

AIMMS Workshop Active Learning

Software tools for active learning

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Which software tools do you already use during your education?

- **Multiple Choice and Open Ended**
 - **Website: [menti.com](https://www.menti.com)**
 - **Code: 39 30 82**



Which software tools do you already use during your education?

Answers:

- A) Student response tool (Mentimeter, GoSoapBox, Socrative, Kahoot, etc.)
- B) Canvas tools (quizzes, assignments, etc.)
- C) Feedback tools (Turnitin, FeedbackFruits, etc.)
- D) Video (YouTube, weblecture, slidecast, kennisclips, etc.)
- E) Plagiarism check (Turnitin, etc.)
- F) Other tools (Perusall, etc.)
- G) I don't use software tools during my education

→ **menti.com – code: 39 30 82**



Activating students using tools

Inside contact hours

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➤ To



Outside contact hours





Activating students using tools

Inside contact hours

- Start: checking prior knowledge
- During: break and testing
- End: self-assessment and testing

➤ Tool: Mentimeter

Outside contact hours

- Assignments
- Feedback

➤ Tools: Turnitin & Feedbackfruits



Advantages of Mentimeter

- + Available for VU employees
 - <https://tinyurl.com/vumentimeter>
- + Browser-based (mobile devices)
- + Many possible question types:



Advantages of Mentimeter

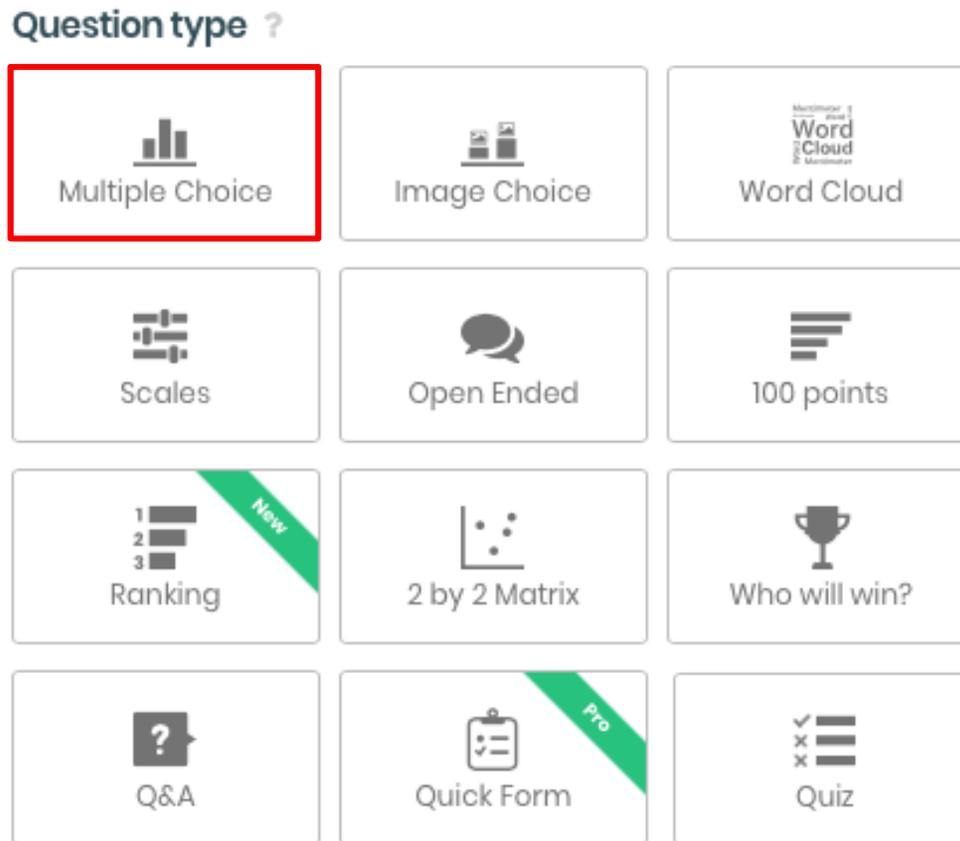
Question type ?

 Multiple Choice	 Image Choice	 Word Cloud
 Scales	 Open Ended	 100 points
 Ranking	 2 by 2 Matrix	 Who will win?
 Q&A	 Quick Form	 Quiz



Mentimeter – multiple choice

Testing (prior) knowledge, self-assessment, etc



Multiple choice results

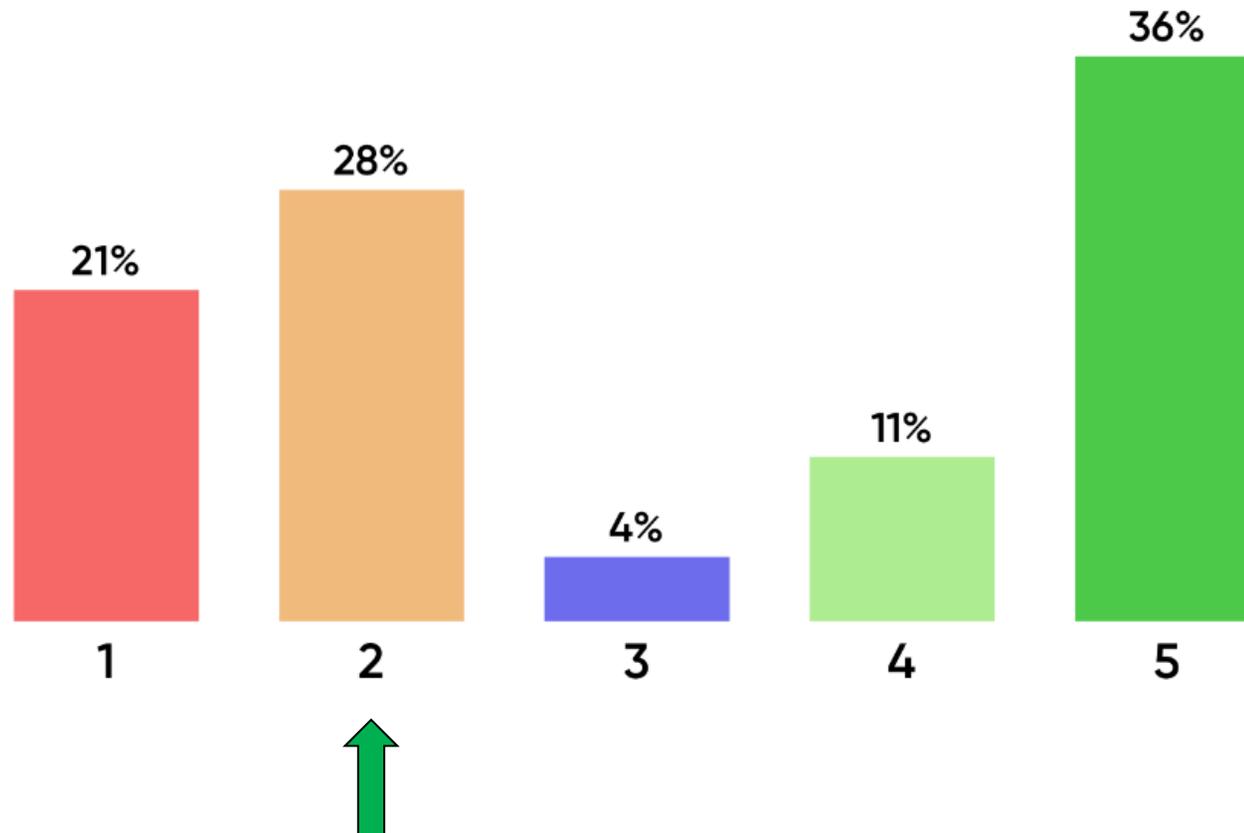
- “Which software tools do you already use during your education?”
- www.mentimeter.com





Example Cellular Biochemistry

Which of the following proteins take part in post-transcriptional gene expression regulation?



Mentimeter – open ended

Open ended

– Answers, opinions, etc

Question type ?

 Multiple Choice	 Image Choice	 Word Cloud
 Scales	 Open Ended	 100 points
 Ranking	 2 by 2 Matrix	 Who will win?
 Q&A	 Quick Form	 Quiz



Results open ended question

- “Specify your answer: which software tools do you already use during education?”
- www.mentimeter.com



Mentimeter – all tools

Question type ?

 Multiple Choice	 Image Choice	 Word Cloud
 Scales	 Open Ended	 100 points
 Ranking <i>New</i>	 2 by 2 Matrix	 Who will win?
 Q&A	 Quick Form <i>Pro</i>	 Quiz





Activating students using tools

Inside contact hours

- Start: checking prior knowledge
- During: break and testing
- End: self-assessment and testing

➤ Tool: Mentimeter

Outside contact hours

- Assignments
- Feedback

➤ Tools: Turnitin & Feedbackfruits



Turnitin

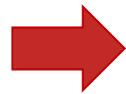
Canvas plugin for feedback/plagiarism

- Centralizing submission and feedback



Making a Turnitin assignment

- Home
- Announcements
- Syllabus
- Modules
- Assignments**
- Grades
- People
- Collaborations



+ Assignment



Submission type

External tool

External Tool Options

Enter or find an external tool URL



Load this tool in a new tab

Manual: <https://tinyurl.com/manuallyturnitin>



Turnitin inbox

Overview of all submissions

Assignment Inbox								Helpdesk	Settings
Search								Download All	Download Selected
<input type="checkbox"/> Author	Paper Title	Paper ID	Uploaded	Viewed	Grade	Similarity	Options		
		979951962	Jul 2nd 2018, 12:37 PM CEST		57	2%	...		
		979758083	Jul 1st 2018, 11:47 PM CEST		51	9%	...		
		979757839	Jul 1st 2018, 11:46 PM CEST		50	13%	...		
		979746262	Jul 1st 2018, 10:54 PM CEST		56	11%	...		
		979743560	Jul 1st 2018, 10:42 PM CEST		66	25%	...		
		979742723	Jul 1st 2018, 10:38 PM CEST		56	58%	...		
		979741597	Jul 1st 2018, 10:33 PM CEST		65	21%	...		



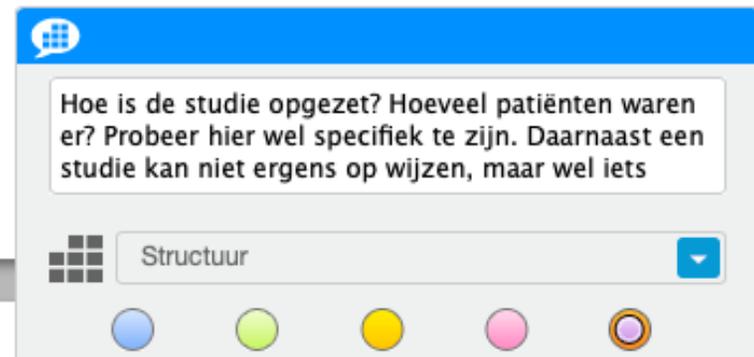
Giving feedback in Turnitin



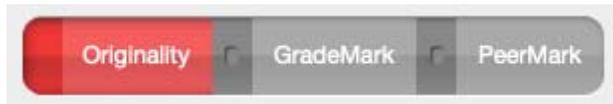
Vele traditionele NSAID's zijn non-selectieve COX-remmers en de ontwikkeling van COX-2 remmers is in volle gang.¹¹ De eerste geïdentificeerde COX-2 selectieve verbindingen waren DuP697 en NS-398. Ondanks dat de ontwikkeling van deze selectieve COX-2 remmers stakte, diende de structuur van DuP679 als een startpunt voor de synthese voor de selectieve remmers.

een geringe hoeveelheid van celecoxib en naproxen.^{2, 13} In een ander onderzoek bij 655 patiënten, blijken celecoxib 2 dd 200 mg en diclofenac 2 dd 75 mg even effectief te zijn.¹⁴

Celecoxib heeft minder gastro-intestinale bijwerkingen.¹³ Endoscopische studies hebben erop gewezen dat celecoxib in vergelijking met een placebo, bij een toxische dosis, geen verschillen oplevert in de maagirritaties. In de



Plagiarism check in Turnitin



Frequentie	Bijwerkingen
Ze er vaak (> 10%)	Hoofdpijn, misselijkheid, braken, diarree, dyspepsie, buikpijn. Periorbitaal oedeem, huiduitslag (o.a. dermatitis en eczeem). Spierspasme en -kramp, spierpijn, gewrichtspijn, botpijn. Vermoeidheid, vochtretentie, gewichtstoename.
Va ak (1-10%)	Duizeligheid, smaakstoornis, hypo-esthesie. slapeloosheid. Anorexie, droge mond, gastro-oesofageale reflux, gastritis,



FeedbackFruits

- Integrated in canvas
- User-friendly & consistent interface
- Facilitates active learning



Interactive study material

-  Interactive Documents
-  Interactive Videos
-  Interactive Audio
-  Comprehension of Documents

Teacher feedback

-  Assignment Feedback
-  Skill Feedback

Peer learning

-  Peer Feedback
-  Group Member Evaluation





Metabolic and Genetic Control of gene expression on a genomic scale

UNFOCUS 1 Annotations

Fischer-Vize, *Science* **270**, 1528 (1995).
 35. T. C. James and S. C. Egin, *Mol. Cell Biol.* **6**, 3962 (1986); R. Paro and D. S. Hogness, *Proc. Natl. Acad. Sci. U.S.A.* **88**, 263 (1991); B. Tschiersch et al., *EMBO J.* **13**, 3522 (1994); M. T. Madred et al., *Cell* **87**, 75 (1993); D. G. Shales, K. D. Tartof, R. P. Perry, *Proc. Natl. Acad. Sci. U.S.A.* **90**, 7137 (1993).
 36. P. M. Palosari et al., *J. Biol. Chem.* **266**, 10750 (1991); A. Schmitz, K. H. Gartmann, J. Fiedler, E.

Grund, R. Eichenlaub, *Appl. Environ. Microbiol.* **58**, 4338 (1992); V. Sharma, K. Suvarna, R. Meganathan, M. E. Hudspeth, *J. Bacteriol.* **174**, 5057 (1992); M. Kanazawa et al., *Enzyme Protein* **47**, 9 (1993); Z. L. Boynton, G. N. Bonnet, F. B. Rudolph, *J. Bacteriol.* **176**, 3015 (1994).
 37. M. Ho et al., *Cell* **77**, 869 (1994).
 38. W. Hendriks et al., *J. Cell Biochem.* **59**, 418 (1995).
 39. We thank H. Skaletsky and F. Lewitter for help with

sequence analysis; Lawrence Livermore National Laboratory for the low-sorted Y control library; and P. Blair, A. Borvin, A. de la Chapelle, G. Fink, K. Jegalan, T. Kawaiuchi, E. Lander, H. Lodish, P. Matsudaira, D. Merke, U. RajBhandary, R. Reijo, S. Rozan, A. Schwartz, G. Sun, and C. Tillyard for comments on the manuscript. Supported by NIH.
 28 April 1997; accepted 9 September 1997

Exploring the Metabolic and Genetic Control of Gene Expression on a Genomic Scale

Joseph L. DeRisi, Vishwanath R. Iyer, Patrick O. Brown*

DNA microarrays containing virtually every gene of *Saccharomyces cerevisiae* were used to carry out a comprehensive investigation of the temporal program of gene expression accompanying the metabolic shift from fermentation to respiration. The expression profiles observed for genes with known metabolic functions pointed to features of the metabolic reprogramming that occur during the diauxic shift, and the expression patterns of many previously uncharacterized genes provided clues to their possible functions. The same DNA microarrays were also used to identify genes whose expression was affected by deletion of the transcriptional co-repressor *TUP1* or overexpression of the transcriptional activator *YAP1*. These results demonstrate the feasibility and utility of this approach to genomewide exploration of gene expression patterns.

The complete sequences of nearly a dozen microbial genomes are known, and in the next several years we expect to know the complete genome sequences of several metazoans, including the human genome. Defining the role of each gene in these genomes will be a formidable task, and understanding how the genome functions as a whole in the complex natural history of a living organism presents an even greater challenge.

Knowing when and where a gene is expressed often provides a strong clue as to its biological role. Conversely, the pattern of genes expressed in a cell can provide detailed information about its state. Although regulation of protein abundance in a cell is by no means accomplished solely by regulation of mRNA, virtually all differences in cell type or state are correlated with changes in the mRNA levels of many genes. This is fortuitous because the only specific reagent required to measure the abundance of the mRNA for a specific gene is a cDNA sequence. DNA microarrays, consisting of thousands of individual gene sequences printed in a high-density array on a glass microscope slide (1, 2), provide a practical and economical tool for studying gene expression on a very large scale (3–6).

Saccharomyces cerevisiae is an especially

favorable organism in which to conduct a systematic investigation of gene expression. The genes are easy to recognize in the genome sequence, cis regulatory elements are generally compact and close to the transcription units, much is already known about its genetic regulatory mechanisms, and a powerful set of tools is available for its analysis.

A recurring cycle in the natural history of yeast involves a shift from anaerobic (fermentation) to aerobic (respiration) metabolism. Inoculation of yeast into a medium rich in sugar is followed by rapid growth fueled by fermentation, with the production of ethanol. When the fermentable sugar is exhausted, the yeast cells turn to ethanol as a carbon source for aerobic growth. This switch from anaerobic growth to aerobic respiration upon depletion of glucose, referred to as the diauxic shift, is correlated with widespread changes in the expression of genes involved in fundamental cellular processes such as carbon metabolism, protein synthesis, and carbohydrate storage (7). We used DNA microarrays to characterize the changes in gene expression that take place during this process for nearly the entire genome, and to investigate the genetic circuitry that regulates and executes this program.

Yeast open reading frames (ORFs) were amplified by the polymerase chain reaction (PCR), with a commercially available set of primer pairs (8). DNA microarrays, containing approximately 6400 distinct DNA sequences, were printed onto glass slides by

using a simple robotic printing device (9). Cells from an exponentially growing culture of yeast were inoculated into fresh medium and grown at 30°C for 21 hours. After an initial 9 hours of growth, samples were harvested at seven successive 2-hour intervals, and mRNA was isolated (10). Fluorescently labeled cDNA was prepared by reverse transcription in the presence of Cy3(green)- or Cy5(red)-labeled deoxyuridine triphosphate (dUTP) (11) and then hybridized to the microarrays (12). To maximize the reliability with which changes in expression levels could be discerned, we labeled cDNA prepared from cells at each successive time point with Cy5, then mixed it with a Cy3-labeled "reference" cDNA sample prepared from cells harvested at the first interval after inoculation. In this experimental design, the relative fluorescence intensity measured for the Cy3 and Cy5 fluor at each array element provides a reliable measure of the relative abundance of the corresponding mRNA in the two cell populations (Fig. 1). Data from the series of seven samples (Fig. 2), consisting of more than 43,000 expression-ratio measurements, were organized into a database to facilitate efficient exploration and analysis of the results. This database is publicly available on the Internet (13).

During exponential growth in glucose-rich medium, the global pattern of gene expression was remarkably stable. Indeed, when gene expression patterns between the first two cell samples (harvested at a 2-hour interval) were compared, mRNA levels differed by a factor of 2 or more for only 19 genes (0.3%), and the largest of these differences was only 2.7-fold (14). However, as glucose was progressively depleted from the growth media during the course of the experiment, a marked change was seen in the global pattern of gene expression. mRNA levels for approximately 710 genes were induced by a factor of at least 2, and the mRNA levels for approximately 1030 genes declined by a factor of at least 2. Messenger RNA levels for 183 genes increased by a factor of at least 4, and mRNA levels for 203 genes diminished by a factor of at least 4. About half of these differentially expressed genes have no currently recognized function and are not yet named. Indeed, more than 400 of the differentially expressed genes have no apparent homology

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Practice moment Required

Are you required to open data you gather in science to everyone?

Practice moment

What other mechanisms regulate protein levels?

Rachida Wahid a year ago

Doesn't whole genome te...

Sorted on location

1

Tiago Araújo (Teacher) 5 months ago

Are you required to open data you gather in science to everyone?

Lara Wilkens a year ago

What other mechanisms regulate protein levels?

Rachida Wahid a year ago

Doesn't whole genome testing require multiple testing correction in statistics?

If you look at the whole genome the chance th...

Chris Colin a year ago

Previously unknown responses with a novel method

If you find previously unknown responses with...

Joshua Weber a year ago

Is it standard procedure to couple mRNA levels to the metabolic state?

I saw plenty of papers that dont do this, while...

Chris Colin a year ago

unusable results?

In the picture you see that two of them have a vague yellow blur on them. this yellow blur co...

Lara Wilkens a year ago

regulating ribosomal activity by genetic modification

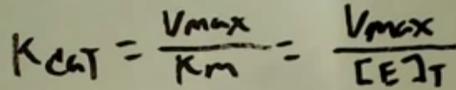
So if you would induce Rap1 in your cel cultur...



Interactive video



← Interactive Video - Calculating enzyme effi... [] FOCUS ^ 2 ⋮



6. Consider the following reaction information about substrate S:

Reaction	Enzyme	K _m	V _{max}
S → P	A	50 mM	100 nM/s
S → Q	B	5 mM	120 nM/s

A reaction is carried out with 100 μM S in a mixture containing equivalent amounts of enzymes A and B. After 1 minute, which product will be more abundant, P or Q? Explain your answer.

Practice moment Required

What is this formula related to?

$$v_0 = \frac{V_{max}[S]}{K_M + [S]}$$

SHOW

1:33 11:07

← Practice question ⋮

Multiple choice question

What is this formula related to?

$$v_0 = \frac{V_{max}[S]}{K_M + [S]}$$

Correct

enzymes (K_m) 1

substrate concentration (V_{max}) 0



Overview for the teacher

Overall student progress

4 out of 11

students have started viewing

55 %

average amount of correct practice questions

20

comments in total

^ Statistics per active student

	Viewed	Marked as done	Practice questions correct	Total comments
 Lara Wilkens	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	25% 0.5/2	6
 Chris Colin	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	50% 1/2	4
 Joshua Weber	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	55% 1.667/3	5
 Rachida Wahid	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	77% 2.333/3	5

← Practice question
⋮

Open question

Managing quality: under which of the 5 functions does this decision fall?

Student answers

Correct	2
Almost	0
Wrong	0





Feedback tools

- **(Peer) Feedback including reflection**
 - + Critical thinking & self-reflection
 - + Students can learn from each other's work
 - + Improve quality of final draft
- **Feedback plugins**
 - + Simple interface
 - + Process guidance & automation
 - + Group & individual assignments

Peer learning



Peer Feedback



Group Member Evaluation

Teacher feedback



Assignment Feedback



Skill Feedback

Using FeedbackFruits

- **Implementation & testing: Jun-Dec 2019**
- **Roll out over faculty: End '19 / start '20**



Activating tools

- Use these tools to:
 - Have students come better prepared to lectures
 - Activate them during and after lectures
- Enables to make (small) changes to your course
- Do you want to:
 - Be updated on FeedbackFruits?
 - Use a tool and want (technical) help?

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Do you have any questions?

Do you envision using these tools?

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