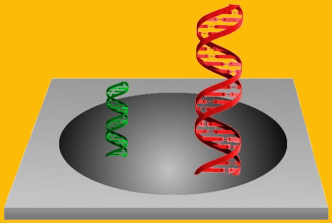
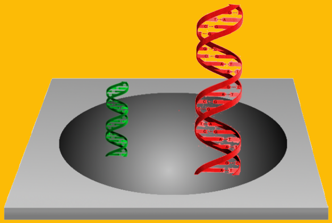
DNA Microarray Image Compression



Miguel Hernández Cabronero

June 19, 2015

DNA Microarray Image Compression



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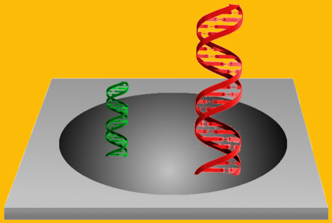

Miguel Hernández Cabronero

June 19, 2015

Supervisor:
Dr. Joan Serra-Sagristà
Co-supervisor:
Dr. Michael W. Marcellin

Committee:
Dr. Manuel Perez Malumbres
Dr. Cristina Fernández Córdoba
Dr. António José Ribeiro Neves

Universitat Autònoma de Barcelona

About this thesis...

Financial support:

- Spanish Government
  - FPU 2010
  - EST13/00180
  - TIN2012-38102-C03-00
- Catalan Government
  - 2014 SGR 691
  - SGR2009-1224
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Development:

2010 BSc Computer Science
BScMathematics

2011 MSc Computer Science

2011 Thesis beginning

2014 Stay in Tucson, AZ, USA

2015 Stay in Aveiro, Portugal

Contents

1. Introduction: DNA Microarrays

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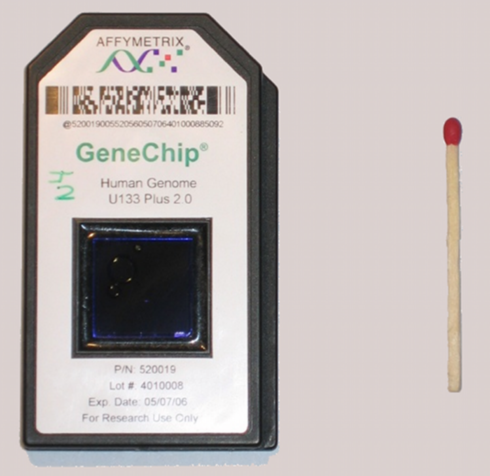
DNA Microarrays

DNA Microarray (match for scale)



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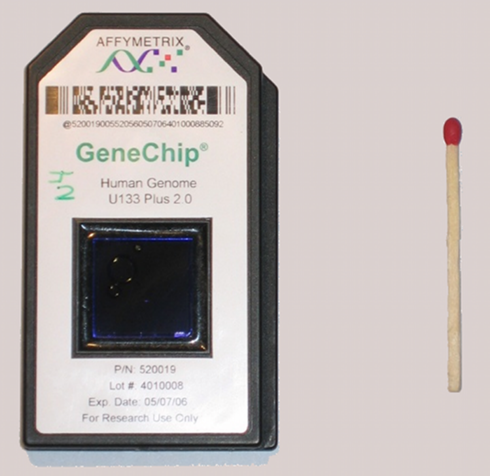

- Quantify genetic expression

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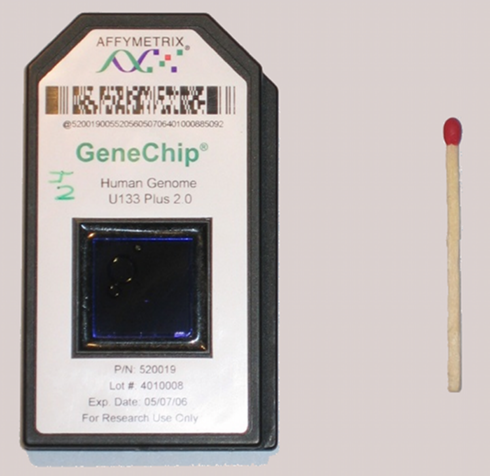

- Quantify genetic expression
- Analyze genetic function and regulation

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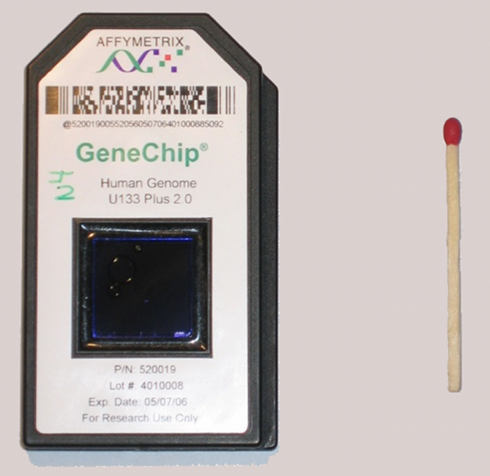


- Quantify genetic expression
- Analyze genetic function and regulation

Some applications:

$\Rightarrow$ Understanding Cancer, HIV, Malaria...

$\Rightarrow$ Drug development

$\Rightarrow$ Evolutionary biology

DNA Microarrays

History:

1975 Southern Blot:
genetic sequence detection

1982 Augentlich:
378 in parallel

1987 Augentlich:
4000 human genes

DNA Microarrays

History:

1975 Southern Blot:
genetic sequence detection

1982 Augentlich:
378 in parallel

1987 Augentlich:
4000 human genes

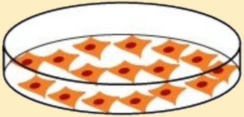
1995 Schena:
Miniaturized chips

1997 Lashkari:
Whole eukaryiotic genome
(∼6000 genes)

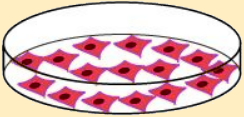
2005 Affymetrix:
Whole human genome
(∼20000 genes)

DNA Microarrays

Biological samples



Tumoral tissue



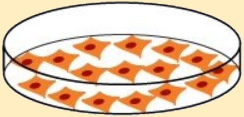
Healthy tissue

Underlying principle:

- Two samples

DNA Microarrays

Biological samples



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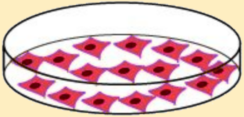


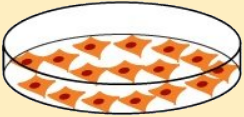
Healthy tissue

Underlying principle:

- Two samples
- Same genes

DNA Microarrays

Biological samples



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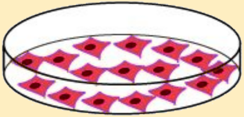

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Underlying principle:

- Two samples
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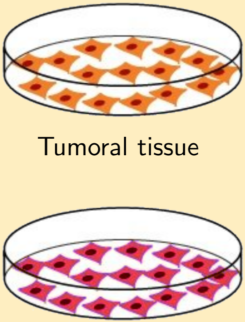
- Different expression intensity

DNA Microarrays

Biological samples



Tumoral tissue

Healthy tissue

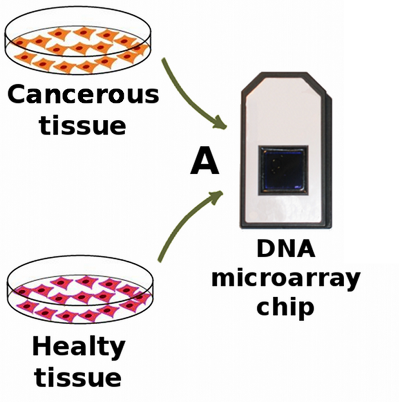
Underlying principle:

- Two samples
- Same genes
- Different expression intensity

Compare expression $\Rightarrow$ understand function

DNA Microarray Experiments

How to obtain the genetic data:



DNA Microarray Experiments

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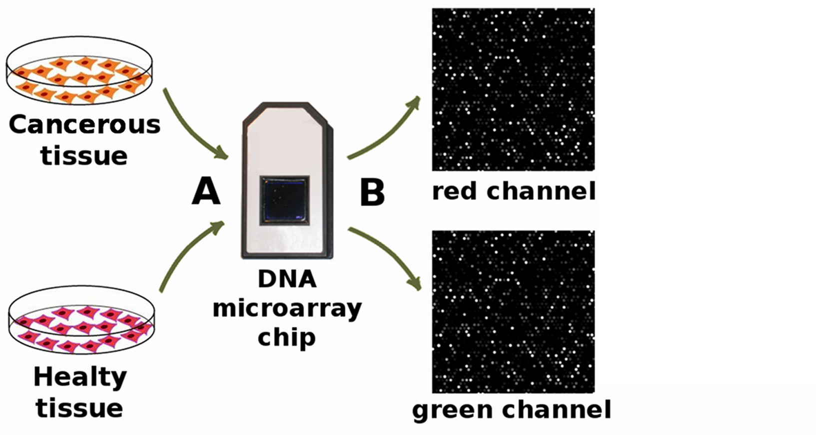

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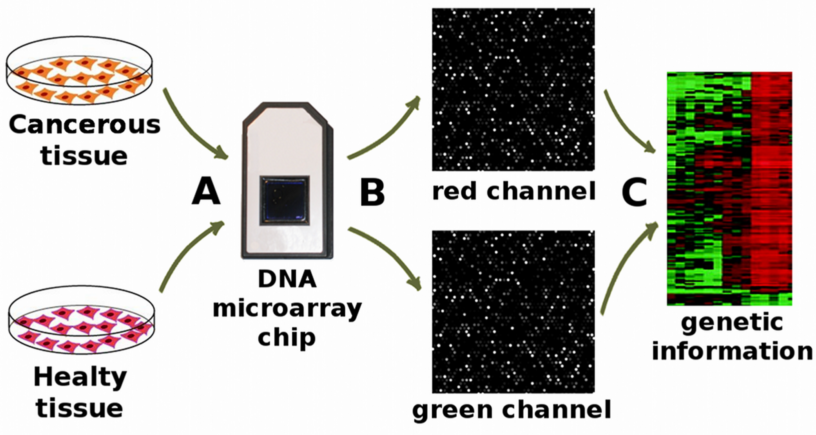

DNA Microarray Experiments

Example of genetic data output:

Gene	Expression intensity Sample 1 μ_1	Expression intensity Sample 2 μ_1	Intensity ratio μ_1/μ_2
Gene 1	245	249	0.98
Gene 2	54	13	4.15
Gene 3	200	1530	0.13
⋮	⋮	⋮	⋮
Gene N	100	103	0.97

DNA Microarray Experiments

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Why Compression?

Why compress DNA microarray images?

Why Compression?

New image analysis methods

Why Compression?

New image analysis methods

- Athanasiadis, 2015
- Fouad, 2015
- Li, 2014
- El-Gawady, 2014

Why Compression?

New image analysis methods $\Rightarrow$ better genetic data

- Athanasiadis, 2015
- Fouad, 2015
- Li, 2014
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Why Compression?

Want to re-analyze

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Want to re-analyze

but

Cannot repeat
experiments

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$\Longrightarrow$ Must keep images

Why Compression?

Want to re-analyze

but $\Longrightarrow$ Must keep images $\Longrightarrow$ Need efficient storage and transmission

Cannot repeat experiments

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Want to re-analyze

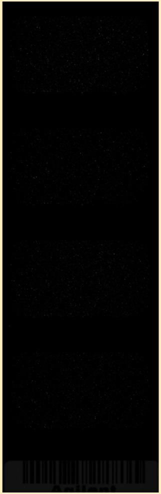
but $\Longrightarrow$ Must keep images $\Longrightarrow$ Need efficient storage and transmission

Cannot repeat experiments

Image compression: natural approach

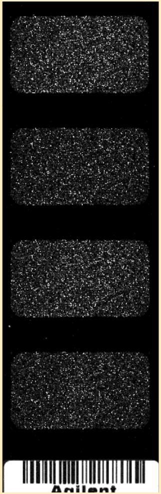
DNA Microarray Images

DNA microarray image



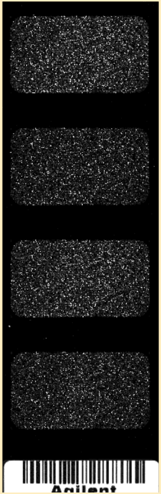
DNA Microarray Images

DNA microarray image (brighter)



DNA Microarray Images

DNA microarray image (brighter)

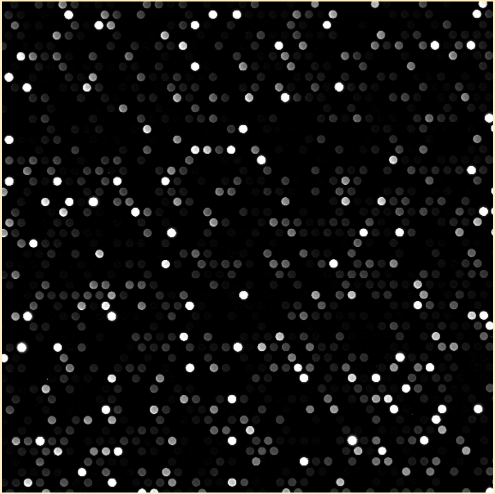


Key properties

- Large dimensions (4400×13800)

DNA Microarray Images

DNA microarray image (crop)

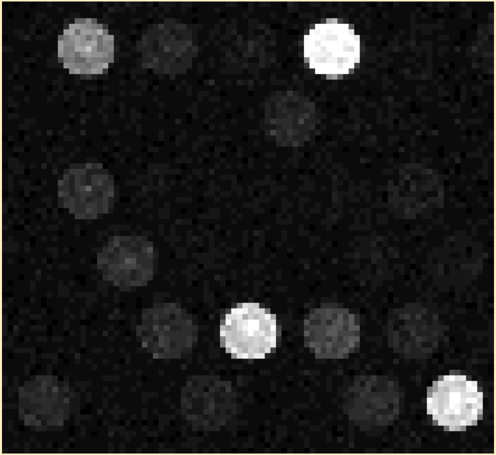


Key properties

- Large dimensions (4400×13800)
- Abrupt changes

DNA Microarray Images

DNA microarray image (detail)



Key properties

- Large dimensions (4400×13800)
- Abrupt changes

DNA Microarray Images

Natural image *vs* Microarray image

Natural images (8 bpp):
$2^8 = 256$ possible intensities

Microarray images (16 bpp):
$2^{16} = 65535$ possible intensities

Key properties

- Large dimensions (4400×13800)
- Abrupt changes
- 16 bits per pixel

DNA Microarray Images

Range of intensities

Natural images (8 bpp):
$2^8 = 256$ possible intensities

Microarray images (16 bpp):
$2^{16} = 65535$ possible intensities

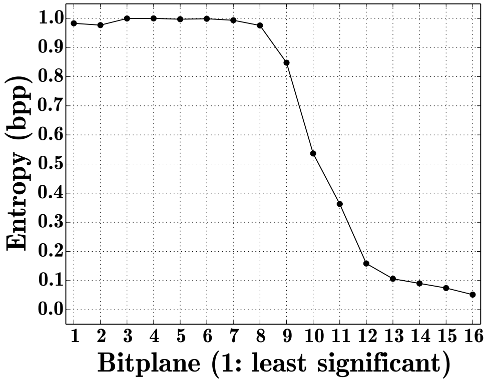
but only 30-80% are used

Key properties

- Large dimensions (4400×13800)
- Abrupt changes
- 16 bits per pixel
- Unused intensities: 20-70%

DNA Microarray Images

Range of intensities



Key properties

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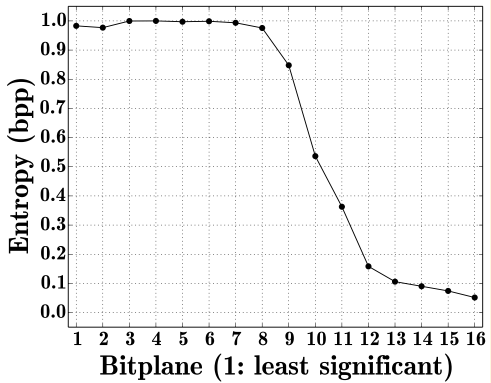
- 16 bits per pixel
- Unused intensities: 20-70%
- Noisy bitplanes: up to 9

DNA Microarray Images

Bitplane entropy



Key properties

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- Abrupt changes
- 16 bits per pixel
- Unused intensities: 20-70%
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Need adapted compressors

Thesis goals

Thesis **main goal**: efficient compression

Thesis goals

Thesis **main goal**: efficient compression

Lossless compression

Lossy compression

Thesis goals

Thesis **main goal**: efficient compression

Lossless compression

✓: Perfect data fidelity

Lossy compression

Thesis goals

Thesis **main goal**: efficient compression

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- ✓: Perfect data fidelity
- ×: Small compression ratios
- ×: Not standard

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Thesis **contributions**: solutions to these problems

Thesis goals

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Thesis **contributions**: solutions to these problems

⇒ Improve standards

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✓: Arbitrary compression ratios

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Thesis **contributions**: solutions to these problems

⇒ Improve standards

⇒ Assess distortion

Thesis goals

Thesis **main goal**: efficient compression

Lossless compression

- ✓: Perfect data fidelity
- ×: Small compression ratios
- ×: Not standard

Lossy compression

- ✓: Arbitrary compression ratios
- ×: Analysis result distortion

Thesis **contributions**: solutions to these problems

- ⇒ Improve standards

- ⇒ Assess distortion
- ⇒ Lossy coder with acceptable distortion

Benchmark Corpora

Image Sets

Name	Year	Images	Size
Yeast	1998	109	1024×1024
ApoA1	2001	32	1044×1041
ISREC	2001	14	1000×1000
Stanford	2001	20	2000×2000
MicroZip	2004	3	1800×1900
Omnibus	2006	25	12200×4320
Arizona	20011	6	4400×13800
IBB	2013	44	2019×6235

Benchmark Corpora

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Representative of many scanner types

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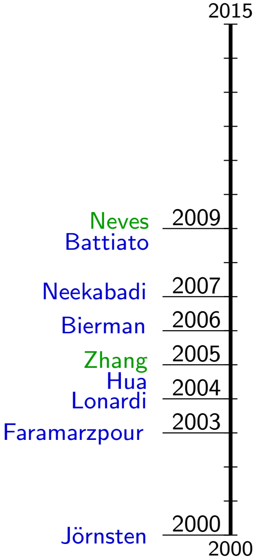
State of the art



Most algorithms:

- Segmentation-based coding
- Context-base coding

State of the art

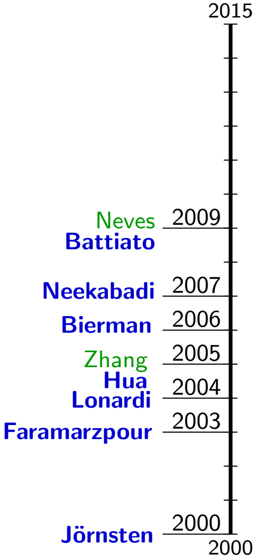
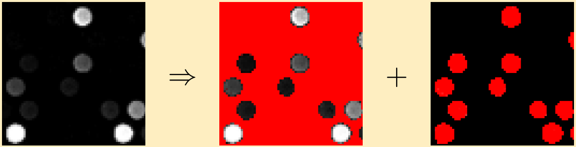


Image segmentation



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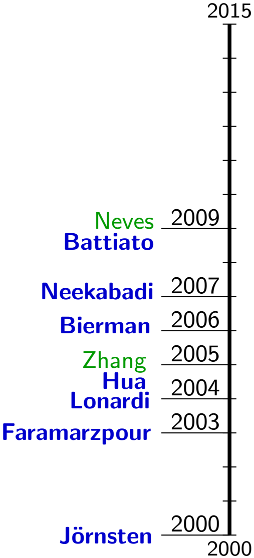

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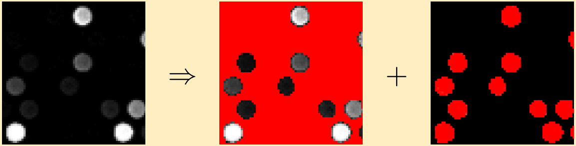
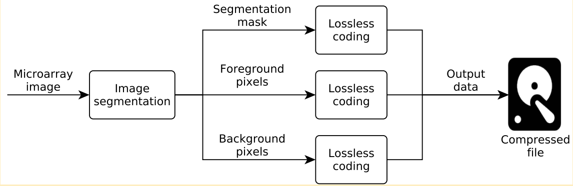


Segmentation-based coding



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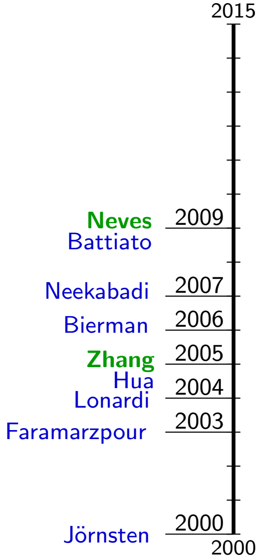
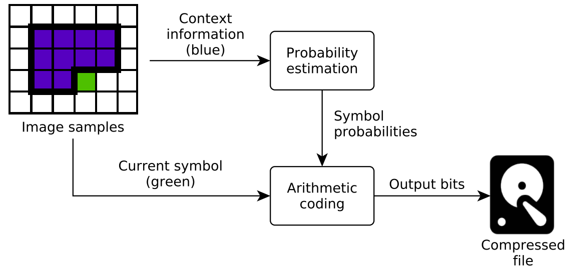


Context-based coding



Standard *vs* microarray-specific coders

Algorithm	Yeast	ApoA1	ISREC	Stanford	MicroZip	Omnibus	AZ	IBB
Generic algorithms and standard image compressors								
Bzip2	6.075	11.067	10.921	7.867	9.394	7.523	8.944	9.081
CALIC	8.502	**10.515**	**10.615**	7.592	9.582	**6.929**	8.767	9.327
JBIG2	6.888	10.852	10.925	7.776	9.747	7.198	8.858	9.344
JPEG-LS	8.580	10.608	11.145	**7.571**	9.441	6.952	**8.646**	9.904
HEVC/H.265	10.660	14.482	14.876	8.897	11.179	8.350	10.592	12.262
JPEG2000	6.829	10.999	10.888	7.969	9.467	8.121	7.549	9.064
Microarray-specific techniques								
Jörnsten	8.556	—	—	—	—	—	—	—
Faramarzpour	9.091	—	—	—	—	—	—	—
Hua	6.985	—	—	—	—	—	—	—
Lonardi	—	—	—	—	9.843	—	—	—
Zhang	6.601	—	—	—	9.587	—	—	—
Neekabadi	—	10.250	10.202	—	8.856	—	—	—
Battiato	—	**9.520**	**9.490**	—	**8.369**	—	—	—
Neves	**5.521**	10.223	10.199	**7.335**	8.667	**7.743**	**8.275**	**8.039**

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Considered the best-performing methods

Standard *vs* microarray-specific coders

Compression results (bpp)

Algorithm	IBB	MicroZip	Arizona
Neves			
JPEG2000			
JPEG-LS			

[a]

Standard *vs* microarray-specific coders

Compression results (bpp)

Algorithm	IBB	MicroZip	Arizona
Neves	8.039		
JPEG2000	9.182		
JPEG-LS	9.904		

[a]

Standard *vs* microarray-specific coders

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[a] Page 44, Table 3.1

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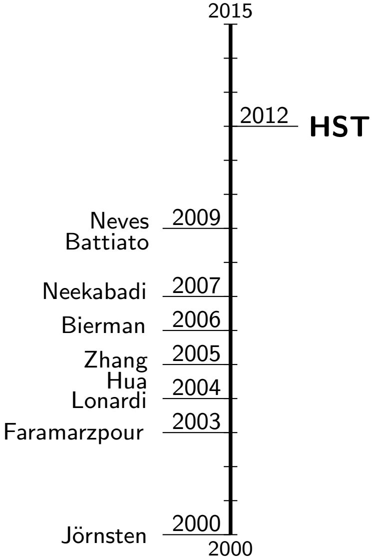
Our approach: improve standards

Contribution 1: Histogram Swap Transform



"DNA microarray image coding,"

Miguel Hernández-Cabronero,
Juan Muñoz-Gómez, Ian Blanes,
Joan Serra-Sagristà,
Michael W. Marcellin

IEEE Data Compression Conference,
DCC, 2012

Contribution 1: Histogram Swap Transform

Why JPEG2000?

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Why JPEG2000?

- DICOM compatible

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- Acceptable base performance

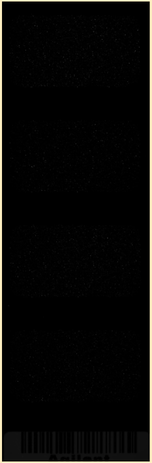
Contribution 1: Histogram Swap Transform

Why JPEG2000?

- DICOM compatible
- Acceptable base performance
- Features and Flexibility

Contribution 1: Histogram Swap Transform

DNA microarray image (original)



Contribution 1: Histogram Swap Transform

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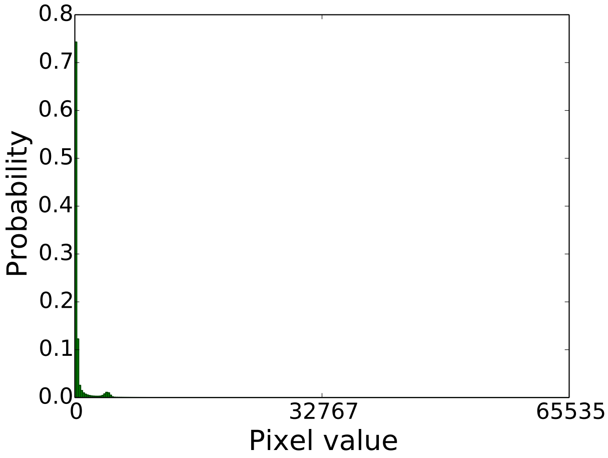

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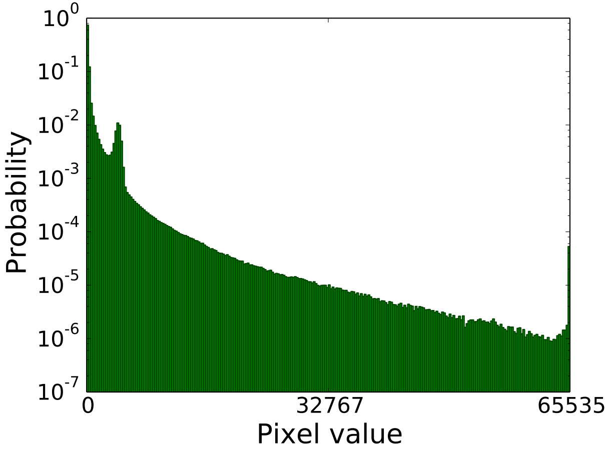
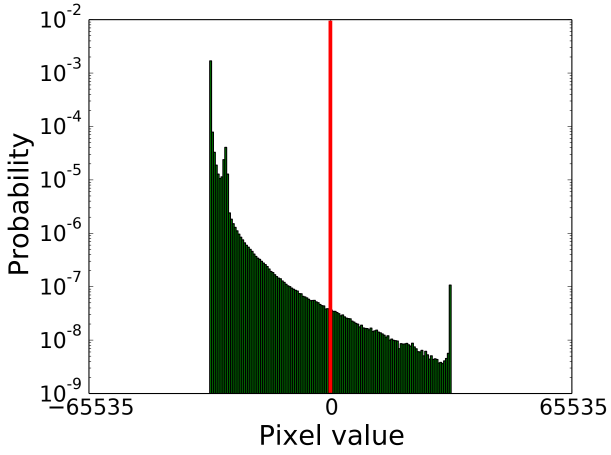


Contribution 1: Histogram Swap Transform

DNA microarray image **(level offset)**

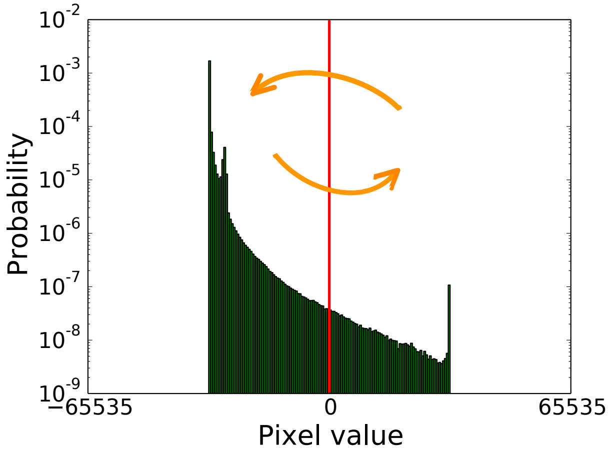


- Asymmetric

$\Rightarrow$ Poor performance

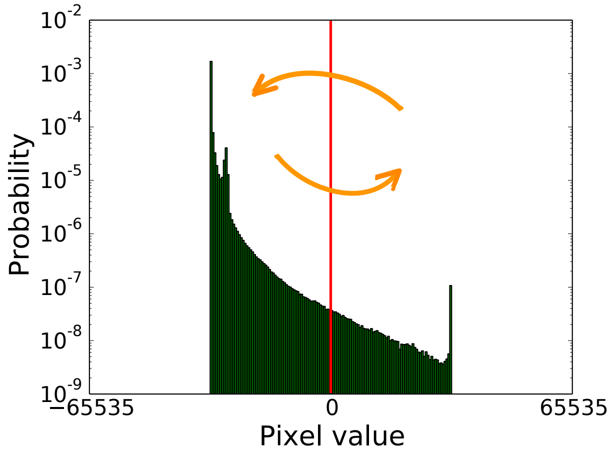
Contribution 1: Histogram Swap Transform

Histogram Swap Transform (before)



Contribution 1: Histogram Swap Transform

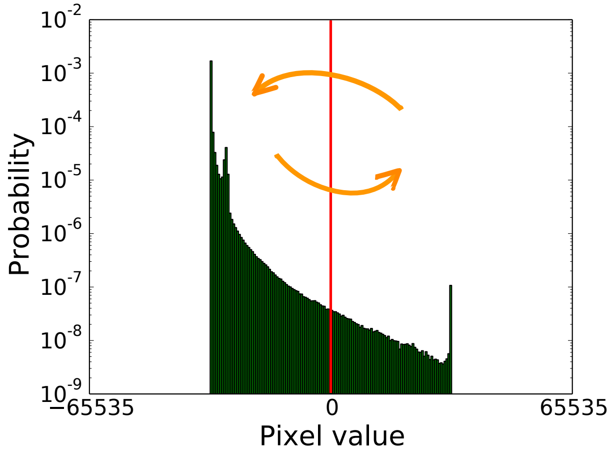
Histogram Swap Transform (before)



- Reversible

Contribution 1: Histogram Swap Transform

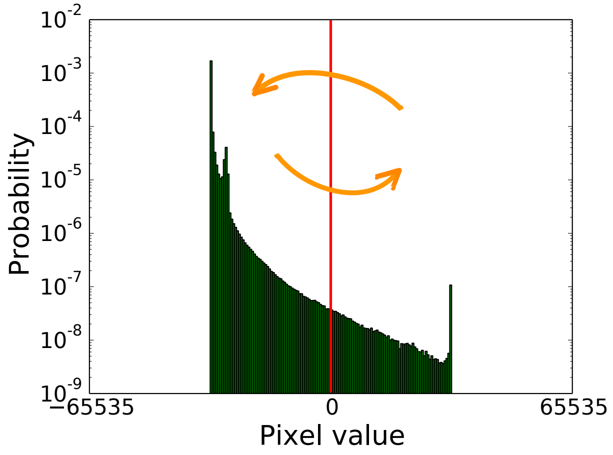
Histogram Swap Transform (before)



- Reversible
- Fast

Contribution 1: Histogram Swap Transform

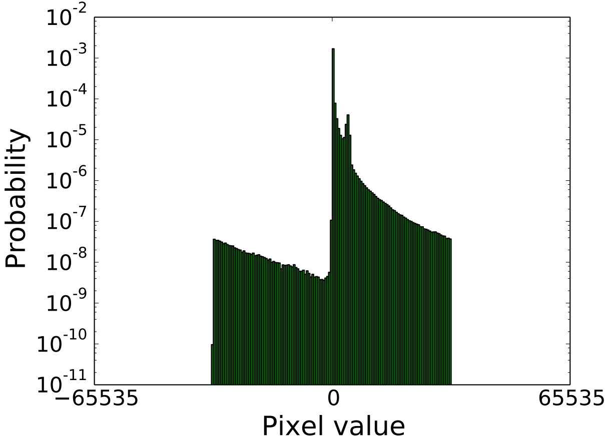
Histogram Swap Transform (before)



- Reversible
- Fast
- JPEG2000 Compatible

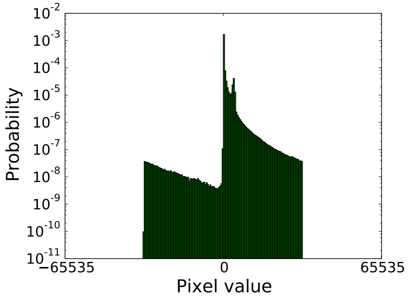
Contribution 1: Histogram Swap Transform

Histogram Swap Transform (after)

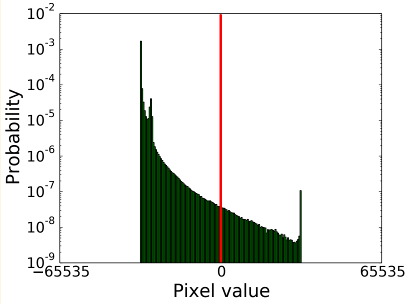


Contribution 1: Histogram Swap Transform

Before



After



Contribution 1: Histogram Swap Transform

JPEG2000 compression results (bpp)

Corpus	Without HST	With HST	Difference	
ApoA1	10.999	10.786	1.97%	-
ISREC	10.888	10.624	2.48%	
Arizona	9.064	8.795	3.06%	
MicroZip	9.467	9.157	3.39%	
Stanford	7.969	7.685	3.70%	
Omnibus	7.549	7.103	6.28%	
IBB	9.182	8.392	9.41%	
Yeast	6.829	5.911	15.53%	+

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- Improvements for **all** datasets (2%-15%)

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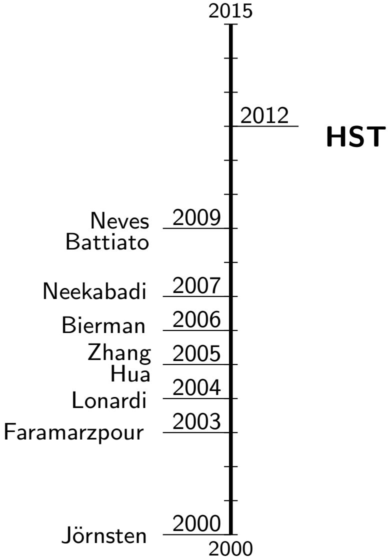
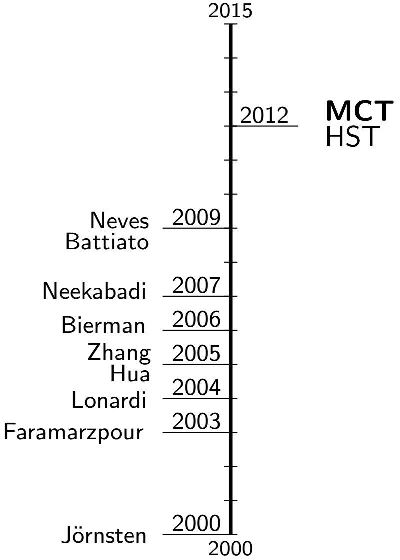
- Improvements for **all** datasets (2%-15%)
- **Can improve further?**

Contribution 1: Histogram Swap Transform



Contribution 2: Multicomponent compression



- "Multicomponent compression of DNA microarray images,"

  Miguel Hernández-Cabronero *et al.*

  CEDI Workshop on Multimedia Data Coding and Transmission, WMDCT, 2012

- "Compression of DNA Microarray Images," Miguel

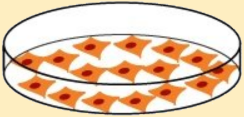
  Hernández-Cabronero, Victor Sanchez, Michael W. Marcellin, Joan Serra-Sagristà

  In Book "Microarray Image and Data

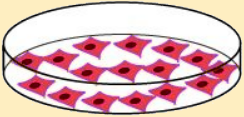
  Analysis: Theory and Practice"

Contribution 2: Multicomponent compression

Biological samples



Tumoral tissue



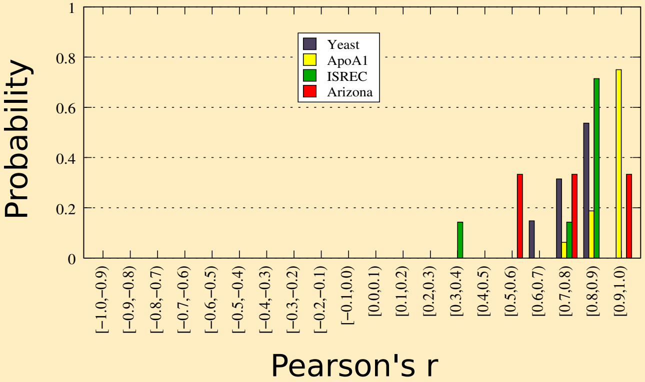
Healthy tissue

Questions:

- Similar images?
- Compress together?

Contribution 2: Multicomponent compression

Correlation (Reg/green pairs only)



Correlation betweeen 0.75-0.92

Contribution 2: Multicomponent transform

JPEG2000 compression results (bpp)

Corpus	No transform	5/3 DWT	RKLT	DPCM	RHaar
Yeast	6.829	6.786	9.279	6.439	6.790
ApoA1	11.524	11.217	10.956	11.289	11.218
ISREC	10.888	11.451	11.468	11.203	11.452
Arizona	9.548	9.649	9.439	9.386	9.649
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Contribution 2: Multicomponent transform

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Results:

- Some improvements
- No "golden" transform

Lossless compression conclusions

Compression results (bpp)

Corpus	JPEG-LS	JPEG2000	HST	Neves
Yeast	8.580	6.829	**5.911**	5.521
ApoA1	10.608	10.999	**10.786**	10.223
ISREC	11.145	10.888	**10.624**	10.199
Stanford	7.571	7.969	**7.685**	7.335
MicroZip	9.441	9.467	**9.157**	8.667
Omnibus	6.952	8.121	**7.103**	7.743
Arizona	8.646	9.064	**8.795**	8.275
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- JPEG2000: Best overall standard
- HST+MCT or HST+DWT: Worse performance

Contents

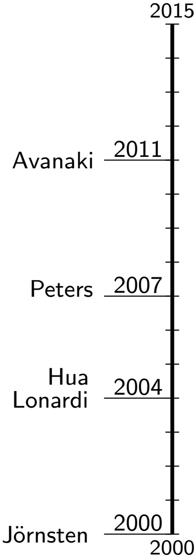
1 Introduction: DNA Microarrays

2 Lossless compression

3 Lossy compression

4 Conclusions

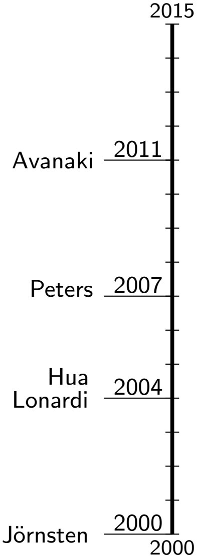
State of the art



Lossless compression

- Perfect fidelity
- Small compression ratios

State of the art



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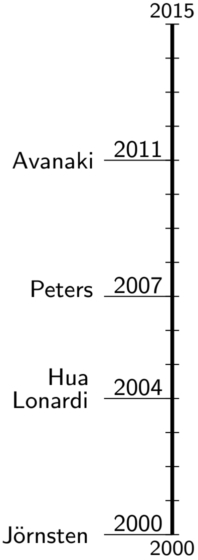

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but image distortion

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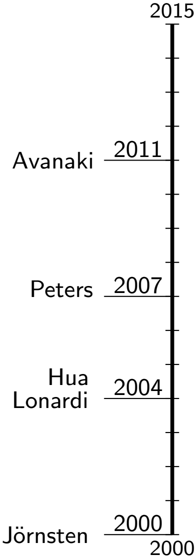

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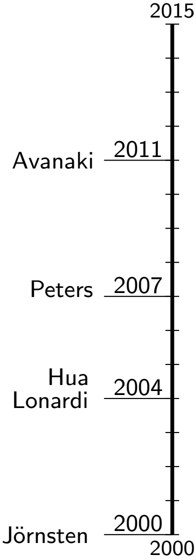
$\Rightarrow$ analysis distortion

State of the art



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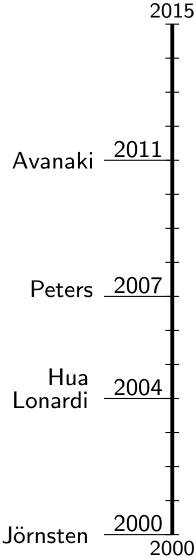
Our contributions:

- Analysis distortion assessment

State of the art



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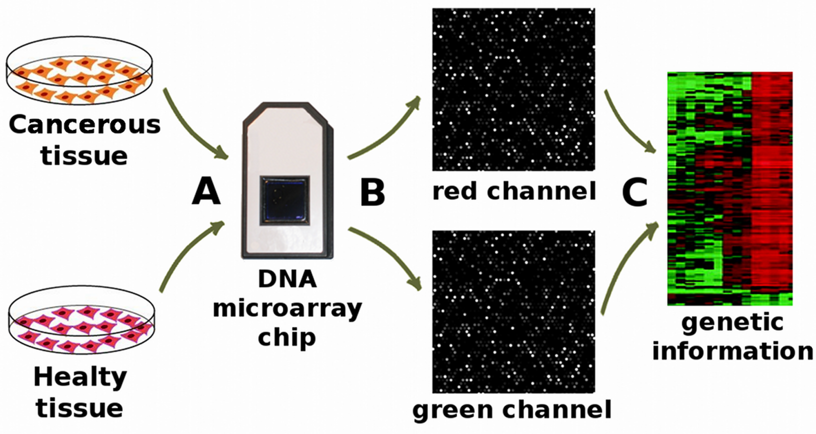
Our contributions:

- Analysis distortion assessment
- Analysis-driven compression

Analysis of DNA Microarray Images

Analysis process



Analysis of DNA Microarray Images

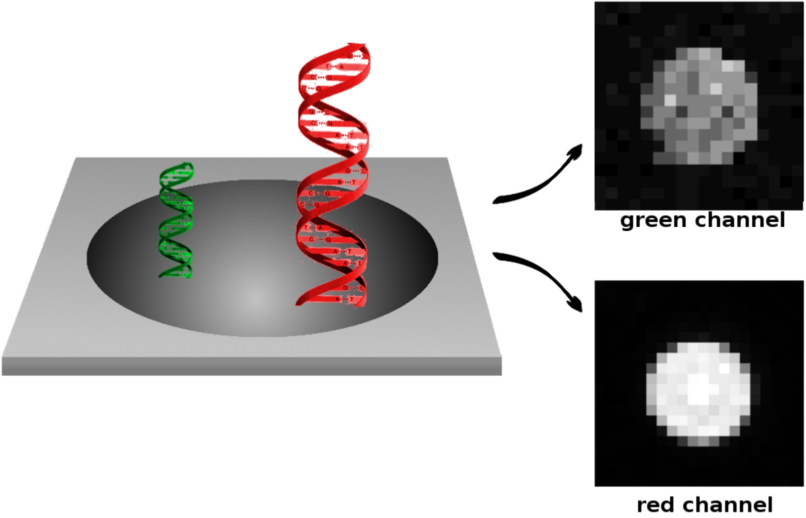
Analysis process

Gene	Expression intensity Sample 1 μ_1	Expression intensity Sample 2 μ_2	Intensity ratio μ_1/μ_2
Gene 1	245	249	**0.98**
Gene 2	54	13	4.15
Gene 3	200	1530	0.13
⋮	⋮	⋮	⋮
Gene N	100	103	0.97

How are they obtained?

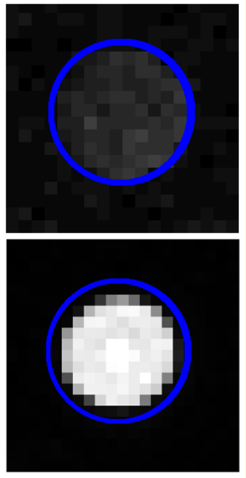
Analysis of DNA Microarray Images

Spot Information



Analysis of DNA Microarray Images

Spot detection

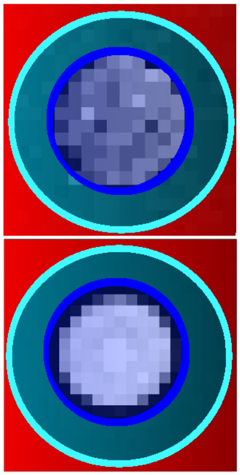


How to obtain the genetic data:

1. Detect the spots

Analysis of DNA Microarray Images

Spot segmentation



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   - Spot
   - Local background
   - Background

Analysis of DNA Microarray Images

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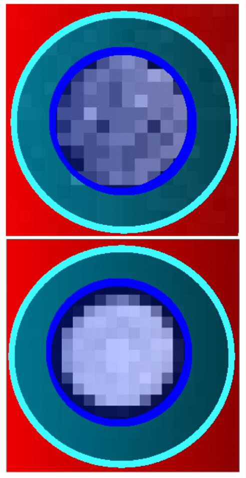

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$$\mathrm{CRM} = \frac{\mu_{\text{spot}}^{\text{green}}}{\mu_{\text{spot}}^{\text{red}}}$$

μ: average intensity

Analysis of DNA Microarray Images

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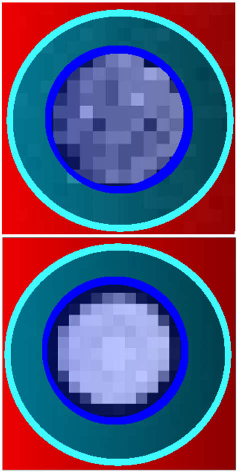

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Analysis of DNA Microarray Images

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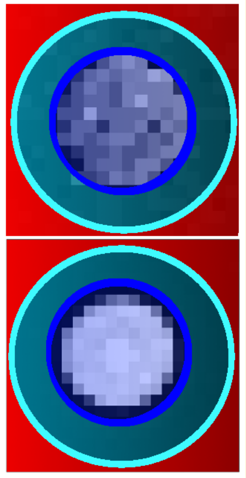

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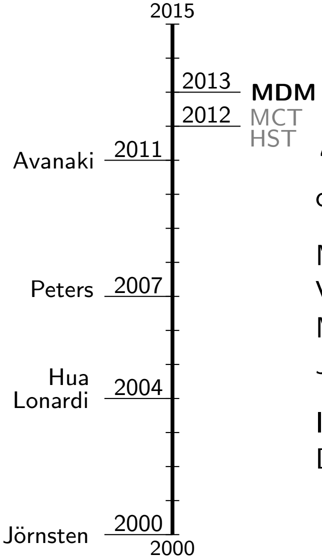
4. normalize

Contribution 3: Microarray Distortion Metric



"A distortion metric for the lossy compression of DNA microarray images"

Miguel Hernández-Cabronero,
Victor Sanchez,
Michael W. Marcellin,
Joan Serra-Sagristà

IEEE Data Compression Conference, DCC, 2013

Contribution 3: Microarray Distortion Metric

How to assess loss importance:

Contribution 3: Microarray Distortion Metric

How to assess loss importance:

- PSNR, MSE

Contribution 3: Microarray Distortion Metric

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How to assess loss importance:

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  2003 Jörnsten
  2004 Hua
  2009 Xu

Contribution 3: Microarray Distortion Metric

How to assess loss importance:

- PSNR, MSE $\Rightarrow$ not enough
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  2003 Jörnsten
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- **Assess loss without analyzing?**

Contribution 3: Microarray Distortion Metric

Calculation

$$MDM = 10 \log_{10} \frac{\text{max\_val}^2}{ME}$$

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$$ME \sim \text{max\_val}^p, \quad p \in [1, 2]$$

- ME: Microarray Error

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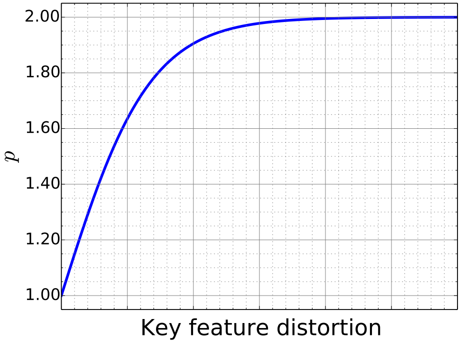
- p: sensitive error exponent



Contribution 3: Microarray Distortion Metric

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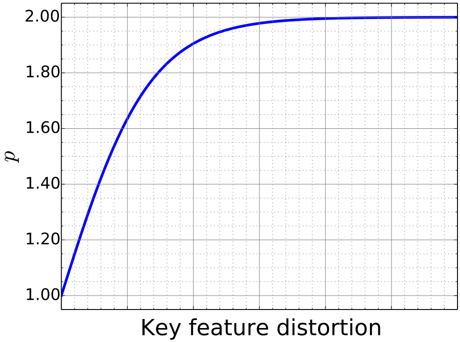
$$MDM = 10 \log_{10} \frac{\text{max\_val}^2}{ME}$$

$$ME \sim \text{max\_val}^p, \quad p \in [1, 2]$$

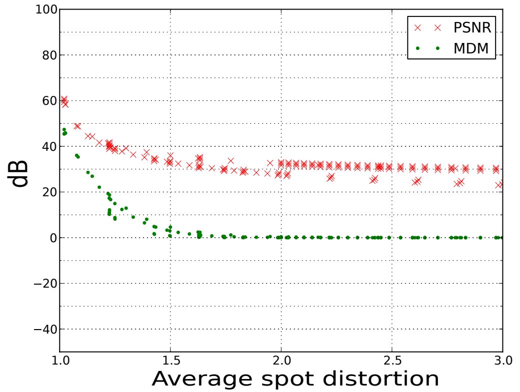
$$p = \text{logistic(feat. distortion)}$$

- ME: Microarray Error
- p: sensitive error exponent



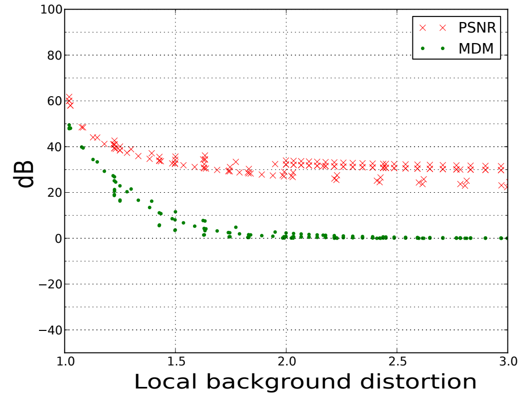
Contribution 3: Microarray Distortion Metric

Results (spots)



Contribution 3: Microarray Distortion Metric

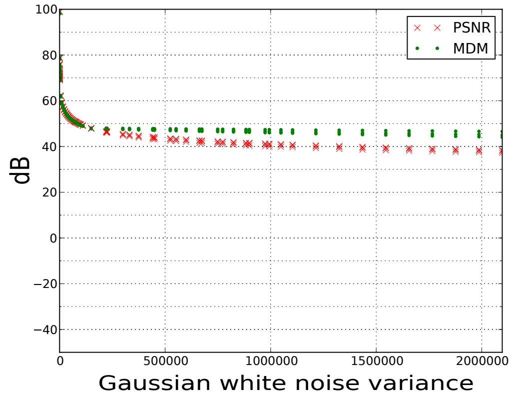
Results (local background)



✓ Important changes

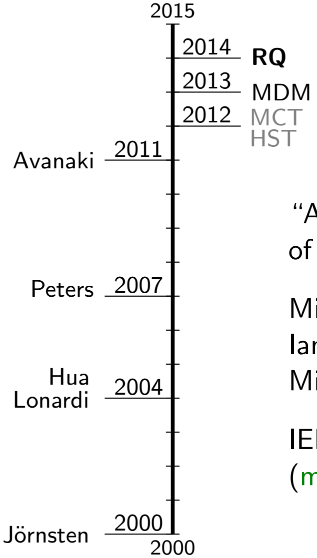
Contribution 3: Microarray Distortion Metric

Results (Gaussian white noise)



- ✓ Important changes
- ✓ Unimportant changes

Contribution 4: Relative Quantization



"Analysis-driven lossy compression of DNA microarray images"

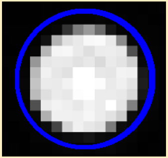
Miguel Hernández-Cabronero
Ian Blanes, Armando J. Pinho
Michael W. Marcellin, Joan Serra-Sagristà

IEEE Transactions on Medical Imaging, 2015 (major revision)

Contribution 4: Relative Quantization

Relative error: important for

Segmentation



(contrast)

Contribution 4: Relative Quantization

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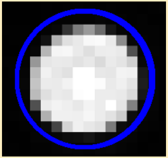

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CRM calculation

$$\mathrm{CRM} = \frac{\mu^{\mathrm{green}}_{\mathrm{spot}} - \mu^{\mathrm{green}}_{\mathrm{localBG}}}{\mu^{\mathrm{red}}_{\mathrm{spot}} - \mu^{\mathrm{red}}_{\mathrm{localBG}}}$$

(error calculation)

Contribution 4: Relative Quantization

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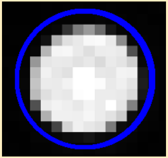

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(error calculation)

Our approach:

$$\text{Control pixel relative error} \Rightarrow \begin{cases} \text{Preserve edge detection} \\ \text{Limit CRM relative error} \end{cases}$$

Contribution 4: Relative Quantization

Keep only k bits from each pixel

MSB	0	0	0
	0	0	0
	⋯	⋯	⋯
	1	0	0
	0	0	0
	1	1	0
	0	1	0
	0	0	0
	1	1	0
	0	1	0
	1	1	0
LSB	1	1	1

Contribution 4: Relative Quantization

Keep only k bits from each pixel

MSB	0	0	0
	0	0	0
	...	...	...
	$\boxed{1}$	0	0
	$\boxed{0}$	0	0
$k = 2$	1	$\boxed{1}$	0
	0	$\boxed{1}$	0
	0	0	0
	1	1	0
	0	1	0
	1	1	0
LSB	1	1	$\boxed{1}$

Contribution 4: Relative Quantization

Keep only k bits from each pixel

MSB	0	0	0		0	0	0
	0	0	0		0	0	0
	…	…	…		…	…	…
	1	0	0		1	0	0
	0	0	0		0	0	0
$k = 2$	1	1	0	$\Longrightarrow$	X	1	0
	0	1	0		X	1	0
	0	0	0		X	X	0
	1	1	0		X	X	0
	0	1	0		X	X	0
	1	1	0		X	X	0
LSB	1	1	1		X	X	1

Contribution 4: Relative Quantization

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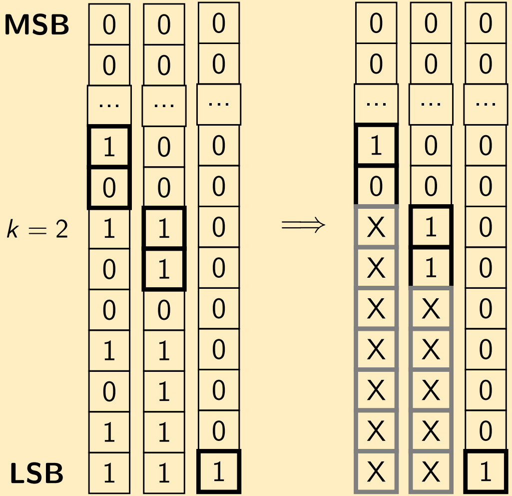


✓ Controlled maximum relative error

k	maximum rel error (2^{-k})
1	0.500
2	0.250
3	0.125
4	0.062
5	0.031
6	0.016
7	0.008

Contribution 4: Relative Quantization

Why call it Relative *Quantization*?

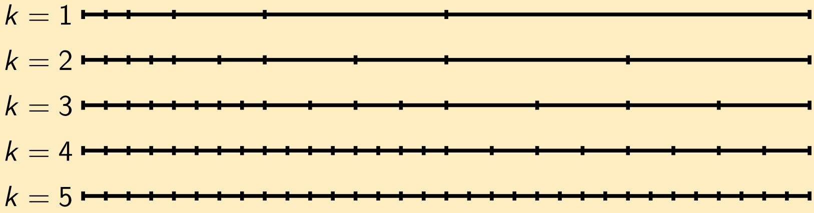
- Same value after discarding $\Rightarrow$ same quantization index

Contribution 4: Relative Quantization

	0	0	0	0	0	0	0		1
	0	0	0	0	0	0	0		1
	⋯	⋯	⋯	⋯	⋯	⋯	⋯		⋯
	0	0	0	0	0	0	0		X
Pixel values	0	0	0	0	0	0	0	⋯	X
	0	0	0	0	0	0	0		X
	0	0	0	0	0	0	0		X
	0	0	0	0	0	0	0		X
	0	0	0	0	0	0	1		X
$(k = 2)$	0	0	0	0	1	1	0		X
	0	0	1	1	0	1	X		X
	0	1	0	1	X	X	X		X
Index	0	1	2	3	4	5	6	⋯	31

Contribution 4: Relative Quantization

Quantization Interval (5 bitplanes)



Contribution 4: Relative Quantization

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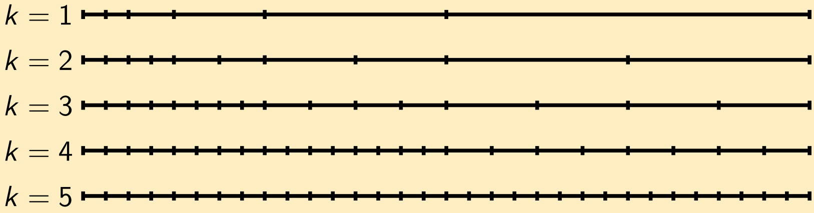

- Effect: $\downarrow$number of symbols $\Rightarrow$ $\downarrow$compressed size

Contribution 4: Relative Quantization

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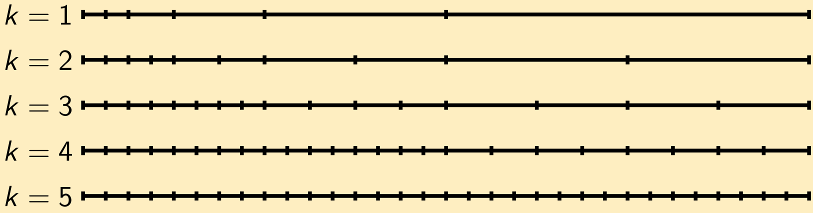

- Effect: ↓number of symbols ⇒ ↓compressed size
- Parameterizable: $k \in \{1, 2, \mathbf{3}, \mathbf{4}, \mathbf{5}, 6, \ldots, 16\}$
  ($\downarrow k \Rightarrow$ more aggressive)

Contribution 4: Relative Quantization

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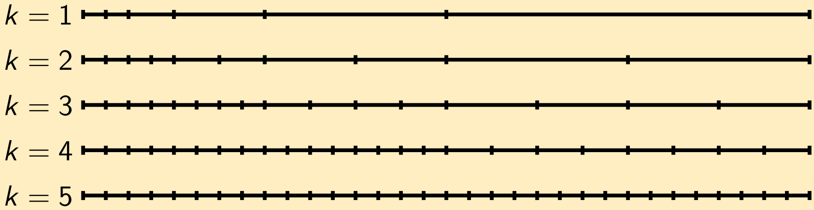

- Effect: $\downarrow$number of symbols $\Rightarrow$ $\downarrow$compressed size
- Parameterizable: $k \in \{1, 2, \mathbf{3}, \mathbf{4}, \mathbf{5}, 6, \ldots, 16\}$
  ($\downarrow k \Rightarrow$ more aggressive)
- Can use any (lossless) coder

Contribution 4: Relative Quantization

Relative Quantization Coder:

1. Quantize images
2. Compress quantization indices

Contribution 4: Relative Quantization

Relative Quantization Coder:

1. Quantize images
2. Compress quantization indices

Compression results (bpp, avg. all sets)

Coder	Relative Quantization k							
	1	**2**	**3**	**4**	**5**	**6**	**7**	**Original**
JPEG2000	2.01	2.75	3.60	4.53	5.51	6.48	7.39	9.76
JPEG-LS	1.87	2.65	3.54	4.47	5.38	6.28	7.13	9.35
Neves	1.51	2.22	3.07	4.01	4.96	5.86	6.60	8.32

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- Good compression performance (*e.g.*, 1.5 bpp vs 8.3 bpp)
- **Acceptable analysis distortion?**

Contribution 4: Relative Quantization

CRM distortion

$$\mathrm{CRM} = \frac{\mu^{\mathrm{green}}_{\mathrm{spot}} - \mu^{\mathrm{green}}_{\mathrm{localBG}}}{\mu^{\mathrm{red}}_{\mathrm{spot}} - \mu^{\mathrm{red}}_{\mathrm{localBG}}}$$

Analysis-based distortion metrics:

- **ARE$_{\mathbf{CRM}}$**
- FWDOC

Contribution 4: Relative Quantization

CRM distortion

$$\mathrm{CRM} = \frac{\mu_{\mathrm{spot}}^{\mathrm{green}} - \mu_{\mathrm{localBG}}^{\mathrm{green}}}{\mu_{\mathrm{spot}}^{\mathrm{red}} - \mu_{\mathrm{localBG}}^{\mathrm{red}}}$$

CRM Average Relative Error:

$$\mathrm{ARE}_{\mathrm{CRM}} = \frac{1}{n} \sum_{i=1}^{n} \frac{|\mathrm{CRM}_i - \widehat{\mathrm{CRM}}_i|}{\delta + |\mathrm{CRM}_i|}$$

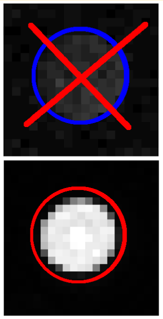
Analysis-based distortion metrics:

- **$\mathrm{ARE}_{\mathrm{CRM}}$**
- FWDOC

Contribution 4: Relative Quantization

How to run an spot:

Wrong detection



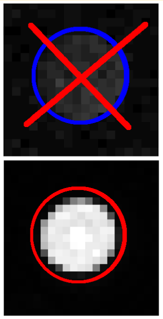
Analysis-based distortion metrics:

- ARE_{CRM}
- FWDOC

Contribution 4: Relative Quantization

How to ruin an spot:

Wrong detection



Wrong classification

A $\mathrm{CRM} < 0.5$

B $0.5 \leq \mathrm{CRM} \leq 2$

C $\mathrm{CRM} > 2$

(should not alter classification)

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Contribution 4: Relative Quantization

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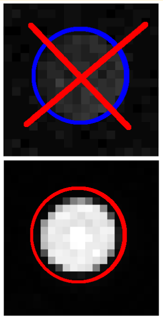

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Fraction of spots
Wrongly Detected Or Classified (FWDOC)

Contribution 4: Relative Quantization

Impact on the image analysis

	CRM error	Detect.+Class. error

Contribution 4: Relative Quantization

Impact on the image analysis

	CRM error	Detect.+Class. error
$k = 1$	0.562	0.148
$k = 2$	0.124	0.100
$k = 3$	0.121	0.064
$k = 4$	0.078	0.044
$k = 5$	0.064	0.030
$k = 6$	0.039	0.019
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Acceptability?

Contribution 4: Relative Quantization

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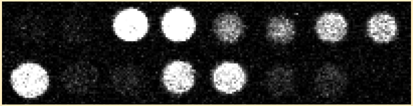

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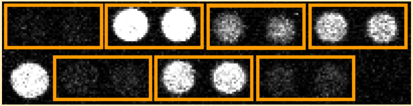
Replicated	0.254	0.212



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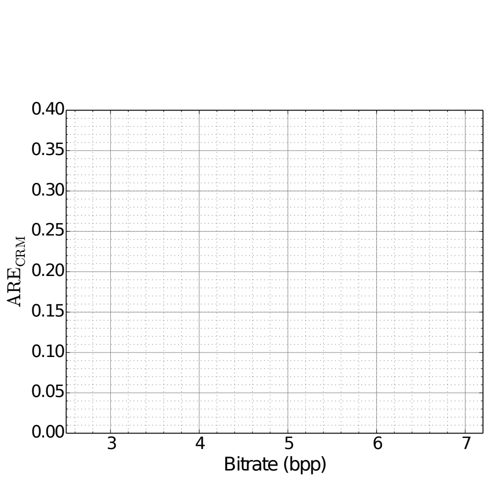
- ✓ Acceptable
- ✓ Good compression performance
- ? Comparison to other coders?

Contribution 4: Relative Quantization

RQ vs Others (CRM)



Contribution 4: Relative Quantization

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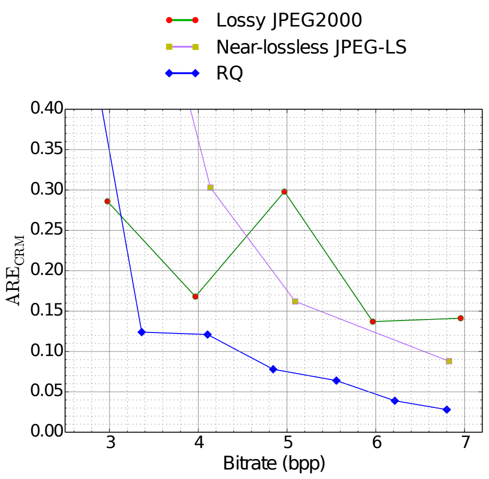
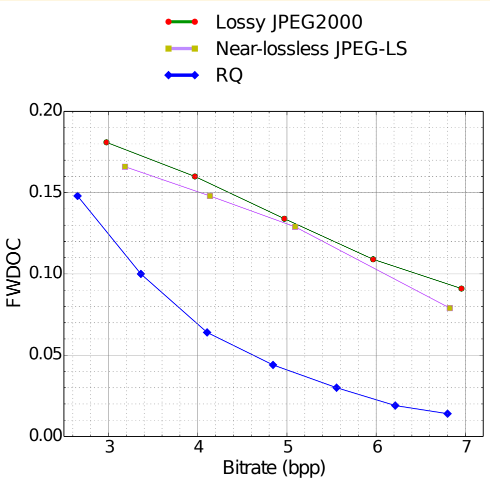


Contribution 4: Relative Quantization

RQ vs Others (detect. or class.)



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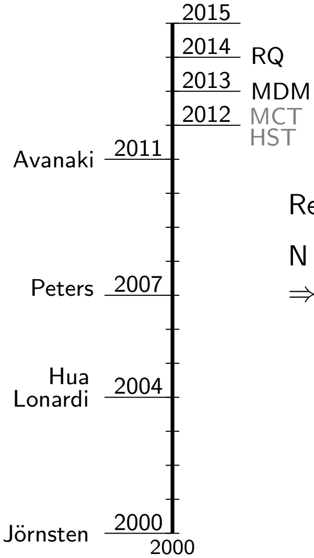
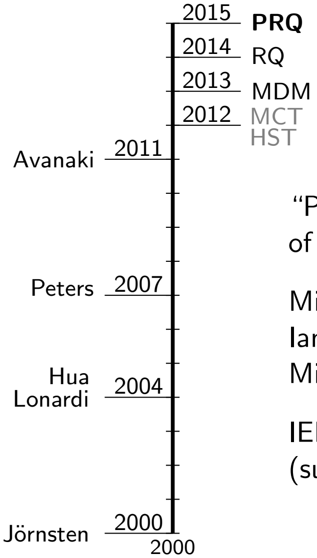


Relative Quantization Coder:

N decompression qualities
$\Rightarrow$ N compressed versions (bad!)

Contribution 5: Progressive RQ



"Progressive Lossy-to-lossless compression of DNA Microarray Images"

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IEEE Signal Processing Letters, 2015 (submitted)

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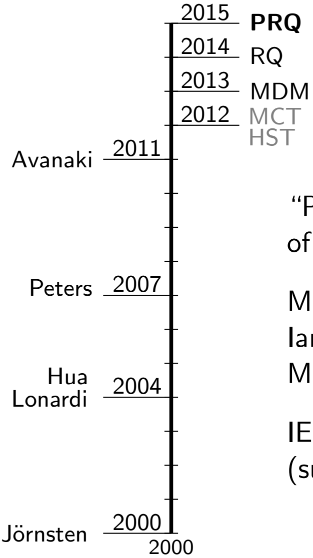

(Last contribution)

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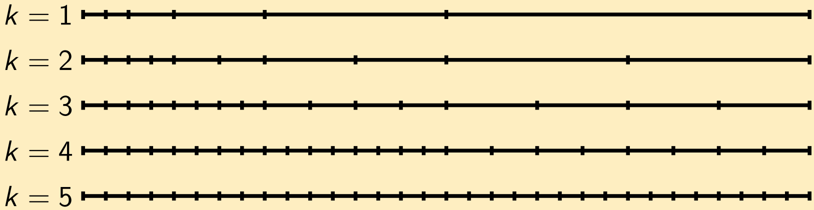
Contribution 5: Progressive Relative Quantization

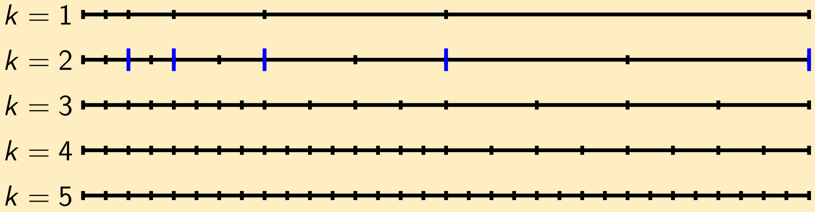
Progressivity (5 bitplanes)



Obs 1: Can refine RQ($k = 1$) into RQ($k = 2$)

Contribution 5: Progressive Relative Quantization

Progressivity (5 bitplanes)



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Contribution 5: Progressive Relative Quantization

Progressivity (5 bitplanes)

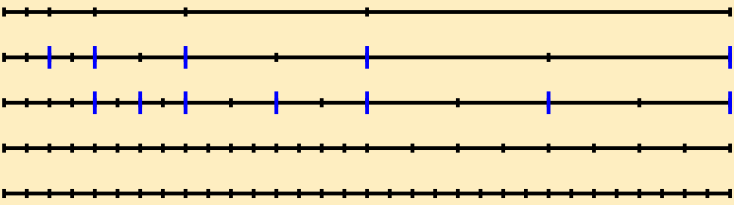
$k = 1$

$k = 2$

$k = 3$

$k = 4$

$k = 5$



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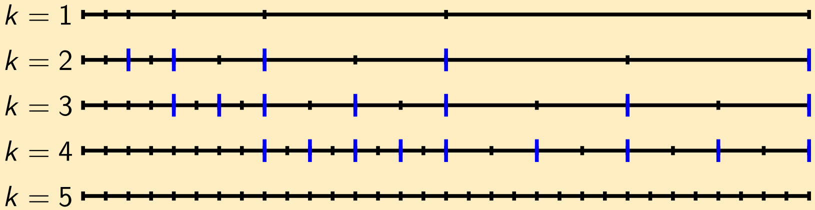

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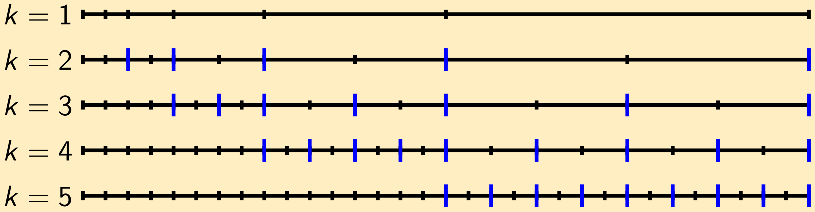

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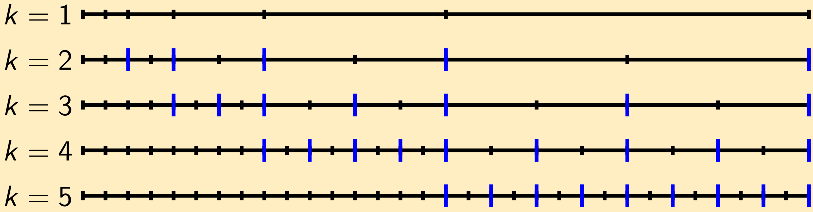


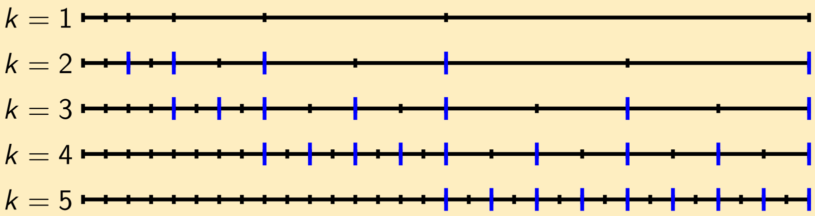
Obs 1: Can refine k into $k+1$ ($\Delta_{k \to k+1}$)

Progressive RQ (PRQ) representation

$$\mathrm{PRQ} = \mathrm{RQ}(k=1), \Delta_{1\to 2}, \ldots, \Delta_{15 \to 16}$$

Contribution 5: Progressive Relative Quantization

Progressivity (5 bitplanes)



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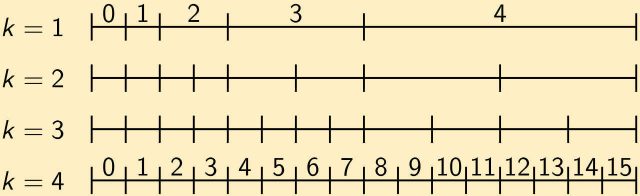
Obs 2: Can reconstruct as RQ(1), RQ(2), ... or RQ(16) = lossless

Contribution 5: Progressive Relative Quantization

Quantization Indices (4 bitplanes)



(Here, $k = 4 \Rightarrow$ quantization index = pixel intensity)

Contribution 5: Progressive Relative Quantization

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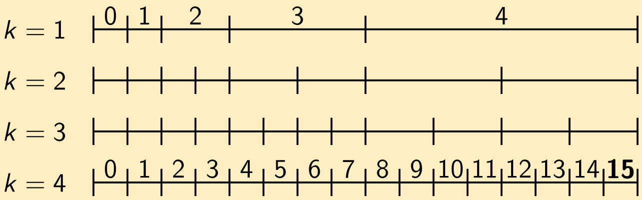

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Ex 1 PRQ(**15**) = 4, right, right, right

Contribution 5: Progressive Relative Quantization

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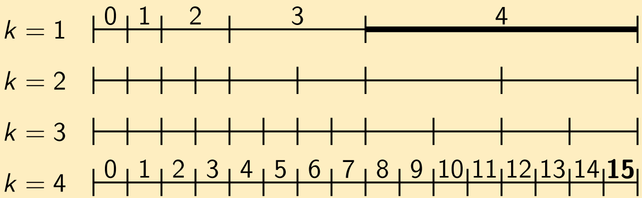

(Here, $k=4 \Rightarrow$ quantization index = pixel intensity)

Ex 1 PRQ(15) = **4**, right, right, right

Contribution 5: Progressive Relative Quantization

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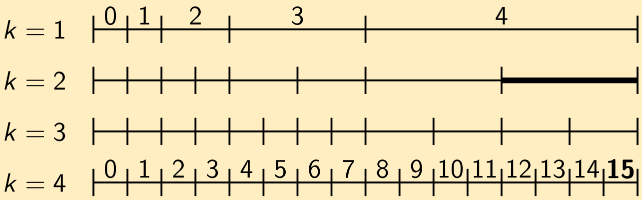

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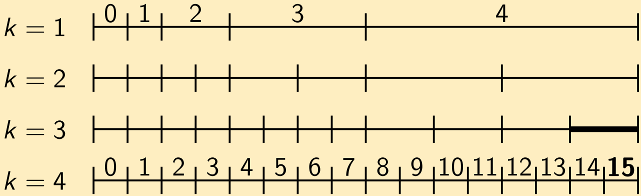

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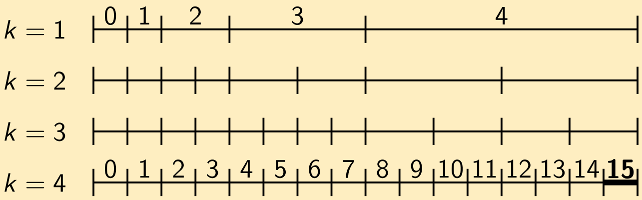
Contribution 5: Progressive Relative Quantization

Quantization Indices (4 bitplanes)

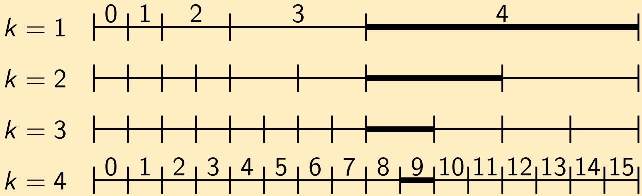


(Here, $k = 4 \Rightarrow$ quantization index = pixel intensity)

Ex 1 PRQ(15) = 4, right, right, **right**

Contribution 5: Progressive Relative Quantization

Quantization Indices (4 bitplanes)



(Here, $k = 4 \Rightarrow$ quantization index $=$ pixel intensity)

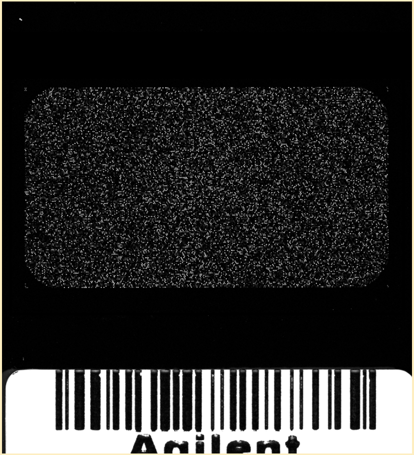
Ex 1 PRQ(15) $=$ 4, right, right, right

Ex 2 PRQ(9) $=$ 4, left, left, right

Contribution 5: Progressive Relative Quantization

How to code the PRQ representation?

DNA Microarray Image



Contribution 5: Progressive Relative Quantization

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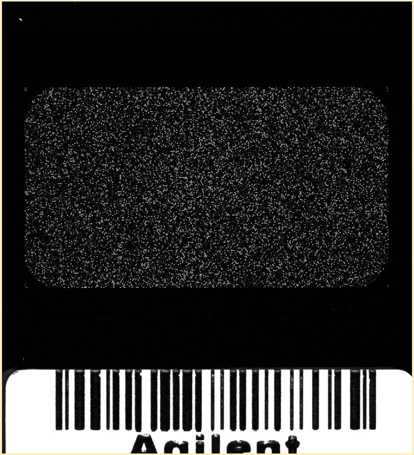

PRQ

All image:

1. RQ($k = 1$)
2. $\Delta_{1\to 2}$
3. $\dots$
4. $\Delta_{15\to 16}$

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PRQ-ROI

First ROI:

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3. $\cdots$
4. $\Delta_{15\to 16}$

Then BG:

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3. $\cdots$
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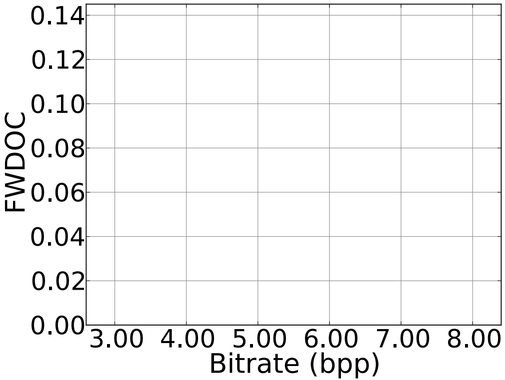
Contribution 5: Progressive Relative Quantizer

Rate-Distortion (Detection+Classification)



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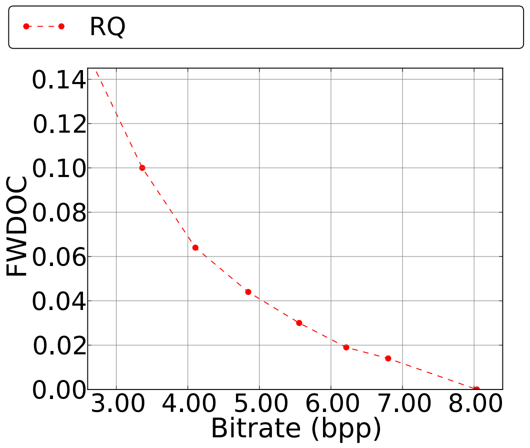

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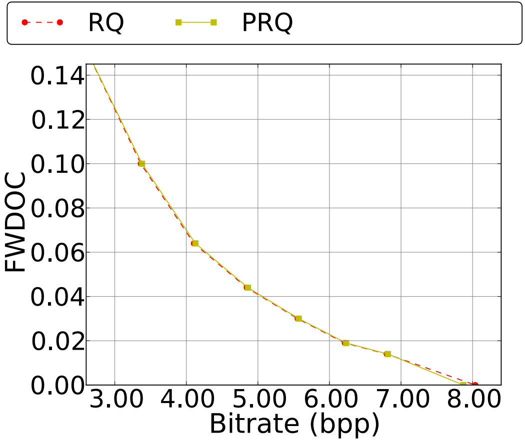

✓ PRQ $\sim$ RQ

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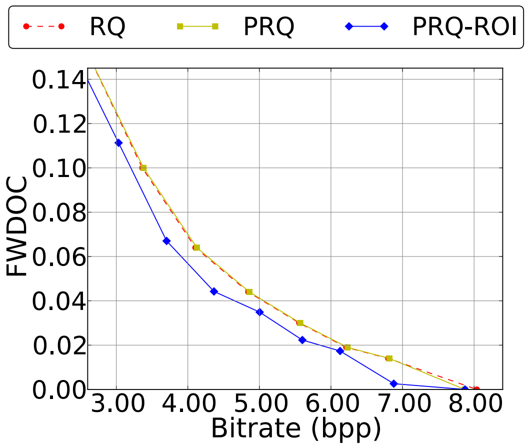

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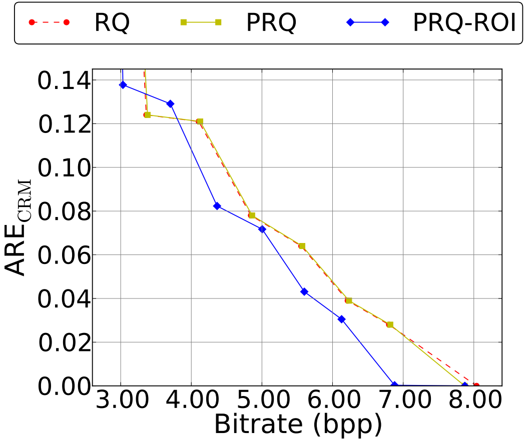

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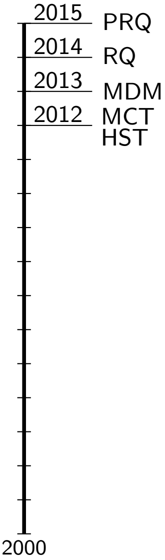
Contents

1. Introduction: DNA Microarrays
2. Lossless compression
3. Lossy compression
4. Conclusions

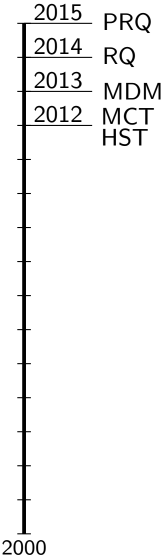
Problems and Goals



Problems

Lossless	**Lossy**
✓: Perfect data fidelity	✓: Arbitrary compression ratios
×: Small compression ratios	×: Analysis result distortion
×: Not standard	

Problems and Goals



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Main goals

- ⇒ Improve standards
- ⇒ Assess distortion
- ⇒ Lossy coder with acceptable distortion

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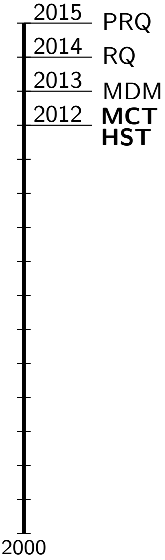

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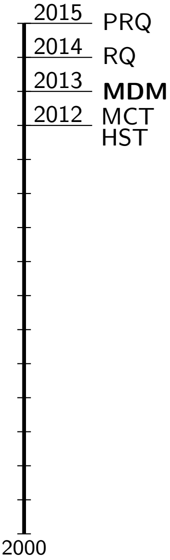

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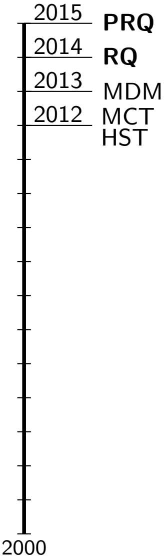

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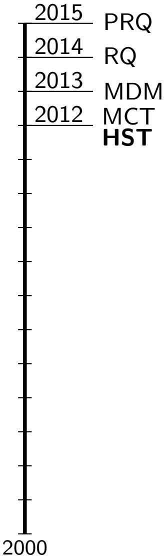

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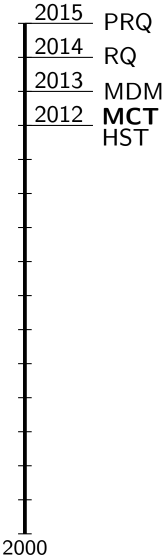

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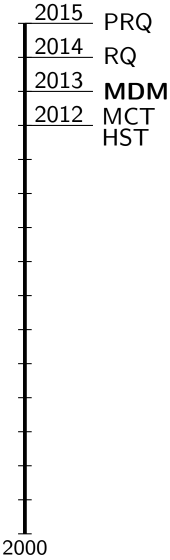

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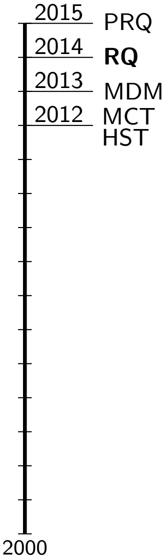

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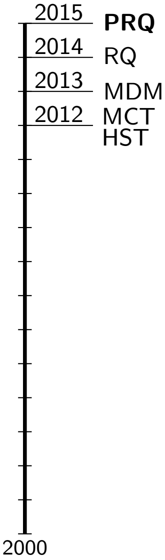

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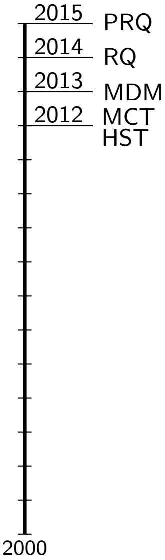

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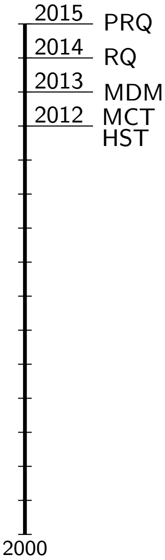

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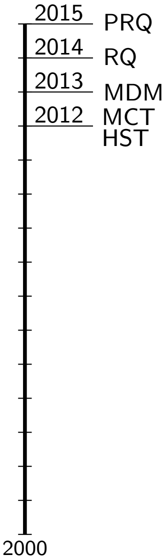

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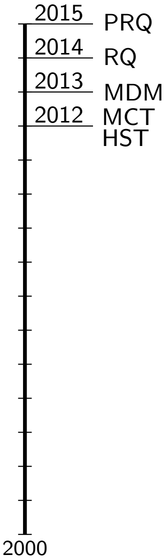

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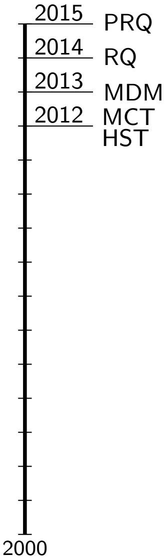

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Book chapters

- 1× CRC Press – 2014

Reflections

Lossless compression

- Performance $\sim$ limit
- Standard - Specific: 0.5 bpp

$\Rightarrow$ Difficult to improve

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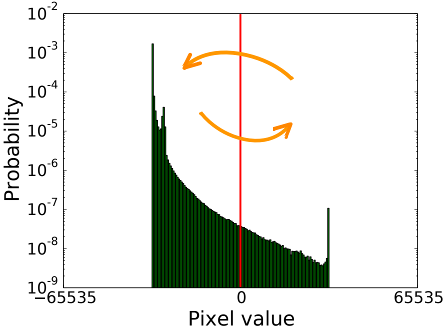
Additional slides

- Image Analysis References
- Compression References
- HST Definition
- HST + DWT?
- MDM Definition
- RQ Definition
- RQ vs PRQ vs PRQ-ROI compression

HST definition

Left part	Right part
1^{st} bit was 0	1^{st} bit was 1
$\Downarrow$	$\Downarrow$
add 8000H	**subtract** 8000H



Histogram Swap Transform

Why not HST + DWT?

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- Range expansion

Histogram Swap Transform

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- Higher % intensities used

Histogram Swap Transform

Why not HST + DWT?

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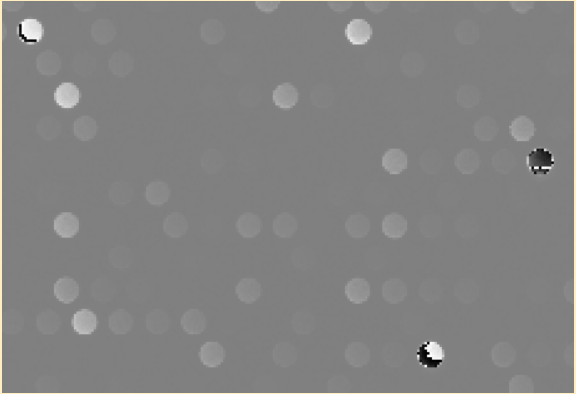
- Abrupt changes

Detail after HST



MDM definition

$$\mathrm{MDM} \quad = \quad 10 \log_{10} \frac{(\mathrm{max\_val})^2}{\mathrm{ME}}$$

$$\mathrm{ME} \quad = \quad (\mathrm{max\_val})^p - \mathrm{max\_val} + \min(\mathrm{max\_val}, \mathrm{MSE}_{\mathrm{image}}).$$

$$p \quad = \quad 2/(1 + exp(-\alpha(r_{\mathrm{spot}} + r_{\mathrm{localBG}} + r_{\mathrm{global}} - 3))),$$

$$\begin{aligned}
r_{\mathrm{spot}} &= \max(\mathrm{max_spot_ratio}, 1/\mathrm{min_spot_ratio}), \\
r_{\mathrm{localBG}} &= \max(\mathrm{max_localBG_ratio}, 1/\mathrm{min_localBG_ratio}), \\
r_{\mathrm{global}} &= \max(\mathrm{global_intensity_ratio}, 1/\mathrm{global_intensity_ratio}).
\end{aligned}$$

RQ Definition

- 2^k intervals of size 1
- 2^{k-1} intervals of size 2
- 2^{k-1} intervals of size 2^2
- $\cdots$
- 2^{k-1} intervals of size 2^{B-k}

Image Analysis References

- **Athanasiadis, 2015**
  Complementary DNA microarray image processing based on the fuzzy gaussian mixture model
- **Fouad, 2015**
  Automaticand Accurate Segmentation of Gridded cDNA Microarray Images Using Different Methods
- **Li, 2014**
  Improvements on segment based contours method for DNA microarray image segmentation
- **El-Gawady, 2014**
  Segmentation of Complementary DNA Microarray Images using Marker-Controlled Watershed Technique

Image Compression References

2003 **R. Jornsten et al.**
Microarray image compression: SLOCO and the effect of information loss,
Signal Processing, vol. 83, no. 4, pp. 859–869

2003 **Faramarzpour, N. et al.**
Lossless DNA microarray image compression
Signals, Systems and Computers

2004 **Hua, J. et al.**
Microarray BASICA: Background Adjustment, Segmentation, Image Compression and Analysis of Microarray Images.
EURASIP Journal on Advances in Signal Processing

2004 **Lonardi & Luo**
Gridding and compression of microarray images.
IEEE Computational Systems Bioinformatics Conference, CSB

2006 **Pinho et al.**
On the use of standards for microarray lossless image compression. IEEE Transactions on Biomedical Engineering

2006 **Bierman, R. et al.**
MACE: Lossless Compression and Analysis of Microarray Images,
ACM Symposium on Applied Computing, 23–27

2006 **Xu, Q. et al.**
Accuracy of differential expression detection with compressed microarray images
Signal Image and Video Processing

2007 **Neekabadi, a. et al.**
Lossless Microarray Image Compression using Region Based Predictors.
IEEE International Conference on Image Processing

2007 **Peters, T. J. et al.**
Microarray image compression using a variation of singular value decomposition.
IEEE Engineering in Medicine and Biology Society Conference

2009 **Neves, A. et al.**
Lossless compression of microarray images using image-dependent finite-context models.
IEEE Transactions on Medical Imaging

2009 **Battiato, S. et al.**
A bio-inspired CNN with re-indexing engine for lossless DNA microarray compression and segmentation.
IEEE International Conference on Image Processing (ICIP)

2011 **Avanaki et al.**
Compression of cDNA Microarray Images based on Pure-Fractal and Wavelet- Fractal Techniques
Journal on Graphics, Vision and Image Processing

2014 **Rueda, L. (editor)**
Microarray Image and Data Analysis: Theory and Practice.
CRC Press

RQ vs PRQ vs PRQ-ROI

Compression results (IBB, bpp)

Algorithm	$k = 1$	$k = 2$	$k = 3$	$k = 4$	$k = 5$	$k = 6$	$k = 7$	Original
RQ	2.653	3.363	4.105	4.844	5.556	6.214	6.800	8.039
PRQ	2.652	3.375	4.119	4.857	5.566	6.230	6.815	8.001
PRQ-ROI	2.380	3.032	3.703	4.365	5.004	5.600	6.128	6.878

Analysis results (IBB, ARE_{CRM})

Algorithm	$k = 1$	$k = 2$	$k = 3$	$k = 4$	$k = 5$	$k = 6$	$k = 7$	Original
RQ	0.526	0.136	0.123	0.073	0.076	0.041	0.029	0
PRQ-ROI	1.356	0.146	0.135	0.076	0.080	0.044	0.032	0

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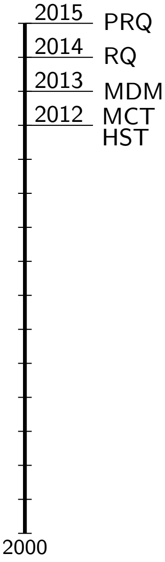

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