



# GP3xCLI

GenePix Post-Processing  
By  
CSIRO Livestock Industries



## Introduction

1. Each microarray hybridisation generates a large amount of data resulting from the scanning of two images (one red, one green).
2. It is both tedious and prone to human error to visually assess the quality of each spot on the microarray.
3. GP3xCLI is an automated AWK-based script to assess the quality of raw microarray data captured using the GenePix optical scanner.
4. Executed from the prompt line, GP3xCLI incorporates tools such as:
  1. A2PS → ASCII to Postscript translator
  2. GNUPLOT → interactive plotting utility
  3. PS2PDF → public domain postscript to PDF converter
5. On execution, GP3xCLI generates a 2-page PDF file.
6. Inspired by GP3 (<http://www.bch.msu.edu/~zacharet/microarray/GP3.html>), GP3xCLI is not intended to perform any real analysis (eg. Correction, filtering, normalisation).
7. Quality assessment is based on standard
  1. Summary Statistics
  2. Diagnostic plots



Summary Statistics

1. Total Number of Spots.
2. Number of Spots by Quality Flag (generated by the scanner).
3. For each channel (Red and Green), Number of Spots for which the foreground is less than the background intensity signal.
4. Optimality of Log-transformation → Amount of data left by each threshold of Mean to Median correlation.
5. Number of Repetitions by Genes
6. N, Mean, Std, Min and Max for Log-Ratio (Red/Green) and average (0.5\*(R+G)) intensities



Summary Statistics

```
#####
#
# GP3xCLI
# GeneFix Processing Program by CSIRO Livestock Industries
# Bioinformatics Group
#
# Enquiries: Tony.Reverter-Gomez@csiro.au
# Copyright (c) 2003-2005 CSIRO Livestock Industries
#
#####

GPR Input:      f12.gpr
Processed on:   Tue Dec 27 22:46:25 EST 2005

===== IMAGE QUALITY =====
Total No. of Spots -----> 19200

  QUALITY FLAG   SPOTS
  -----
    0             14467
   -100            12
    -50            4721

Red dye with Background >= Foreground ---> 892
Green dye with Background >= Foreground ---> 915

Median to Mean Correlation Analysis:

          DATA LEFT
          RED          GREEN
Corr     Raw  Log2    Raw  Log2
> 0.00  19200 19200   19200 19200
> 0.20  19199 19200   19199 19200
> 0.40  19193 19200   19192 19200
> 0.60  19008 19200   19102 19200
> 0.80  17061 19199   18541 19198
> 0.85  14466 19193   17872 19196
> 0.90  10491 19137   15786 19181

===== VALID SPOTS* =====
Total No. of Valid Spots -----> 14432
Percentage of Valid Spots -----> 75.2

Total No. of Genes -----> 7215
Mean No. Repetitions -----> 2 for 6596 Genes
Min. No. Repetitions -----> 1 for 579 Genes
Max. No. Repetitions -----> 28 for 1 Genes

          Log(R/G) vs 0.5*Log(R+G)
          N             14432             14432
          Mean          -0.017            10.327
          Std           0.617             2.079
          Min           -8.711            3.246
          Max            4.030            15.994
          Correlation   0.362

          Log(R/G) across Intensity Values
          Intensity   Spots   % <0   % >0
( 0 , 4)             4       100.0   0.0
( 4 , 8)            1499       74.1   25.9
( 8 , 12)           9846       40.4   59.6
(12 , 16)           3083       17.3   82.7
```

Valid Spots:  
 - Foreground > Background  
 - Quality Flag = 0

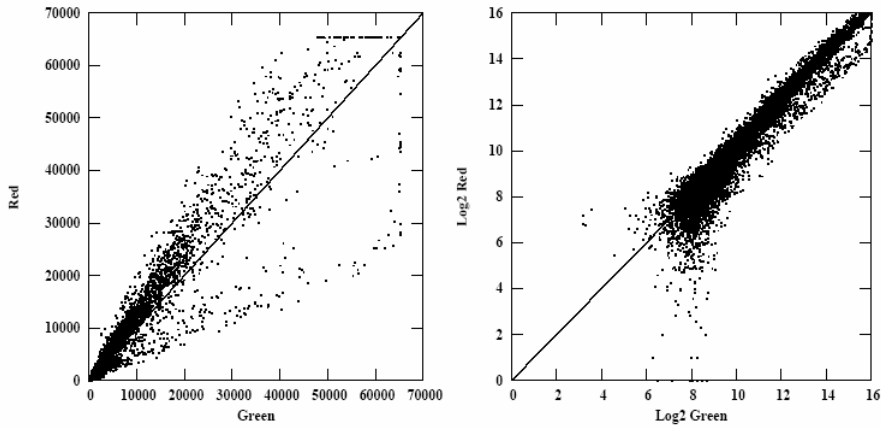
===== VALID SPOTS\* =====



Diagnostic Plots

NB: Only for Valid Spot:  
- Foreground > Background  
- Quality Flag = 0

Scatters: **RED** versus **GREEN**



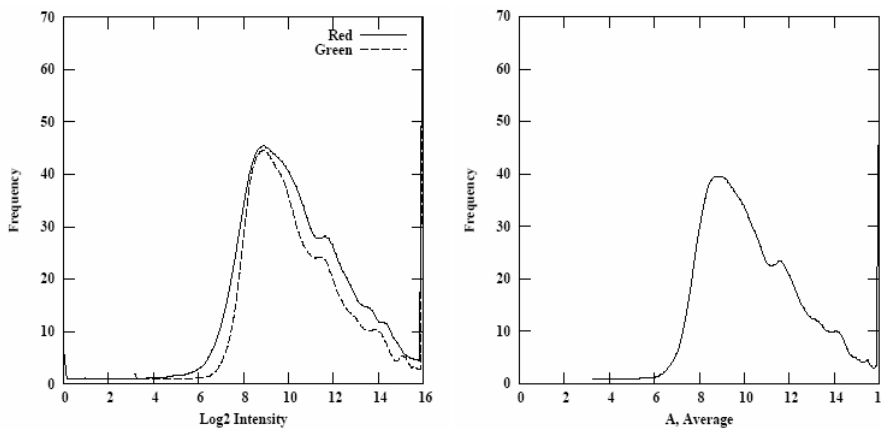
A. Reverter - Sept. 2006, UAB, Barcelona, Spain



Diagnostic Plots

NB: Only for Valid Spot:  
- Foreground > Background  
- Quality Flag = 0

Densities: **RED** and **GREEN**



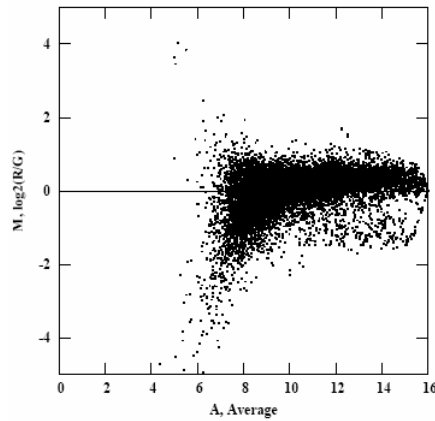
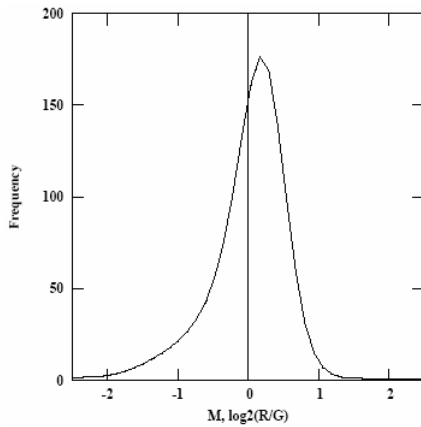
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Diagnostic Plots

NB: Only for Valid Spot:  
- Foreground > Background  
- Quality Flag = 0

Ratios: **RED** to **GREEN**



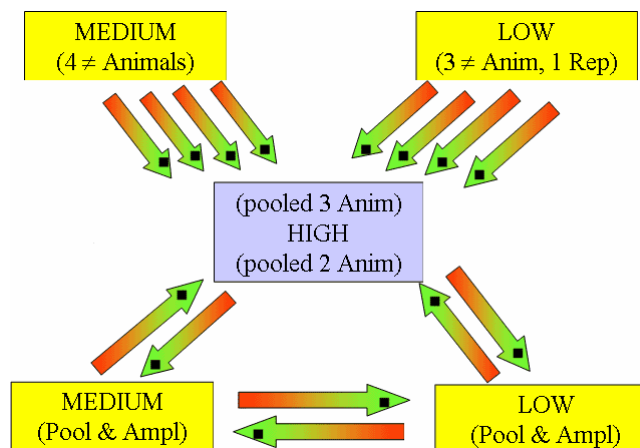
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Application

*The Diets Experiment*

3 Diets, 10 Animals, 14 Microarrays



Available at: <http://www.livestockgenomics.csiro.au/courses/Keren/>

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