

les: Loci of Enhanced Significance
Identification of Differential Effects in
Tiling Microarray Experiments

Julian Gehring Clemens Kreutz Jens Timmer

Faculty of Biology and Institute of Physics

University of Freiburg, Germany

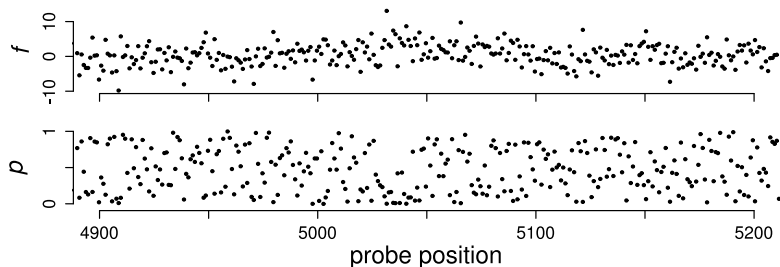
November 18, 2010



General Analysis of Tiling Microarray Data

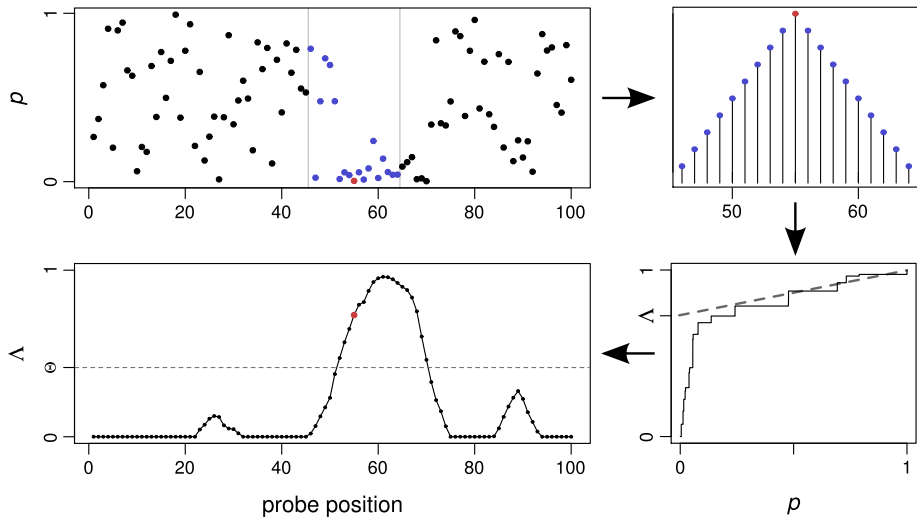
analysis of differential design experiments

- assessing the effect for each probe individually



- combining information of neighboring probes

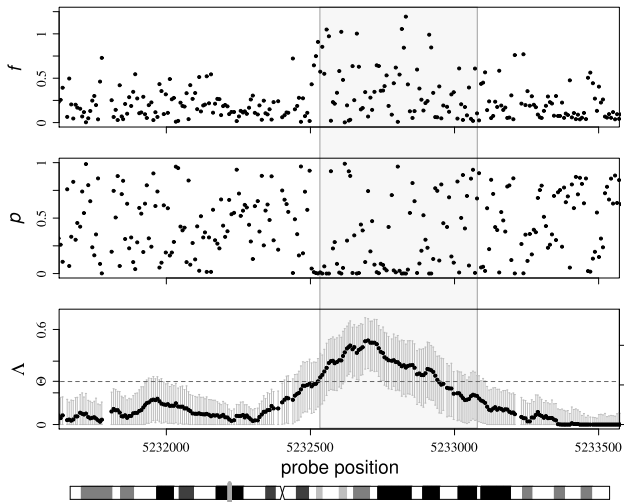
From Probe Level p-values to Loci of Enhanced Significance



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

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, ...)
```