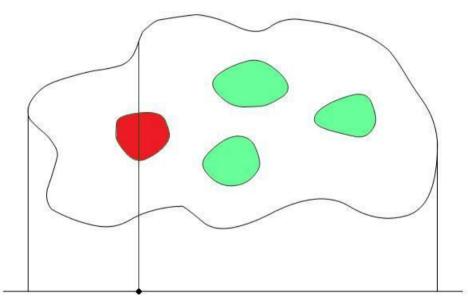
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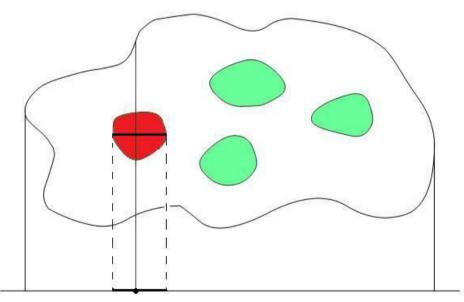
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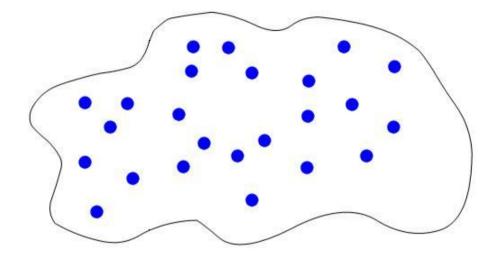


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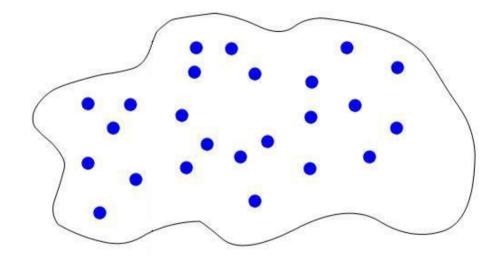


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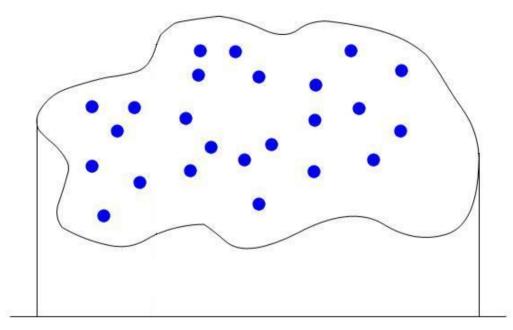




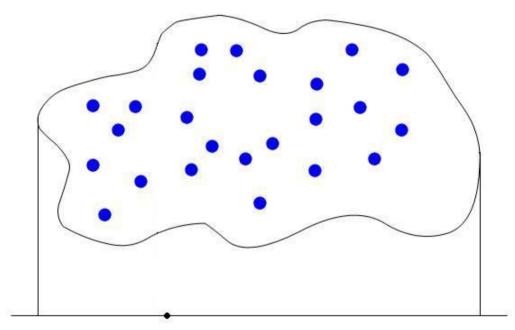
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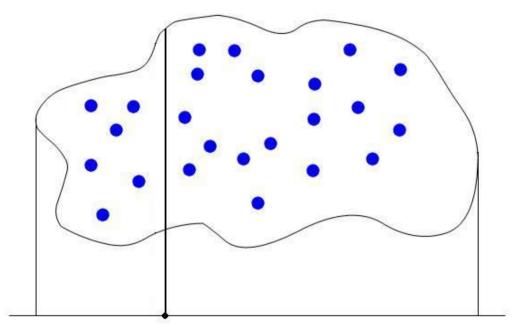
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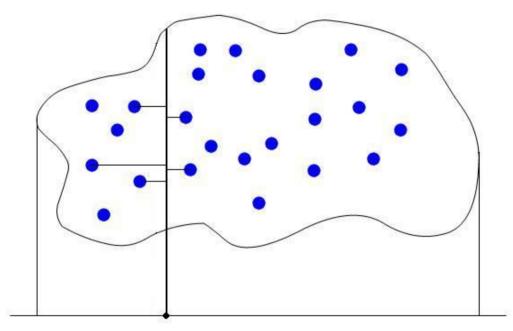
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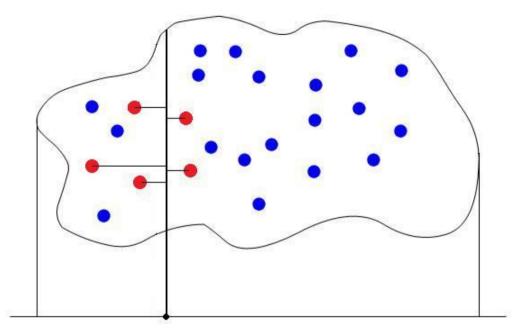
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### **HORVITZ-THOMPSON ESTIMATION**

- S sample of animals or plants selected from a point, plot or transect
- S<sub>1</sub> sample of units from species 1
- S<sub>k</sub> sample of units from species k
- $\pi_j$  inclusion probability (known for each selected unit)

 $\hat{N}_l = \sum_{j \in S_l} \frac{1}{\pi_j}$  HT estimator of abundance of species *l* 

$$\hat{N}_l = 0$$
 if  $S_1 = \emptyset$  (lost species)

$$\hat{\mathbf{N}} = \begin{bmatrix} \hat{N}_1, \dots, \hat{N}_k \end{bmatrix}^{\mathrm{T}}$$
 vector of abundance estimator

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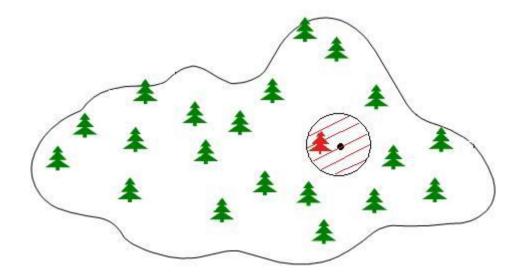
•  $\Sigma$  depends on the sampling scheme as well as on the characteristics of the ecological community (spatial distribution of the individuals over the study area)

•  $\Sigma$  cannot be unbiasedly estimated by a unique sample S

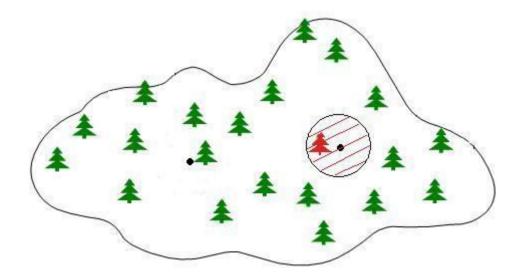
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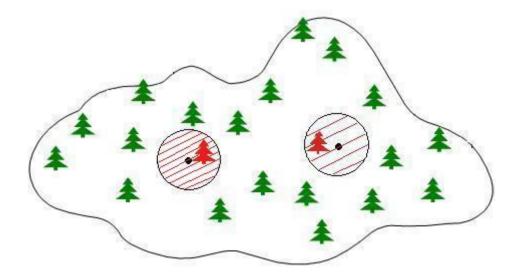
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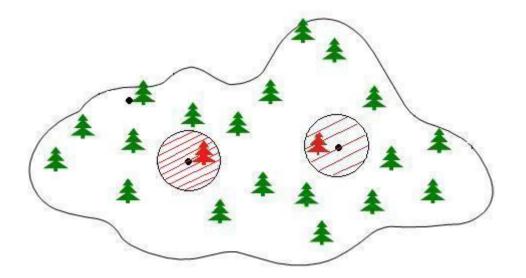
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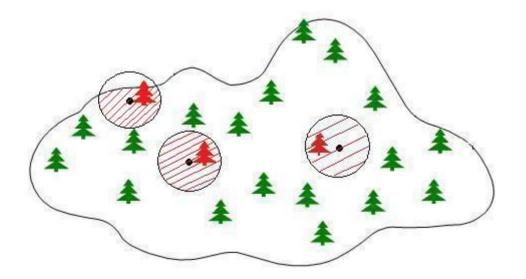
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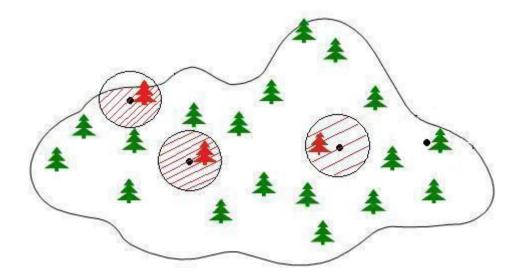
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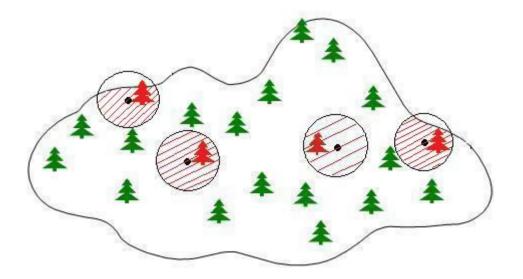
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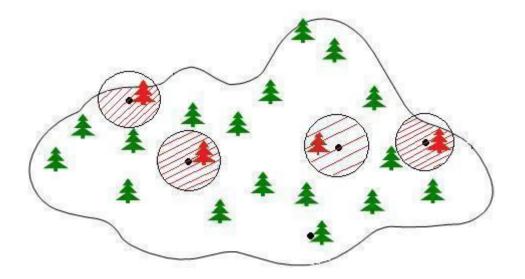
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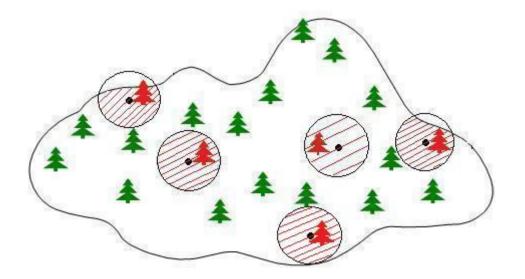
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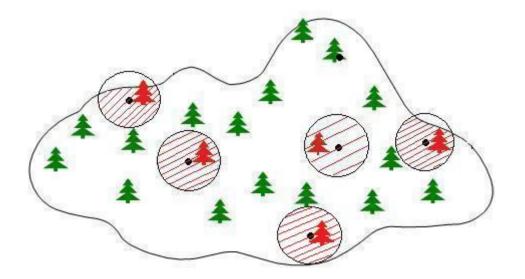
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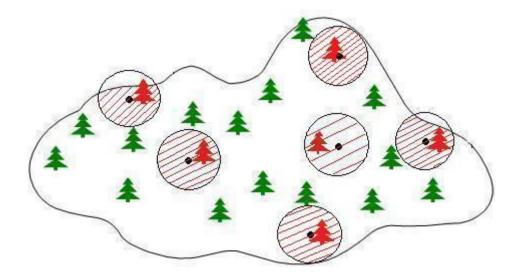
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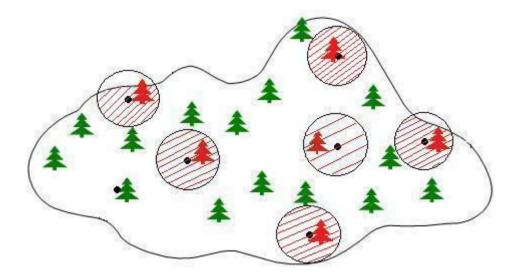
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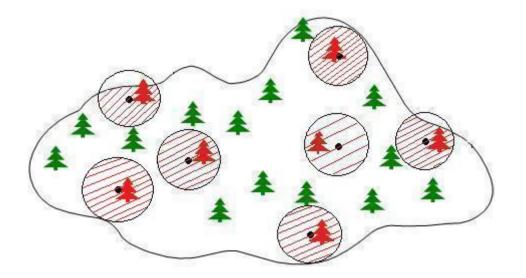
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*n* replications = *n* samples

*n* estimates  $\hat{N}_1, \ldots, \hat{N}_n$ 

arithmetic mean  $\hat{N}$ 

$$\hat{\mathbf{N}}_n = \frac{1}{n} \sum_{i=1}^n \hat{\mathbf{N}}_i$$

Central Limit Theorem: as *n* increases  $\hat{N}_n$  converges to N

 $\hat{\mathbf{N}}_n \to \mathbf{N}$ 

## **GENERAL RESULTS**

$$\Delta(N_1,...,N_k) = \Delta(N_1,...,N_k,0,...,0)$$

• estimation does not require the knowledge of k since the missing species may be ignored when computing  $\hat{\Delta}_n = \Delta(\hat{\mathbf{N}}_n)$ 

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• Delta Method: if  $\hat{N}_n \rightarrow N$  then

$$\hat{\Delta}_n = \Delta(\hat{\bar{\mathbf{N}}}_n) \to \Delta$$

### **JACKKNIFE** (deleting one replication at time)

•  $\hat{\Delta}_n$  is asymptotically unbiased but a bias occurs for finite samples and decreases with *n* 

standard results on jackknife (Shao and Tu, 1995):

• the bias of  $\hat{\Delta}_{jack}$  decreases with  $n^2$  !!

$$\hat{\Delta}_{jack} \pm 2v_{jack}$$
 95% ci

 $\hat{\Delta}_{jack} v_{jack}^2$ 

these results hold for the most familiar diversity indexes

Site	SRF(ha)	R	SH	SE	Crops (ha)	R	SH	SE
1	6.13	7	1.19	26%	361.59	21	2.67	11%
2	61.45	7	2.41	12%	100.97	15	1.95	29%
3	52.47	10	2.43	5%	460.39	17	1.91	17%
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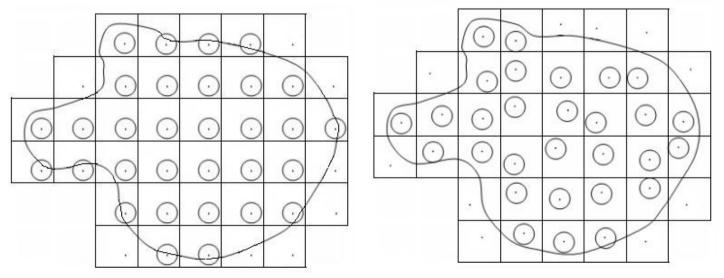
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• more complex sampling schemes should be adopted in order to ensure a systematic search over the study area (e.g systematic grid sampling or tessellation stratified sampling  $\rightarrow$ pseudoreplications)



• the use of pseudo-replications instead of genuine replications requires more refined methodological tools, because the estimates derived from these plots, points or lines cannot be considered equally distributed and in the aligned case they are even dependent

extension to the diversity index estimation of the results by Barabesi (2003), Barabesi and Marcheselli (2005, 2008), Gregoire and Valentine (2008, Chap. 10), Mandallaz (2008, Sec 4.2), Barabesi and Franceschi (2011)

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