les: Loci of Enhanced Significance

Identification of Differential Effects in Tiling Microarray Experiments

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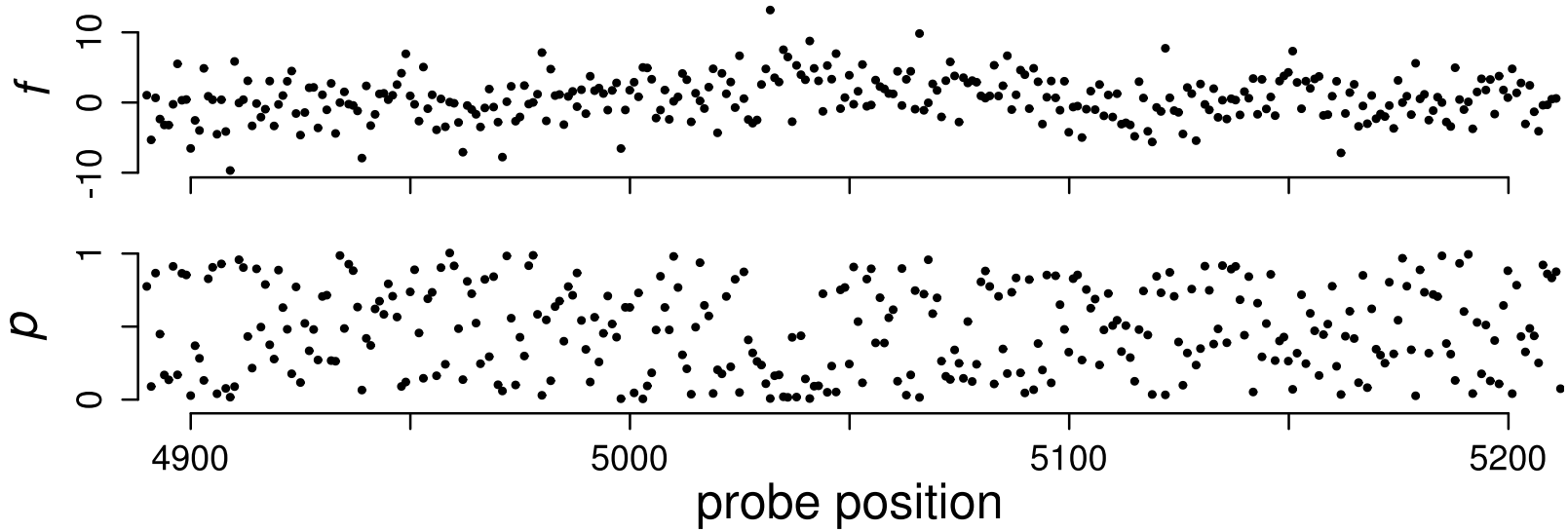
November 18, 2010

General Analysis of Tiling Microarray Data

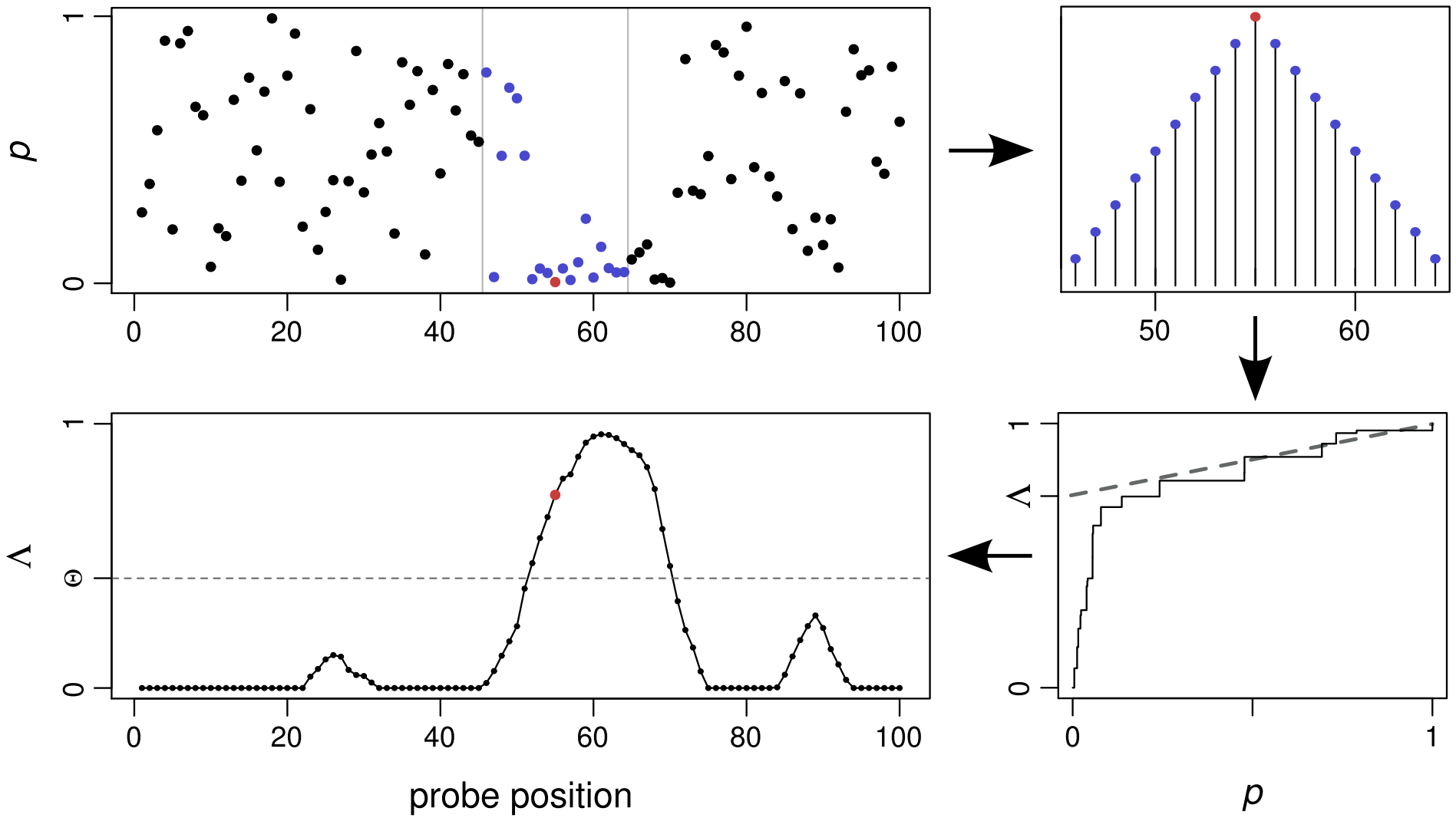
analysis of differential design experiments

- assessing the effect for each probe individually



- combining information of neighboring probes

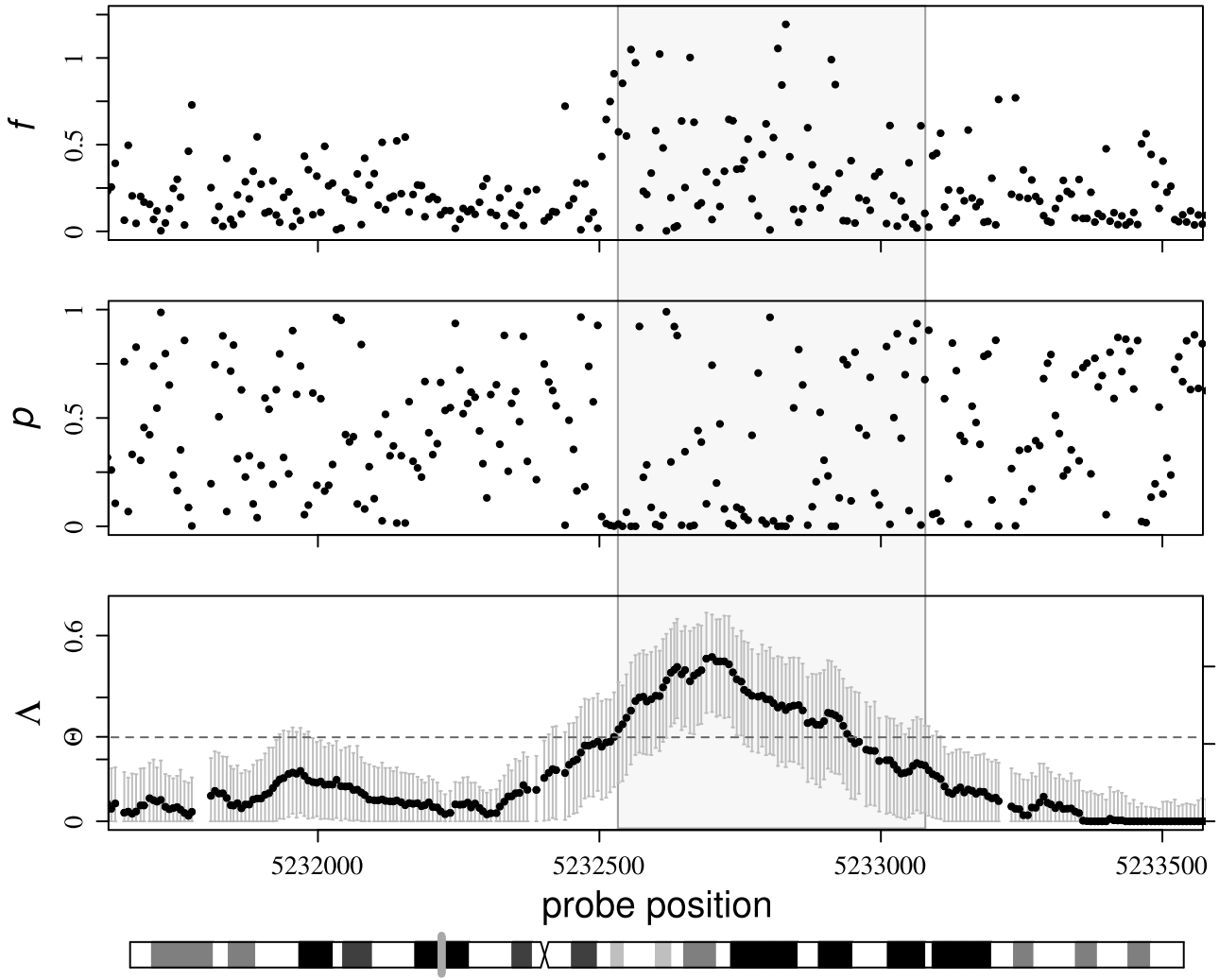
From Probe Level p-values to Loci of Enhanced Significance



Characteristics of the LES Approach

- estimator for the fraction of significant probes in the local surrounding of the genome
- confidence intervals computed with bootstrapping
- statistics allow a meaningful interpretation
- independent of the analysis at the probe level
- accounts for the dependency of probes through weighting, flexible in the definition of the weighting window
- all parameters can be estimated from the data

Results for ChIP-chip Data



data: Johnson et al., 2008

Implementation in R

les package

- identification of differential effects in tiling microarray experiments based on probe-level p-values
- features:
  - object oriented, S4 classes
  - high-level plotting
  - export of results to standard formats
  - scalable, speed and memory efficient
  - support of multicore processing
- published with bioconductor release 2.7 in October 2010

Usage of the *les* Package

```
library(les)

x <- Les(pos, pval, chr)

x <- estimate(x, weighting=rectangWeight, win=100, ...)
x <- ci(x, conf=0.95, ...)

x <- threshold(x, ...)
x <- regions(x, ...)

region <- x[“regions”]
export(x, file, format, ...)
plot(x, ...)
```