

	Prince <i>et al.</i> , 2010	Mahajan and Bachtrog, 2015
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Method	Microarray	RNA-Seq
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	Prince <i>et al.</i> , 2010	Mahajan and Bachtrog, 2015
Method	Microarray	RNA-Seq

Sample

Whole Body

Abdominal and
Prothoracic Glands

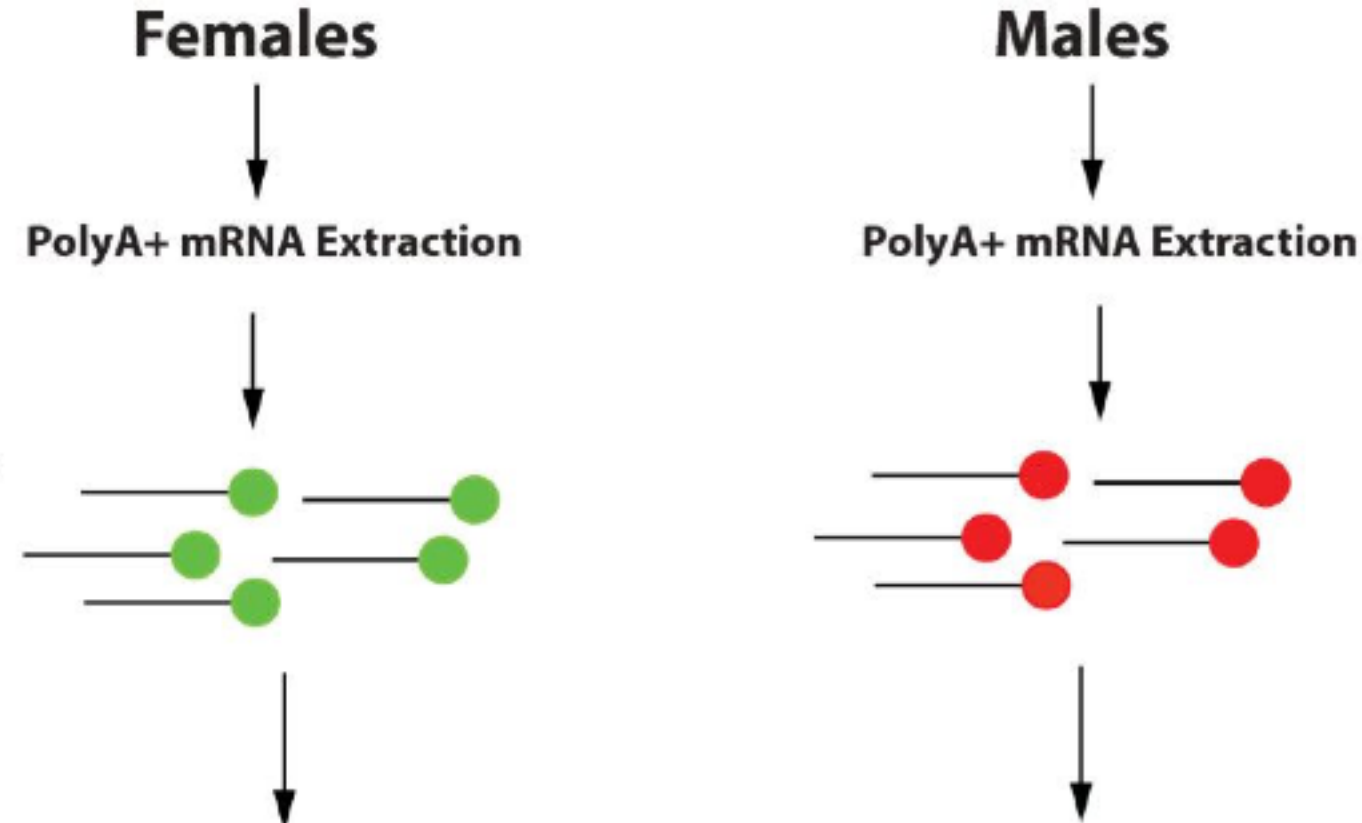
Reasons for Discrepancy:

	Prince <i>et al.</i> , 2010	Mahajan and Bachtrog, 2015
Method	Microarray	RNA-Seq
Sample	Whole Body	Abdominal and Prothoracic Glands

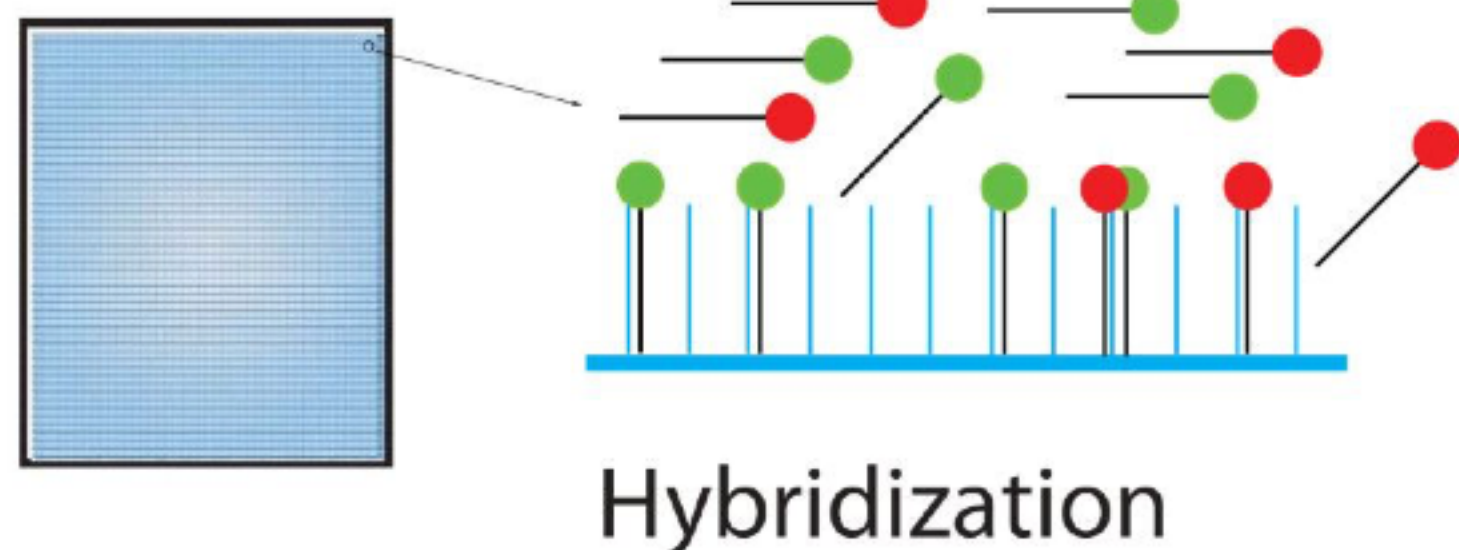
Microarrays

Sample Prep

Convert to cDNA by
RT and random
priming and Label

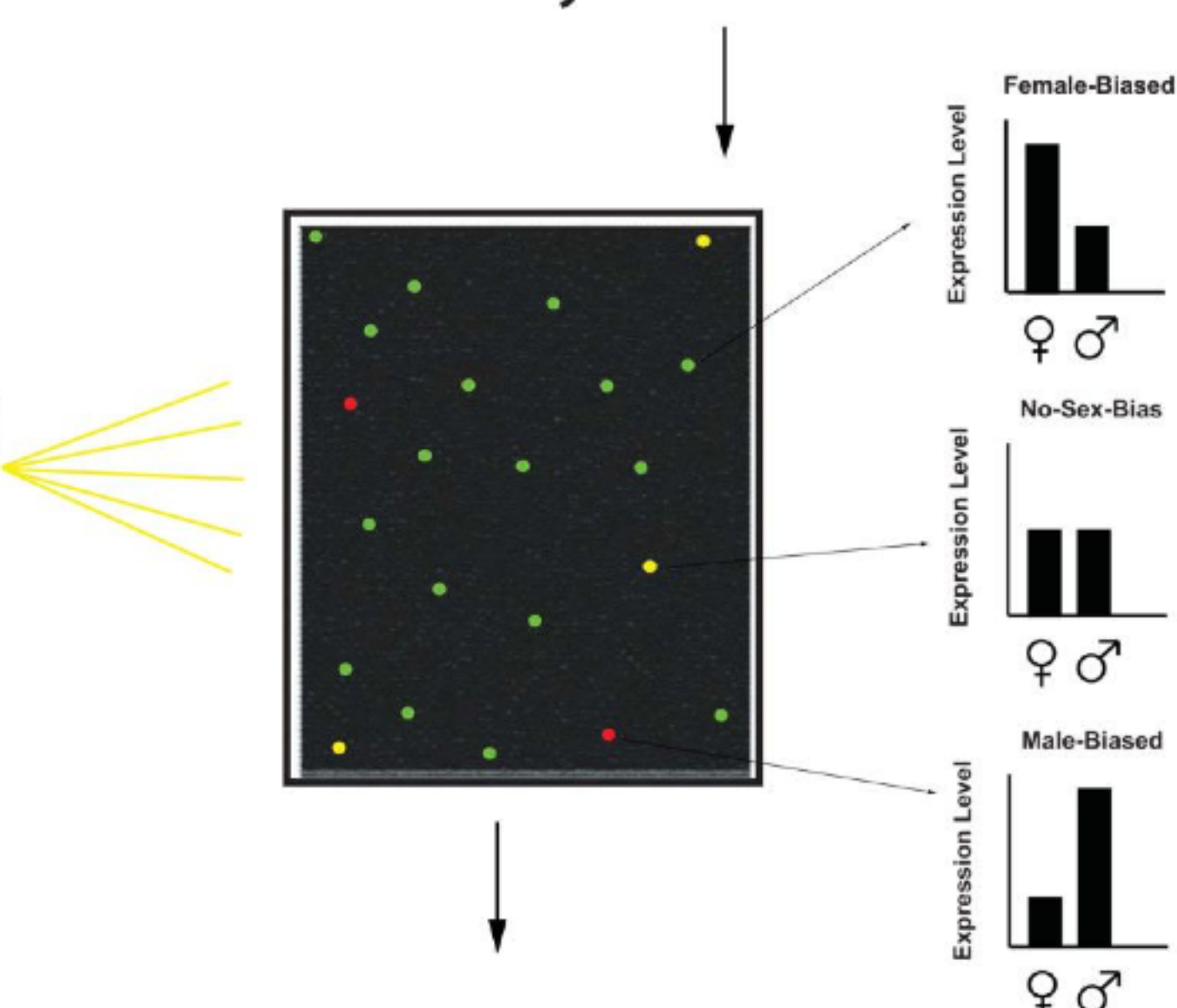


Procedure



Acquisition

Scanning
by laser



Data

Raw: Image files (a few megabytes in size) with fluorescent intensities
Processed: Text files with intensities of gene expression

mRNA-Seq

Sample Prep

Fragment RNA

Convert to cDNA
by RT and
random priming

Ligate Adapters

Procedure

Cluster
(solid phase
clonal amplification)

Flow cell

Acquisition

Sequence
by
Synthesis

Cycle 1:
Add sequencing reagents
First base incorporated
Remove unincorporated bases
Detect signal with laser

Cycle 2-n:
Add sequencing reagents
and repeat

Data

Raw: FASTQ files of millions of sequences (1-10s of Gigabytes / lane)
Processed: Mapping, Junction Detection, Quantification

Read Coverage
Gene Models

