

**BLENDED LEARNING 'A LA CARTE' -  
COURSEWORK ASSESSMENT OF A  
DIFFERENT KIND**

**Dr. Henry Keil, Brunel University**

# Two different definitions of blended learning

## Traditional:

Learning involving a combination of traditional face-to-face tuition with on-line learning

In regards to **Biology coursework: experimental (lab/field) work + lab/field-report**

## New:

A **combination of media and tools** employed in an e-learning environment and **a combination of different pedagogic approaches**, irrespective of the learning technology employed (Whitelock and Jelfs, 2003).

# Research question

Does such a redefined blended learning approach

- **support students' individual learning styles**
- **facilitate and enhance their learning**
- **lead to an improvement in their academic performance?**

Setting:

Coursework on the topic: **Microbial Genetics**

# The approach

## Combination of media and tools

- Wet labs
- Dry labs
- Powerpoint presentation
- Oral presentation
- Online discussion

## Combination of different pedagogic approaches

- Individual project work
- Collaborative group work
- Factual recall
- Problem solving

# 'A LA CARTE'

- Element of choice – menu 1  
**Choice of how many**  
- with a minimum of two or three out of a total of six
- Element of choice – menu 2  
**Free choice of the type of coursework assignment** they wish to undertake and to be assessed in
- The dessert - assessment  
The **best three assignments** submitted determine coursework mark

# WebCT VISTA - the e-learning 'Interface'

## MICROBIAL GENETICS

Please work your way through the icons below, from left to right and top to bottom during the course of this module.

It is suggested you make regular use of the calendar tool in the menu bar on the left side menu bar. For optimal viewing please read the footer at the bottom of this page.



Study Preparation  
to be used before start of module



Content Delivery  
PP-files and Web-sites



Wet and dry labs  
all schedules and instructions are found here



On-line discussion  
for Bacterial Genomics



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Assessment  
contains the 3 MCQs



Problem solving  
for those who like to think laterally



Print material  
PP-files in print format



WebCT-based submissions  
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Grades awarded



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# Wet/dry labs – assignments 1 and 2

## MICROBIAL GENETICS

Please work your way through the icons below from left to right and top to bottom during the course of this

Table of Contents for  
Wet and dry labs - please print out files below

### 1. Laboratory work

- 1.1. [Safety Guidelines](#)
- 1.2. [Practical schedule](#)
- 1.3. [Datasheet](#)
- 1.4. [Circular Map of E. coli](#)
- 1.5. [The grades for your practical](#)

### 2. Bioinformatics

- 2.1. [Instructions](#)
- 2.2. [Bioinformatics tasks](#)
- 2.3. [Bioinformatics Website](#)
- 2.4. [Project allocations for Bioinformatics](#)

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Wet and dry labs  
all schedules and instructions  
are found here

Your location: [Course Content Home](#) > [Wet and dry labs - please print out files below](#) > [Bioinformatics](#) > [Bioinformatics Website](#)



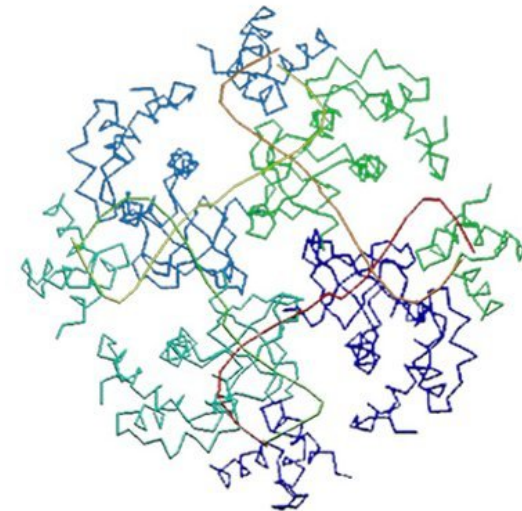
## Bacterial Genomics

On-line learning  
Additional Web-sites

GATC

Funded by:

**ltsn**  
Bioscience  
teaching  
development  
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October 2002



Background: *E. coli* RuvA tetramer, with bound DNA forming a Holliday junction

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# On-line discussion – assignment 3

Your location: [Course Content Home](#) > [On-line discussion](#) > [Genomics Papers](#)

## Genomics Papers

[Pseudomonas](#) (31 Messages / **31 New**)

[Salmonella](#) (40 Messages / **40 New**)

[Yersinia](#) (49 Messages / **49 New**)

[Helicobacter](#) (37 Messages / **37 New**)

[Rickettsia](#) (0 Messages)

[Campylobacter](#)

[Streptomyces](#)

[B. subtilis](#)

[B. anthracis](#)

Your location: [Course Content Home](#) > [On-line discussion](#) > [Genomics Papers](#) > [Yersinia](#)

### Yersinia

[Expand All](#) [Collapse All](#)

Display: [Threaded](#) [Unthreaded](#) [All](#) [Unread](#)

<input type="checkbox"/>	Subject	Messages	Author	Date
<input type="checkbox"/>	<a href="#">Instructions (New)</a>		Keil, Henry	13 March 2006 10:02 AM
<input type="checkbox"/>	<a href="#">Yersinia group (New)</a>	2 ( <b>2 Unread</b> )	IMACHUKWU, AMY	13 March 2006 7:16 PM
<input type="checkbox"/>	<a href="#">Some hints (New)</a>		Keil, Henry	14 March 2006 10:28 AM
<input type="checkbox"/>	<a href="#">lets make a start! (New)</a>	3 ( <b>3 Unread</b> )	TAYLOR, EMMA	15 March 2006 4:42 PM
<input type="checkbox"/>	<a href="#">new message (New)</a>		Keil, Henry	17 March 2006 3:30 PM
<input type="checkbox"/>	<a href="#">Insertion sequences?! (New)</a>		TAYLOR, EMMA	17 March 2006 7:36 PM
<input type="checkbox"/>	<a href="#">Genome Sequence (New)</a>	4 ( <b>4 Unread</b> )	TAVAKOLI, KHASHAYAR	17 March 2006 7:53 PM
<input type="checkbox"/>	<a href="#">response to ashi (New)</a>	2 ( <b>2 Unread</b> )	TURNER, KARA	18 March 2006 5:35 PM
<input type="checkbox"/>	<a href="#">ashis message (New)</a>		TURNER, KARA	18 March 2006 5:36 PM
<input type="checkbox"/>	<a href="#">Reminder guys (New)</a>		TAVAKOLI, KHASHAYAR	18 March 2006 6:07 PM

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## Genome sequence of *Yersinia pestis*, the causative agent of plague

J. Parkhill<sup>1</sup>, B. W. Wren<sup>2</sup>, N. R. Thomson<sup>3</sup>, R. W. Tibball<sup>4</sup>, M. T. G. Holden<sup>5</sup>, M. B. Prentice<sup>6</sup>, M. Sebatian<sup>7</sup>, K. D. James<sup>8</sup>, C. Churcher<sup>9</sup>, K. L. Mungall<sup>10</sup>, S. Baker<sup>11</sup>, D. Basham<sup>12</sup>, S. D. Bentley<sup>13</sup>, K. Brooks<sup>14</sup>, A. M. Cerdeño-Tarraga<sup>15</sup>, T. Chillingworth<sup>16</sup>, A. Croxin<sup>17</sup>, R. M. Davies<sup>18</sup>, P. Davis<sup>19</sup>, G. Dougan<sup>20</sup>, T. Feltwell<sup>21</sup>, H. Hamlin<sup>22</sup>, S. Holroyd<sup>23</sup>, K. Jagels<sup>24</sup>, A. V. Karlyshev<sup>25</sup>, S. Leather<sup>26</sup>, S. Moule<sup>27</sup>, P. C. F. Oyston<sup>28</sup>, M. Quail<sup>29</sup>, K. Rutherford<sup>30</sup>, M. Simmonds<sup>31</sup>, J. Skelton<sup>32</sup>, K. Stevens<sup>33</sup>, S. Whitehead<sup>34</sup> & B. G. Barrell<sup>1</sup>

<sup>1</sup> The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK

<sup>2</sup> Department of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, Keppel Street, London WC1E 7HT, UK

<sup>3</sup> Chemical and Biological Sciences, Durr Forton Down, Salisbury, Wiltshire SP4 0JQ, UK

<sup>4</sup> Department of Medical Microbiology, St Bartholomew's and the Royal London School of Medicine and Dentistry, London EC1A 7BE, UK

<sup>5</sup> Centre for Molecular Microbiology and Infection, Department of Biological Sciences, Imperial College of Science, Technology and Medicine, London SW7 2AZ, UK

The Gram-negative bacterium *Yersinia pestis* is the causative agent of the systemic invasive infectious disease classically

infected cat.

The general features of the genome are shown in Fig. 1 and Table 1. The most striking large-scale features in the genome are anomalies in GC bias. All bacterial genomes sequenced to date have a small but detectable bias towards G on the leading strand of the bidirectional replication fork<sup>5</sup>. Anomalies in this plot can be caused by the very recent acquisition of DNA (such as prophages) or by the inversion or translocation of blocks of DNA. The three anomalies visible in the *Y. pestis* plot (see Supplementary Information; see also [http://www.sanger.ac.uk/Projects/Y\\_pestis/](http://www.sanger.ac.uk/Projects/Y_pestis/)) are each bounded by insertion sequence elements, suggesting that they could be the result of recent recombination between these perfect repeats. To investigate this, we designed polymerase chain reaction (PCR) primers to test for the presence and absence of the predicted translocation, and for the orientation of the two inversions (see Supplementary Information). PCR confirmed the position of the translocation, but, intriguingly, the results for the two inversions showed that both orientations were present in the same DNA preparation, with the inverse orientation predominating. This suggests genomic rearrangement during growth of the organism. The results were similar in DNA from three different subcultures of CO92 and investigation of other strains indicated that similar rearrangements may have occurred (see Supplementary Information). These results demonstrate that the *Y. pestis* genome is fluid, and capable of frequent intragenomic recombination *in vitro*; the rapid emergence of new ribotypes of *Y. pestis* biovar Orientalis in the environment following pandemic spread<sup>7</sup> shows that chromosomal rearrangements are common *in vivo*. The effects of these rearrangements on the biology

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# Group presentations – assignment 4

## Presentations

1. [Guidelines to the Bacterial Genomics](#)
2. [Guidelines for MP4 file viewing](#)
3. [Pseudomonas](#)
  - 3.1. [Powerpoint Pseudomonas](#)
  - 3.2. [Pseudomonas video talk](#)
4. [Helicobacter](#)
  - 4.1. [Powerpoint Helicobacter](#)
  - 4.2. [Helicobacter video talk](#)
5. [Yersinia](#)

Your location: [Course Content Home](#) > [Presentations](#) > [Pseudomonas Article](#)

Acrobat Reader - [aeruginosa[1].pdf]

File Edit Document Tools View Window Help

117%

articles

## Complete genome sequence of *Pseudomonas aeruginosa*

## Pseudomonas Aeru

- **Opportunistic pathogen** – rarely infects healthy people.
- Ideal environment is the hospital
- In a survey conducted in the U.S. results showed :
  - 2<sup>nd</sup> most common cause of nosocomial pneumonia
  - 3<sup>rd</sup> most common cause of U.T.I.
  - 4<sup>th</sup> most common cause of surgical site infections.

WebCT - Mozilla Firefox

https://weblearn.brunel.ac.uk/webct/cobaltMainFrame.dowebct

Brnel UNIVERSITY WEST LONDON School of Health Sciences and Social Care

BB2403 Molecular and Cellular Biology - BB2403 2005-6 YEAR

Your location: [Course Content Home](#) > [Presentations, both oral and PP](#) > [Pseudomonas Talk](#)

pseudomonas

00:00:00

weblearn.brunel.ac.uk

# Online MCQs – assignment 5

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# Frequency of choices made

No. of assignments chosen	No. of students
1	5
2	11
3	42
4	15
5	1

*The relative frequency of choices made by the students taking part in the coursework activities. Students needed to take a minimum of two elements.*

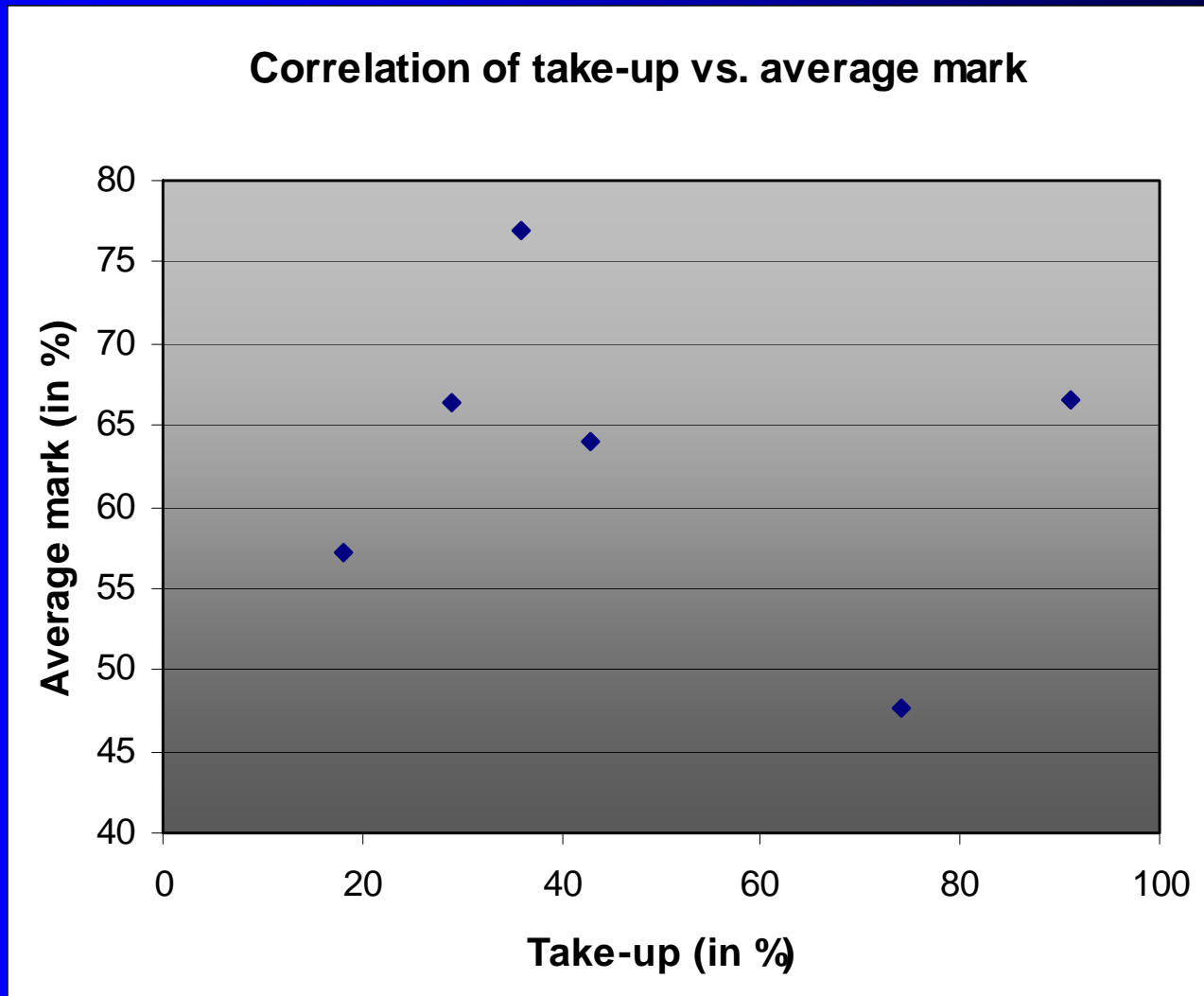
*Total no. of assignments: 218, i.e. 2.95 per student*

# Students' preferences and marks

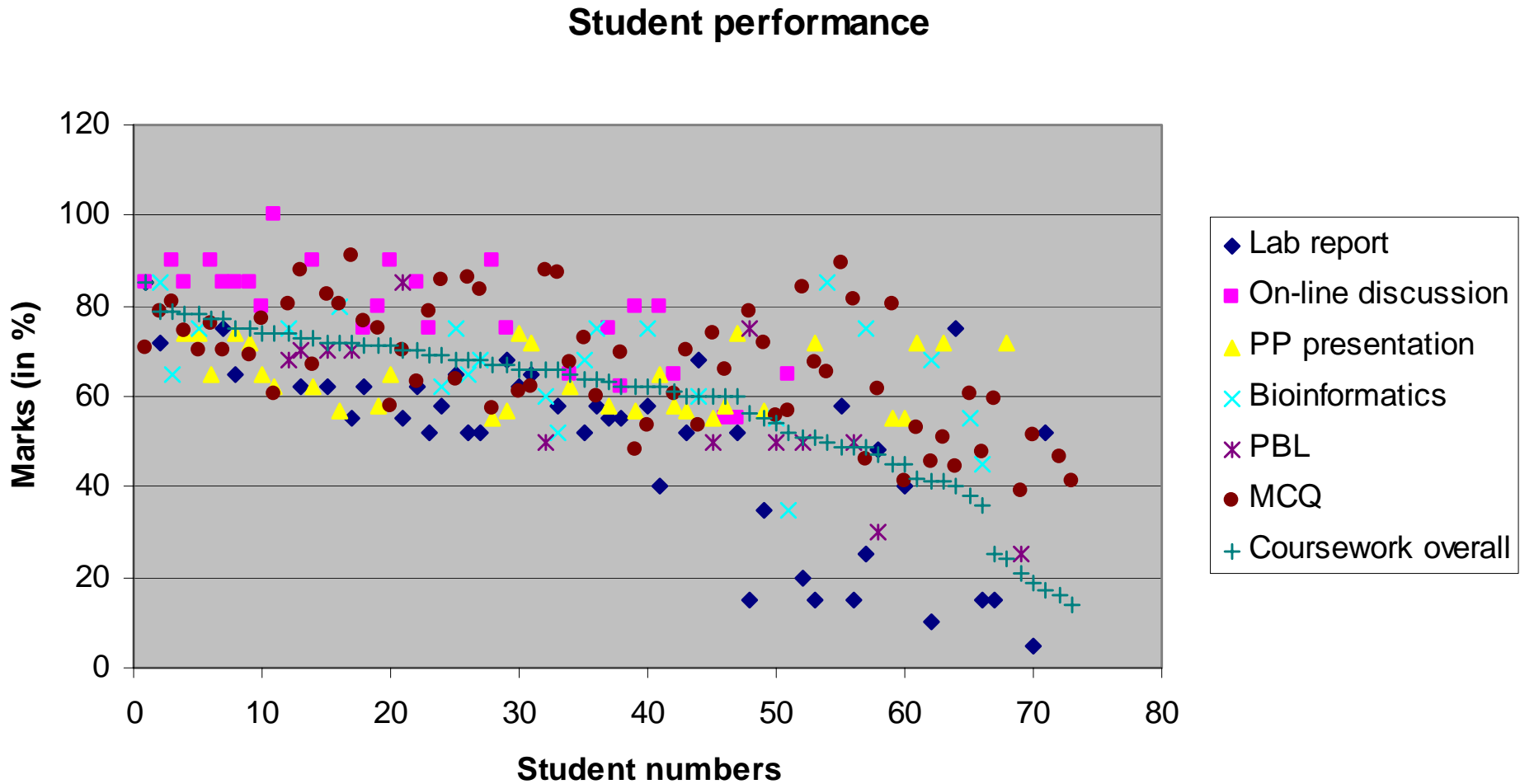
Category	% of class participating	Average mark	SD
Online MCQs	91	66.5	13.9
Laboratory report	74	47.7	19.6
PowerPoint presentation	43	64.0	7.2
Online discussion	36	77.0	12.5
Bioinformatics	29	66.3	12.6
Problem solving	18	57.3	17.6

*The proportion of students taking part in the coursework activities on offer and their respective average mark and standard deviations. The group work activities are highlighted in red.*

# Correlation between popularity of choice and average mark?

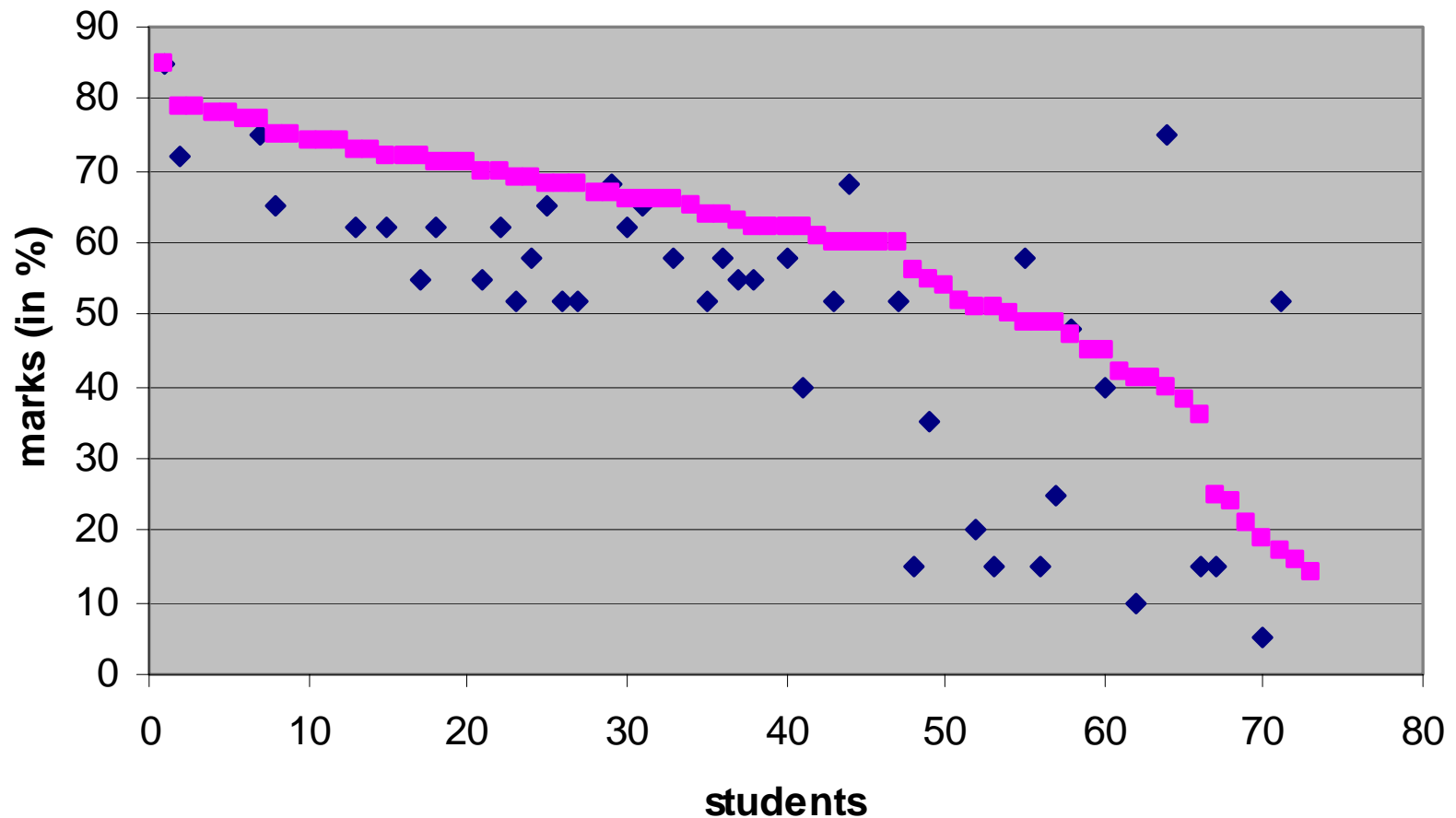


# Comparing the six assignments



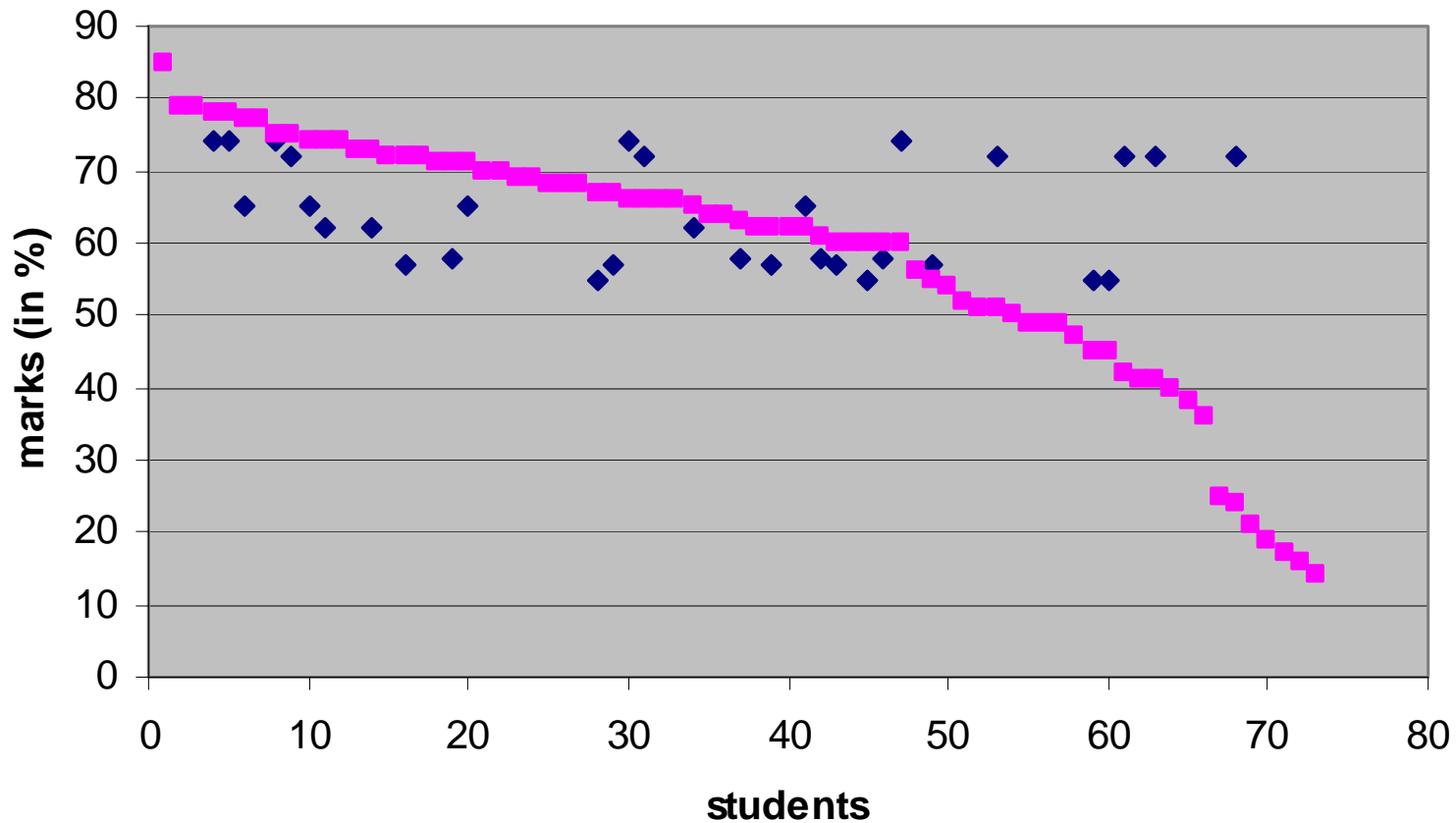
# Writing lab reports was challenging

Lab report vs coursework average



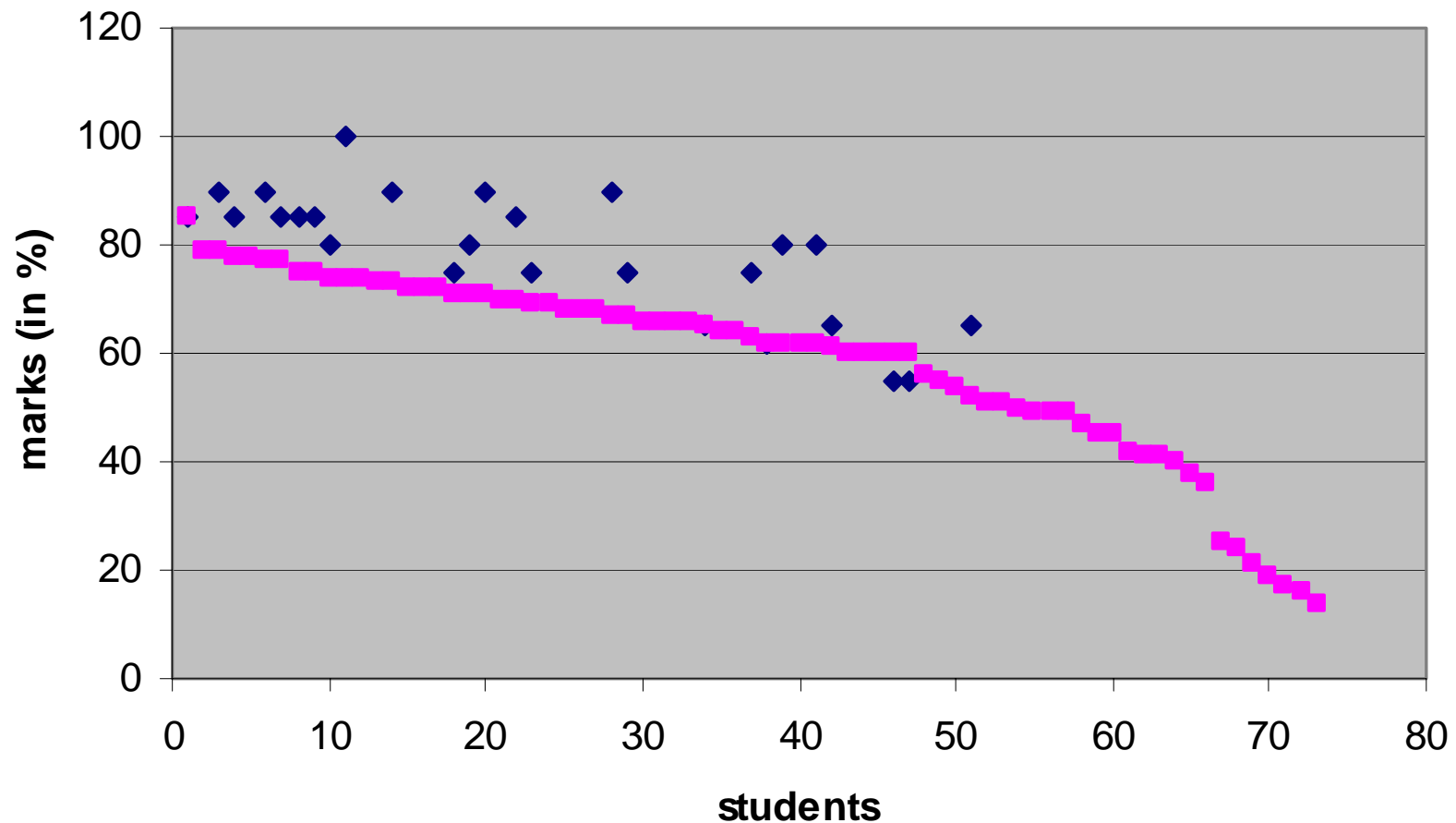
# Powerpoint presentation – the great leveller

Powerpoint vs coursework average



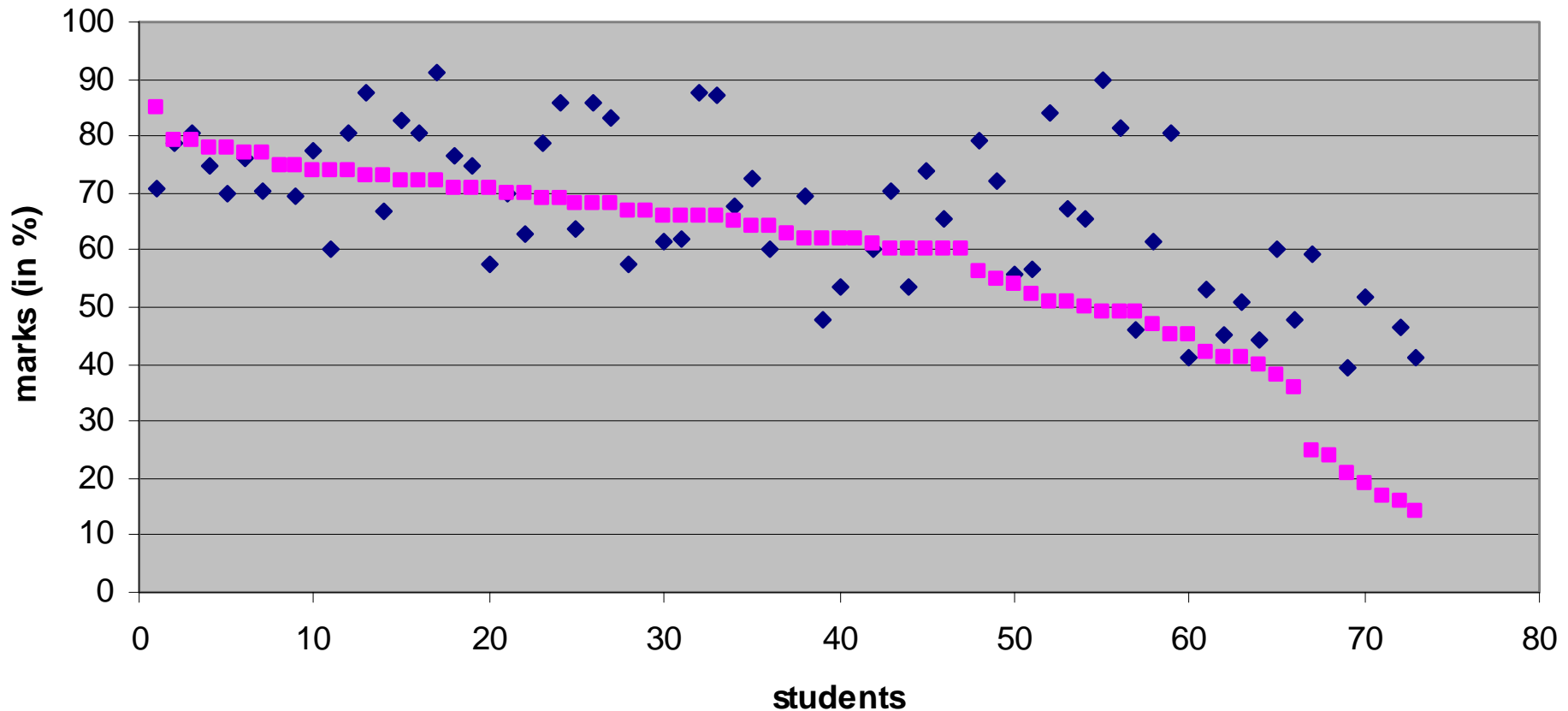
# Online discussion – preferred by good students

Online discussion vs coursework average

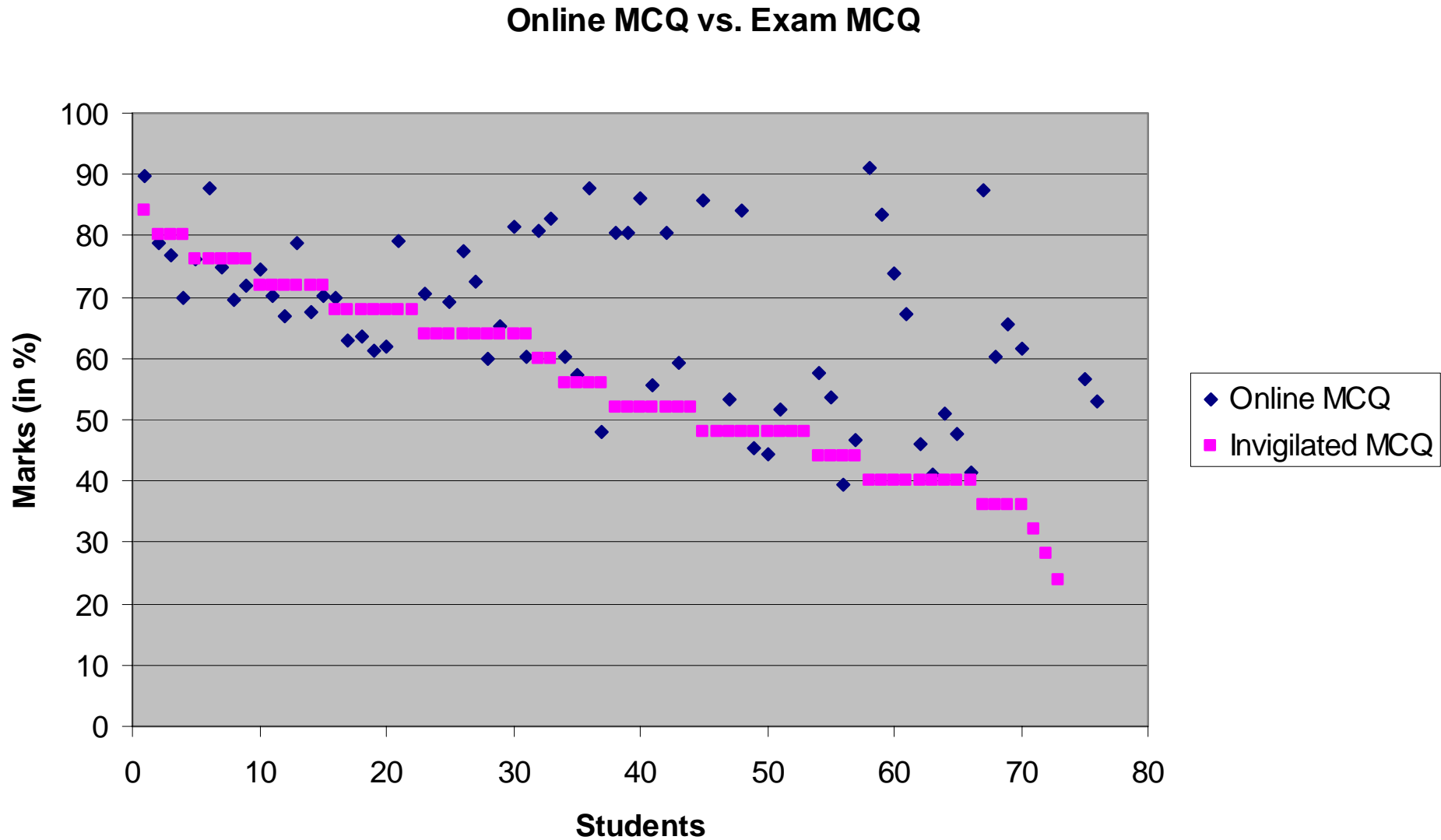


# Online MCQ – marks way above average

Online MCQ vs coursework average



# Poor correlation of online MCQ with exam MCQ



# Comparative student performance

Year of assessment	2003	2004	2005	2006
Overall coursework average	50.0	50.5	47.1	56.1
Failed coursework (%)	23	21	28	9

*Comparative student performance over the past four years; data from this study are highlighted in red.*

*Note that lab coursework on its own (2006) has an overall average of 47.7%*

*Numbers based on lab-report only*

# Conclusion - 1

- The element of choice was exercised by a vast majority of students
- Marking involves the equivalent of **two medium length lab reports**
- The number of failed coursework has more than halved
- Choice helps to cater for students' different learning styles – academically strong students take advantage of extra option(s) to increase overall mark – see Online Discussion

# Conclusions 2

- The online MCQ was used by academically weaker students as an 'insurance activity' towards the end of the assessment period; however there is suspicion of collusion
- Omitting the online MCQ from the calculation reduces the overall coursework average from **56.1 to 55%**
- As expected the award of group marks in the PowerPoint presentation had a levelling effect on student assessment
- The lab exercise showed the poorest overall student performance (and highest SD)

# Possible improvements

- To increase fairness the on-line MCQ assessment should either be invigilated or else be used in formative assessment only
- Informal student feedback suggested that for the credit value given a format for the **best two out of four/five** was preferable
- Some refinements to increase discriminatory effect in Powerpoint presentation may be required

# **Pros & Cons of 'A La Carte' Provision**

- **Putting students in control of their learning – better learning experience**
- **More flexibility in course provision as most assignments do not require a physical presence of students**
- **Improvement in overall average mark profile**
- **Fewer resit assessments**

# **Pros & Cons** of 'A La Carte' Provision

- **Comparability of assessment?**
- **Are learning outcomes adequately specified – skills profile?**
- **Extra time required to create additional assignments**
- **Good organisational skills required to keep track of activities**

# Way Forward

- Initially extra options may be added over time starting with a simpler format (**one out of two**)
- For higher level credit modules range of choices may be different (**three out of seven?**)
- Extra e-learning elements to be added could include student blogging, collaborative authoring using Wikis, project work in online 'virtual worlds', podcasting, webinars etc