

Services Provided by the Genomics Core

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Instruments & Services

1. **Real-time PCR** – Applied Biosystem 7900HT Seq Detection System
2. **Affymetrix GeneChip service:**
Hybridization Oven 640, Fluidics Station 450, Scanner 7G
3. NanoDrop **Spectrophotometer** ND-1000
4. GeneMachine **miroarray slide spotter**
5. **Robotic Pipettor** (Beckman Coulter Biomek FX)
6. Bio-Rad Experion Automated **Electrophoresis Station**
7. ScanArray Express **Microarray Scanner** (Perkin Elmer)
8. **WebArray/WebArrayDB** online platform for data analysis
9. **Customized data analysis**

QPCR (Applied Biosystem 7900HT Seq Detection System)



Responsibility:

1. Setting up account.
2. Demo of the software

Charge:

1. \$10 for the first three hours
 2. \$5 for each additional hour
- (* double charge for outsider)

Affymetrix GeneChip Work Station



Accept:

1. total RNA (Full service)
 - 5–10 ug in 10 uL (Affy kits)
 - 10–100 ng in 5 uL (Nugen kits)
2. amplified cRNA or cDNA
(hybridation and scan)

Charge (for expression chips):

1. \$380 for full service
(\$456 for outsider)
2. \$150 for hybridization and scan
(\$180 for outsider)

NanoDrop Spectrophotometer

Sample:

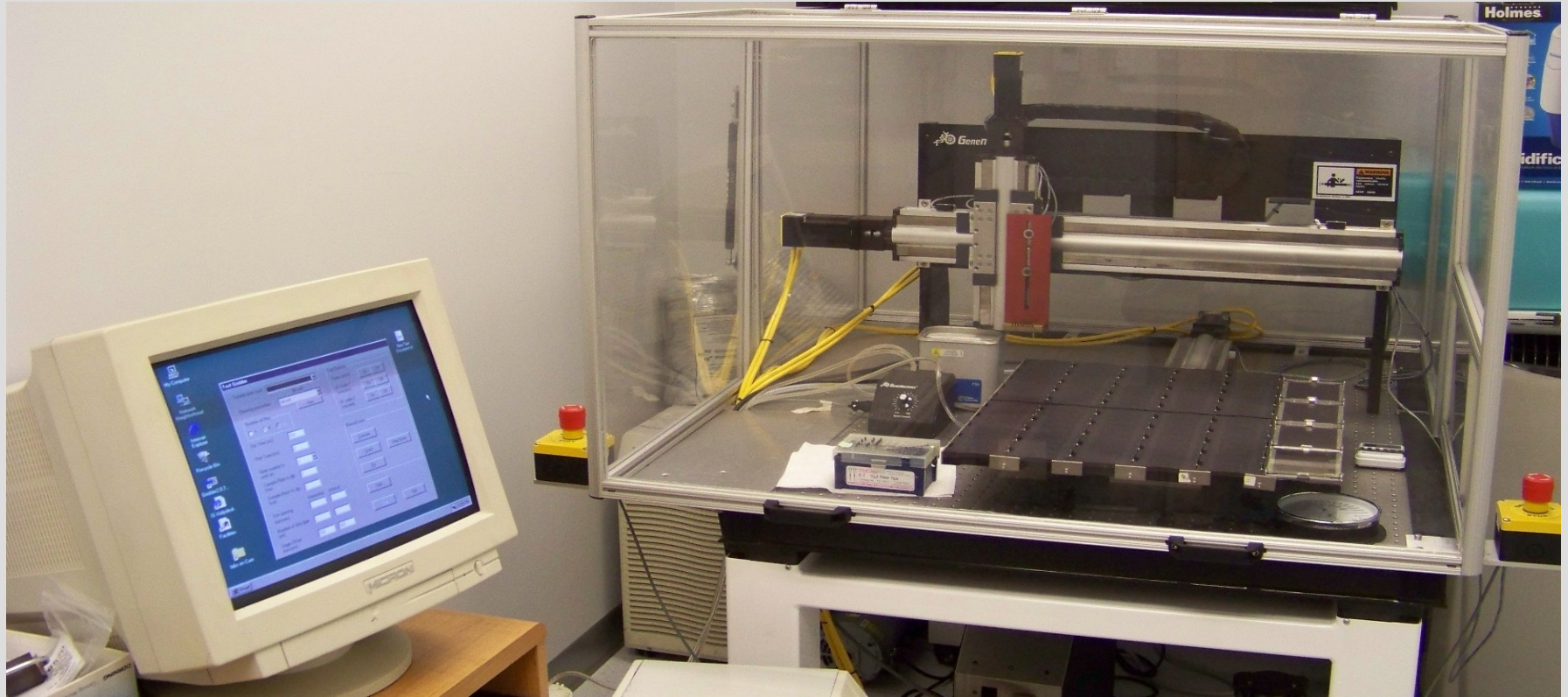
1. 1 uL Nucleic Acid (2 to ~ 3000 ng/uL)
2. Protein (methods: A280, BCA, lowry, Bradford)
3. Cell culture

Charge:

free



GeneMachine Microarray Spotter



Accept:

sample solution
in 384-well plates

Charge (per slide):

1. \$12 for slide
2. \$3 for printing (machine wear-out)
3. \$2 for personnel if printed by the Core.

Biomek FX Robotic Pipettor

Sample requirement:

samples in plates
(96/384-well)

Charge:

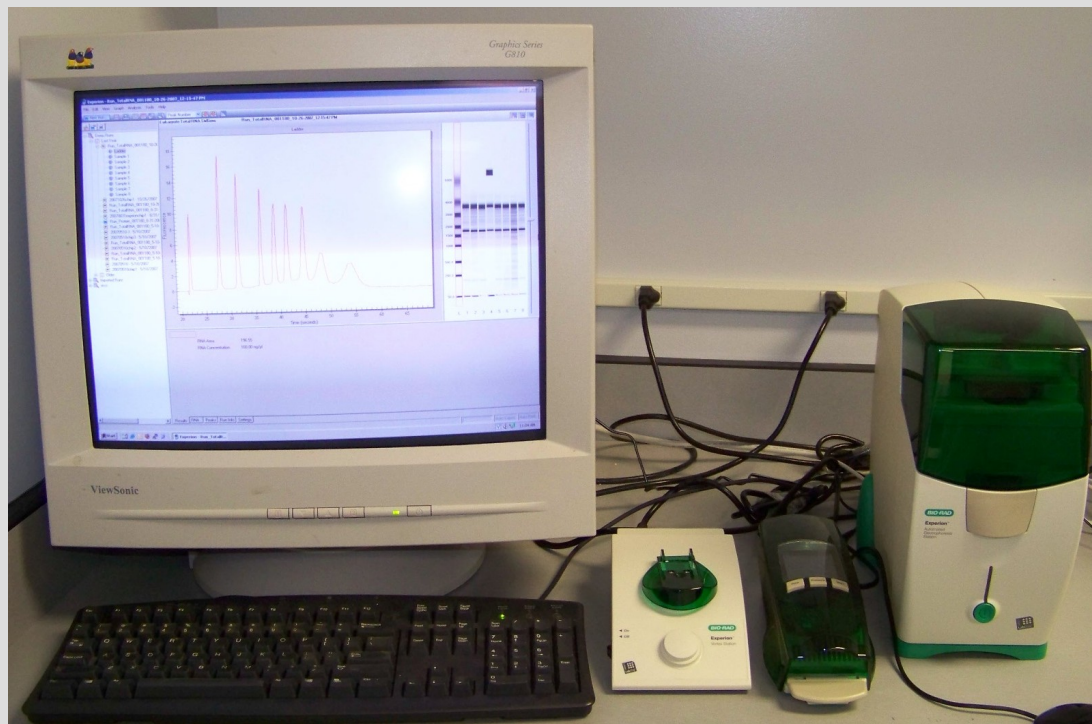
1. \$4 for each tip box
2. \$10 per hour for personnel if operated by the Core member.



Bio-Rad Experion Automated Electrophoresis Station

Features:

1. Chip-based electrophoresis system
2. Multiple samples — 1 to 11 or 12 each time (in 30 minutes)
3. Qualitative range:
 - 5–500 ng/ μ L total RNA for StdSens analysis kit
 - 100–5000 pg/ μ L total RNA for HighSens



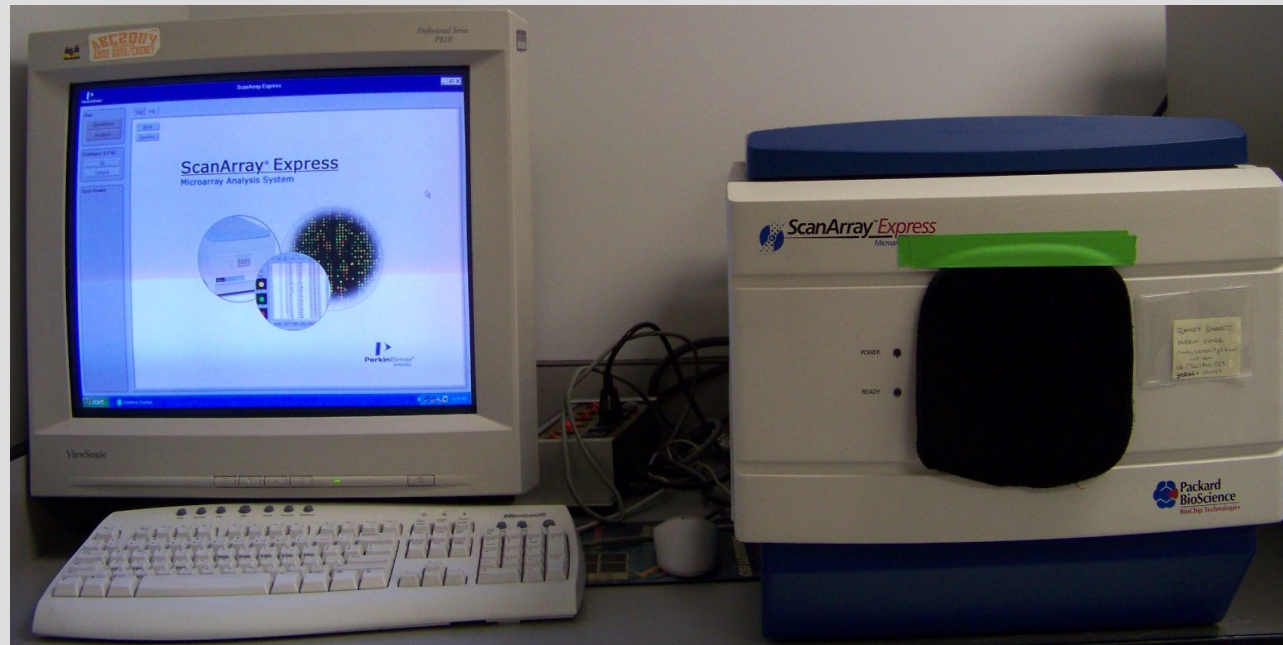
Samples:

total RNA (eukaryotic/prokaryotic)
mRNA
protein

Charge:

Free

ScanArray Express Microarray Scanner



Features:

4 channels of laser
5 um resolution

Status & Problems:

Reason:

a) too old (10 years old)
b) heavily using

Result:

out of order frequently

Conclusion:

need to be upgraded!

WebArray

- An online computation platform for microarray data
- Computation based on uploaded files
(two-color data and Affymetrix GeneChip CEL files)
- Algorithm is eBayes-moderated t-test (LIMMA package)
- <http://bioinformatics.skcc.org/webarray>
- more than 300 registered users (increasing) all over the world
and 1 guest account can be used by anybody



WEBARRAY

Welcome back, guest

logoff

Home

User Profile

Upload Data

Manage Data

Submit Requests

• Affymetrix Data

• Dual Color Array Data

Browse Results

Help

1 File Selections

Intensity files format:

- Agilent
- ArrayVision
- Genepix
- ImaGene
- QuantArray
- SMD
- Specific Format
- SPOT
- spot.close.open

Intensity files and experiment design:

Choose from following entries:

<input type="text"/>	in which C
<input type="text"/>	in which C
<input type="text"/>	in which C
<input type="text"/>	in which C
<input type="text"/>	in which C
<input type="text"/>	in which C

More files

OR use following files:

targets file:

design file :

Contrast design (optional):

Gene list file:

File format: GAL Specific Format

Please select file:

Spot type file (optional):

Genome/chromosome location file (optional):

WebArrayDB

WebArrayDB (<http://10.0.1.127/webarray>) was developed on the base of WebArray

New features:

1. **data repository** (storing, browsing, searching)
2. computation **based on databases** (rather than on files with WebArray)
3. **more data types**, 1 or multiple colors/channels data.
4. alignment and computation ability across **multiple platforms**
5. **more algorithms** for differential analysis
6. allows much **more flexible experimental design**
7. **parallel computation** on SMP or Linux cluster
8. probe searching with GO (Gene Ontology) terms

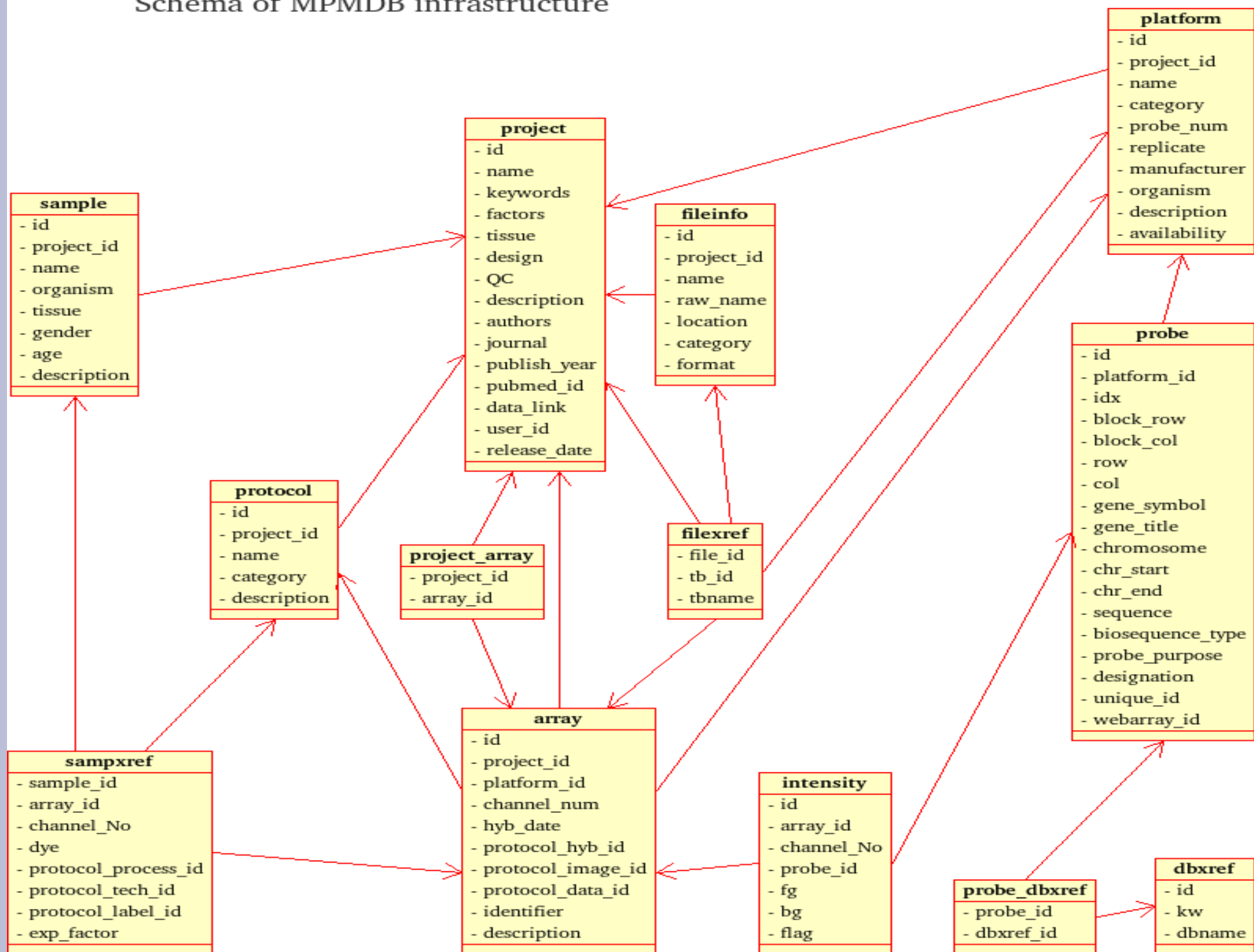
.....

WebArrayDB

Microarray data repository

- maintaining multiple specialized databases
- store parsed data in databases tables and files on server's file system.
- database contents:
 - a) project description
 - b) microarray platform definition
 - c) samples
 - d) protocols
 - e) intensity data and raw files

Schema of MPMDB infrastructure



WebArrayDB

Differential analysis of microarray data

Based on intensity:

- a) t-test
- b) eBayes-moderated t-test(LIMMA) (which is used in WebArray)
- c) SAM
- d) AN(C)OVA (fixed-effect model and mixed-effect model)
- e) non-parametric tests

Based on ratio:

Use paired data for analysis

all the above algorithms were implemented or in developing

WebArrayDB

Steps for analysis:

1. Searching from databases
2. Background correction
3. Within-array normalization
4. Between-array normalization (within-platform)
5. Align cross-platform data
6. Between-array normalization (cross-platform)
7. Differential analysis

There are many options to select at each step



WEBARRAY

Welcome back, tt1

[logoff](#)

Quick Start

[Home](#)

[User Profile](#)

Files

- [Upload](#)
- [Delete](#)

Data Repository

[Reference databases](#)
[Databases](#)

- [Generic](#)
- [Bacteria](#)
- [Prostate cancer](#)

Data Analysis

- [By databases](#)
- [By files](#)
 - [Affymetrix](#)
 - [Two Color](#)

[Results](#)

[Help](#)

```
nim_a3d - Ch1 (nim_pf1d::webarray)
nim_a3d - Ch2 (nim_pf1d::webarray)
nim_a3u - Ch1 (nim_pf1u::webarray)
nim_a3u - Ch2 (nim_pf1u::webarray)
nim_a4u - Ch1 (nim_pf1u::webarray)
nim_a4u - Ch2 (nim_pf1u::webarray)
nim_a4d - Ch1 (nim_pf1d::webarray)
nim_a4d - Ch2 (nim_pf1d::webarray)
nim_a4 - Ch1 (nim_pf1::webarray)
nim_a4 - Ch2 (nim_pf1::webarray)
nim_a5 - Ch1 (nim_pf1::webarray)
```

```
>> nim_a2u - Ch2 (nim_pf1u::webarray)
nim_a2d - Ch2 (nim_pf1d::webarray)
<< nim_a2 - Ch2 (nim_pf1::webarray)
nim_a3 - Ch2 (nim_pf1::webarray)
nim_a3d - Ch2 (nim_pf1d::webarray)
nim_a3u - Ch2 (nim_pf1u::webarray)
nim_a4u - Ch2 (nim_pf1u::webarray)
```

[search](#)

[remove](#)

2 Options

Data match

Match probes for across-platform data: Yes No

Method to match data from different platform:

Method to merge replicate values:

Data normalization

Background correction and normalizations within platform: [more](#)

Platform	Background	Within array	Between arrays	
<input type="text" value="nim_pf1u::webarray"/>	<input type="text" value="none"/>	<input type="text" value="loess"/>	<input type="text" value="none"/>	Remove

Normalization method across platforms:

Number of bin:

Data analysis

[Show/Hide advanced options](#)

Method for analysis:

Contrasts:

3 Request name

You may give a name for this analysis request:

Customized data analysis

Analysis:

1. differential analysis
2. clustering and classification

Charge:

\$50 per hour for personnel
or
coauthors ?

Plans and Expectation for the Recent Future

1. A new microarray scanner to replace the old one
2. Upgrade WebArray on bioinformatics to WebArrayDB to offer services for registered and new internet users
3. A much powerful server to host WebArrayDB, ideally
 - a) 16 CPU cores and
 - b) at least 16G memory
 - c) RAID hard disks
4. Build a two specialized microarray databases with WebArrayDB – bacteria and cancer open to public access.
5. More meta-analysis functions, including
 - a) clustering & classification
 - b) pathway analysis