INSTITUTE OF MARINE RESEARCH

Estimating evolutionary change

Nordic Marine Academy course on *Modelling marine populations from physics to evolution*
10-16.10.2005 Espegrend, Norway

What to measure?

- Evolution=genetic change
- Phenotypic data “contaminated” by non-genetic effects
  - Clean your data
  - Focus on traits that are least affected
    - E.g., reaction norms

What to measure?

- *Darwins* (Haldane 1949)
  - $\ln(\text{trait}_{now}/\text{trait}_{then})/(\text{now-ten [yr]})*10^6$
  - Simple
- *Haldanes* (Haldane, ...)
  - $(\text{trait}_{now} - \text{strait}_{then})/(\text{sd} \times \#\text{generations})$
    where sd=pooled phenotypic standard deviation
  - A bit more complex, but avoids comparisons between apples and oranges

Estimating maturation reaction norms when age at maturation is unknown

- Barot, S., Heino, M., O'Brien, L. & Dieckmann, U. 2004: Estimating reaction norms for age and size at maturation when age at first reproduction is unknown. *Evolutionary Ecology Research* 6:659-678.
- Barot, S., Heino, M., O'Brien, L. & Dieckmann, U. 2004: Long-term trend in the maturation reaction norm of two cod stocks. *Ecological Applications* 14:1257-1271.

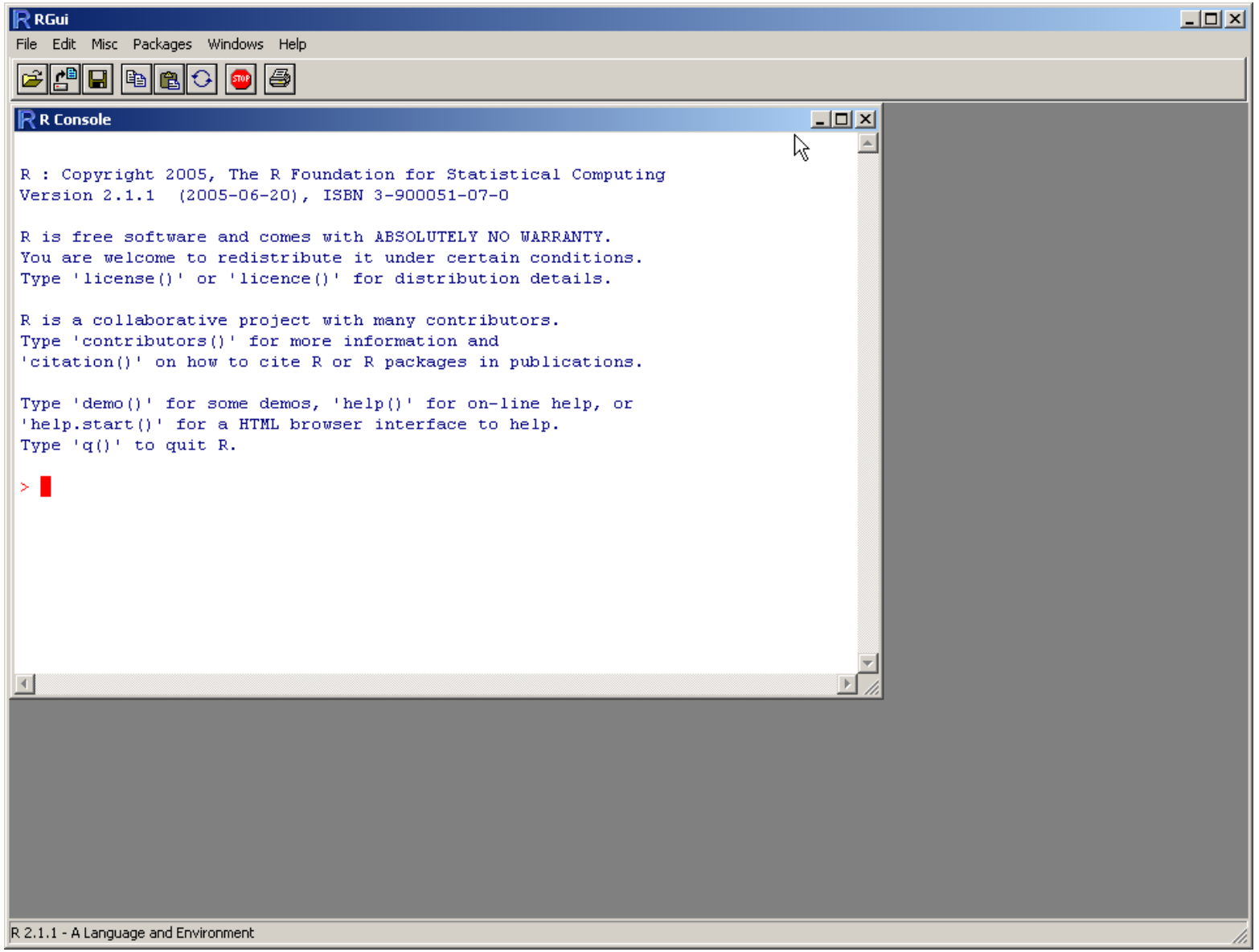
$$m(a,s) = \frac{o(a,s) - o(a-1, s-\delta s)}{1 - o(a-1, s-\delta s)}$$

- This formulate suggests a 4-step procedure
  1. Estimate growth increments δs
  2. Estimate ogives $o(a,s)$
  3. Plug the results in the equation to obtain the maturation reaction norm
  4. Estimate uncertainty

$$m(a,s) = \frac{o(a,s) - o(a-1, s-\delta s)}{1 - o(a-1, s-\delta s)}$$

- We do now something slightly different
  1. Get to know the data
  2. Estimate growth increments δs
  3. Estimate ogives $o(a,s)$
  4. Plug the results in the equation to obtain the maturation reaction norm

R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R 2.1.1 - A Language and Environment

R

- R is an open-source implementation of the language S with command line GUI
- S+ is a bit more user-friendly, commercial implementation with handy menus etc.
- The basic functionality is the same
- ... but ordinary users are likely to use high-level functions that are not necessarily the same

Some very basics #1

- Everything is based on objects. For example, if you type `a<-2` then an object named `a` is created, and it has value 2. `<-` is the assignment operator.
- Objects have class, like `a` is “numeric”. Usually R decides that automatically and you don’t need to bother.
- To see what is in a stored object, just type its name.

Same very basics #2

- Objects can be complex. For example if you do a regression, you get an object in return that contains parameters estimates, residuals, etc. Regression analysis itself is just another object that is pre-programmed.
- You can access individual elements. For example, `a[2]` gives you the second element in object `a`
- Data frames are a useful class of objects, much like spreadsheets. If `d` is a data frame that has column ‘age’ and ‘length’, then you can access these by typing `d$age` etc.