

Image Processing in Bioinformatics

part of “Fortgeschrittene Methoden in der Bioinformatik”

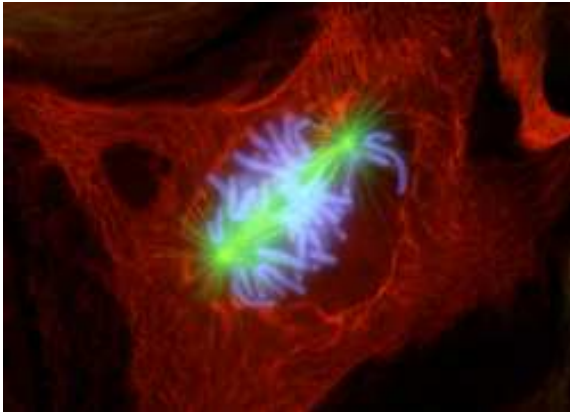
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University Leipzig

Leipzig, WS 2009/10

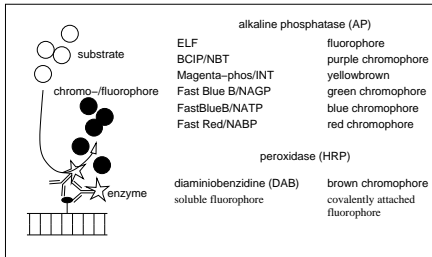
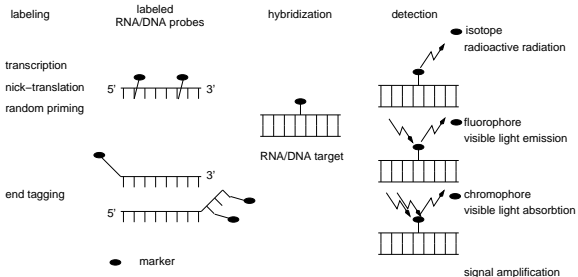
- *in situ* hybridization (ISH)
 - localization of DNA/RNA targets
 - DNA/RNA probes
 - radio-, fluorescence- or antibody-labeling
 - for light- and electron microscopy
 - multicolor ISH
 - tissue slices, whole-mount objects
 - live-cell imaging
- immunohistochemistry (IHC)
 - localization of protein targets
 - anti-target antibodies as labels
 - detection systems as for ISH
 - Multi-Epitope-Ligand-Cartography/Toponomics
 - tissue slices, whole-mount objects

Example

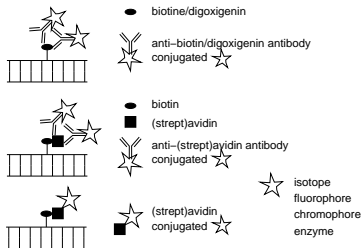


<http://www.youtube.com/watch?v=P7m3WfzgZdI>

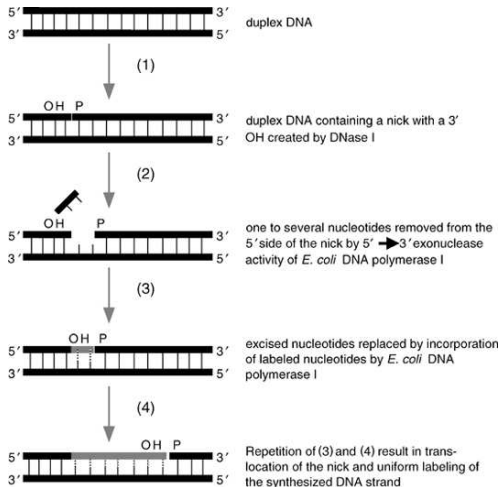
Concept of *in situ* hybridization



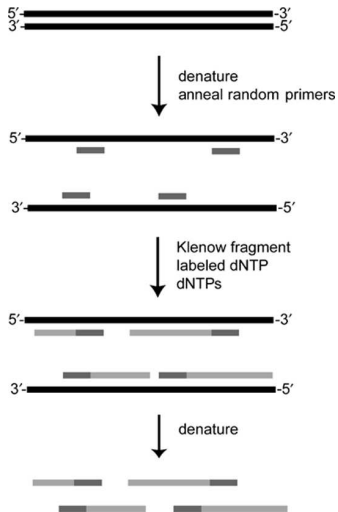
signal amplification



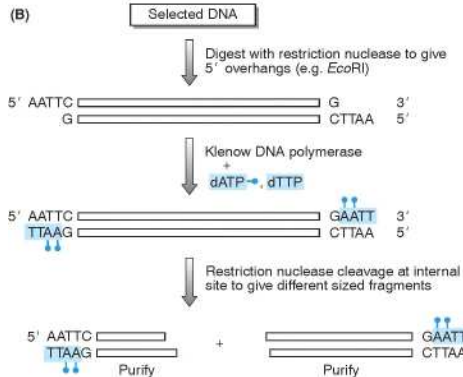
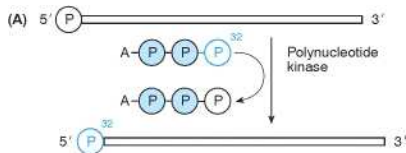
Labeling: Nick Translation



Labeling: Random Priming



Labeling: 5'-end Labeling



Labeling: Radioactive Labeling

- ^{35}S – 87.2 days
- ^{32}P – 14.3 days
- ^3H – 12.43 years

disadvantages

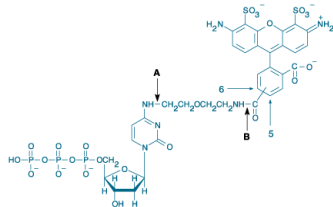
- safety problems
- isotopes vary in exposure time and stability only
- instability
- time-consuming

advantages

- high sensitivity, signal amplification
- lower probe concentration (10-50 fold)
- chemically identical probes
- easy access to the target

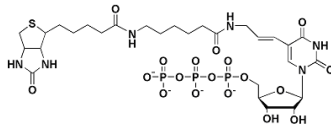
Labeled Nucleotides

Fluorophore

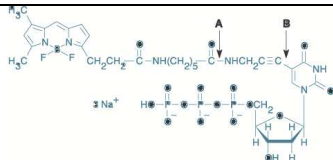


Alexa Fluor dCTP

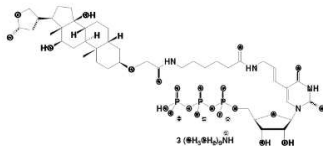
Marker



Biotin UTP



BODIPY dUTP

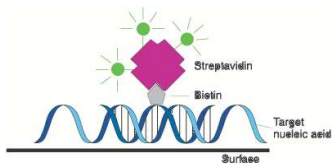


Digoxigenin UTP

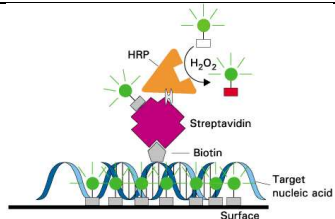
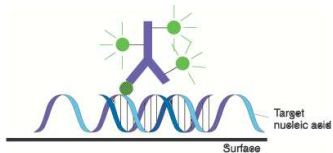
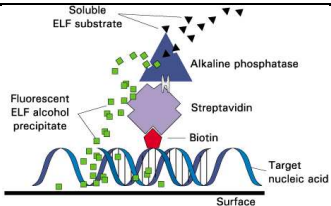
Spacer arms allow base pairing and make the marker accessible to detection.

Detection Systems: Signal Amplification

several dye moities per marker

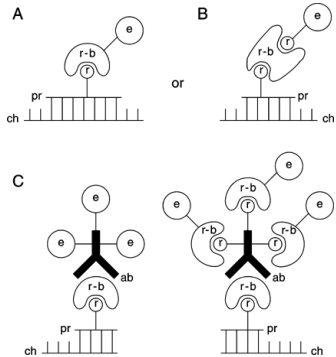


enzymatic amplification

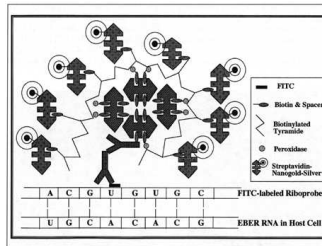


Detection Systems: Strong Signal Amplification

light microscopy



electron microscopy



Why is this interesting to bioinformaticians?

- biotin labeling: endogenous biotin can cause false positives
- digoxigenin labeling: only in *Digitalis sp.*, otherwise less false positives
- unspecific binding events? (avidin versus streptavidin)
- Can low amounts of targets be detected?
- Do labeling and amplification steps allow quantitative analysis?
- Is the amount of target in a linear relationship to the staining intensity?

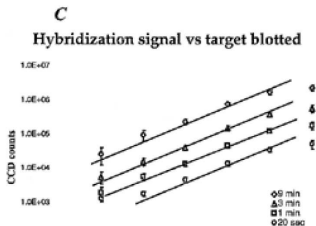
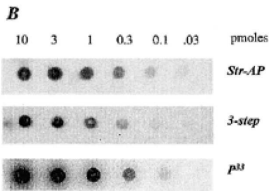
Amount of Target RNA/DNA Versus Staining Intensity

A

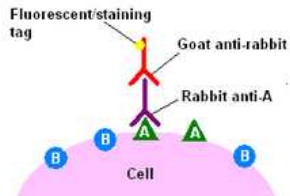
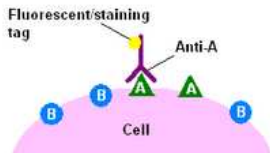
target G
target C
target A
target T

5' - CAGGGXTTCCCACT - 3'

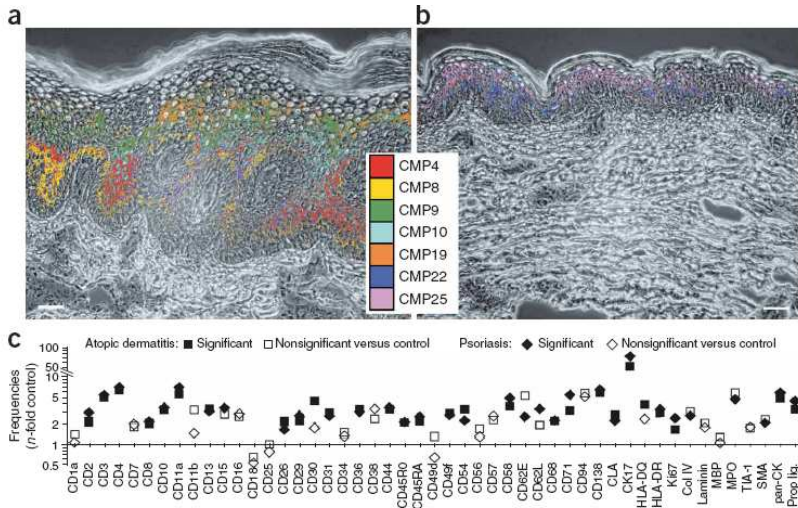
probe G 3' - ccGaaagggt - biot
probe A 3' - ccAaaagggt - biot
probe N 3' - ccNaaagggt - biot



Direct and Indirect Immunohistochemistry

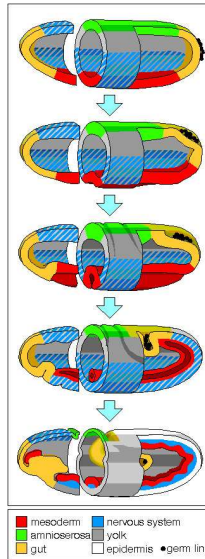
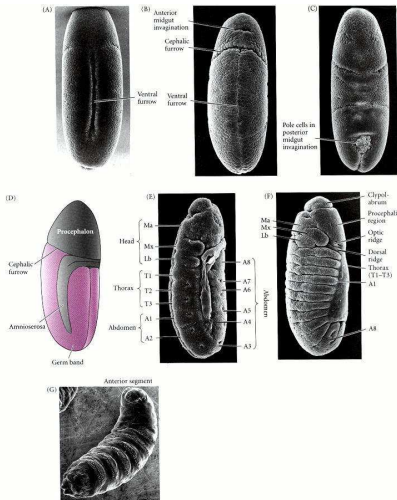


MELK and Toponomics



- BDGP - FlyExpress (fly)
- ZFIN (zebrafish)
- GEISHA (chicken)
- EMAGE (mouse)

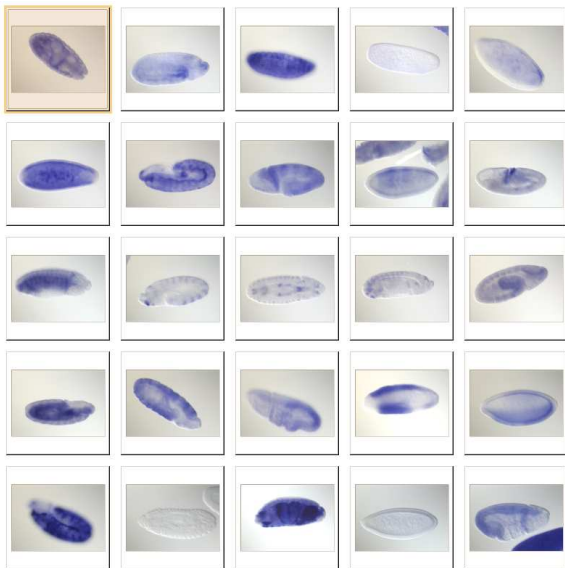
Drosophila Development



Youtube:

<http://www.youtube.com/watch?v=Ib6TJzTLg>

BDGP Raw Data



From the *in situ* image to the comparison of spatial expression patterns

pay attention to:

- images from the same developmental stage and
- same view
- alignment of anterior – anterior, ventral – ventral, etc.
- inference of target localization/concentration from staining
- quantitative/qualitative measure of similarity/correlation

From the *in situ* image to the comparison of spatial expression patterns

processing steps:

- cut out embryo
- determine view, orientation
- standardize embryos
- extract staining
- compare distribution of stain from embryo 1 and embryo 2

Be Careful with Biological Conclusions

- mRNA distribution does not necessarily reflect protein distribution
- mRNAs *in situ* patterns are found to overlap
 - does not necessarily mean interaction of the gene products (A interacts with B)
 - does not necessarily indicate co-regulation (A and B are regulated by a set of common TFs)
 - does not necessarily indicate a positive regulatory interaction (A enhances B or B enhances A)