E-Learning in Bioinformatics

vs.

What I find problematic …


TMZ.com

- 1.5h lectures too long
- mixed audience
- booooring …
  - too elementary
  - same content every year
- no time for discussion / deeper understanding

A possible solution

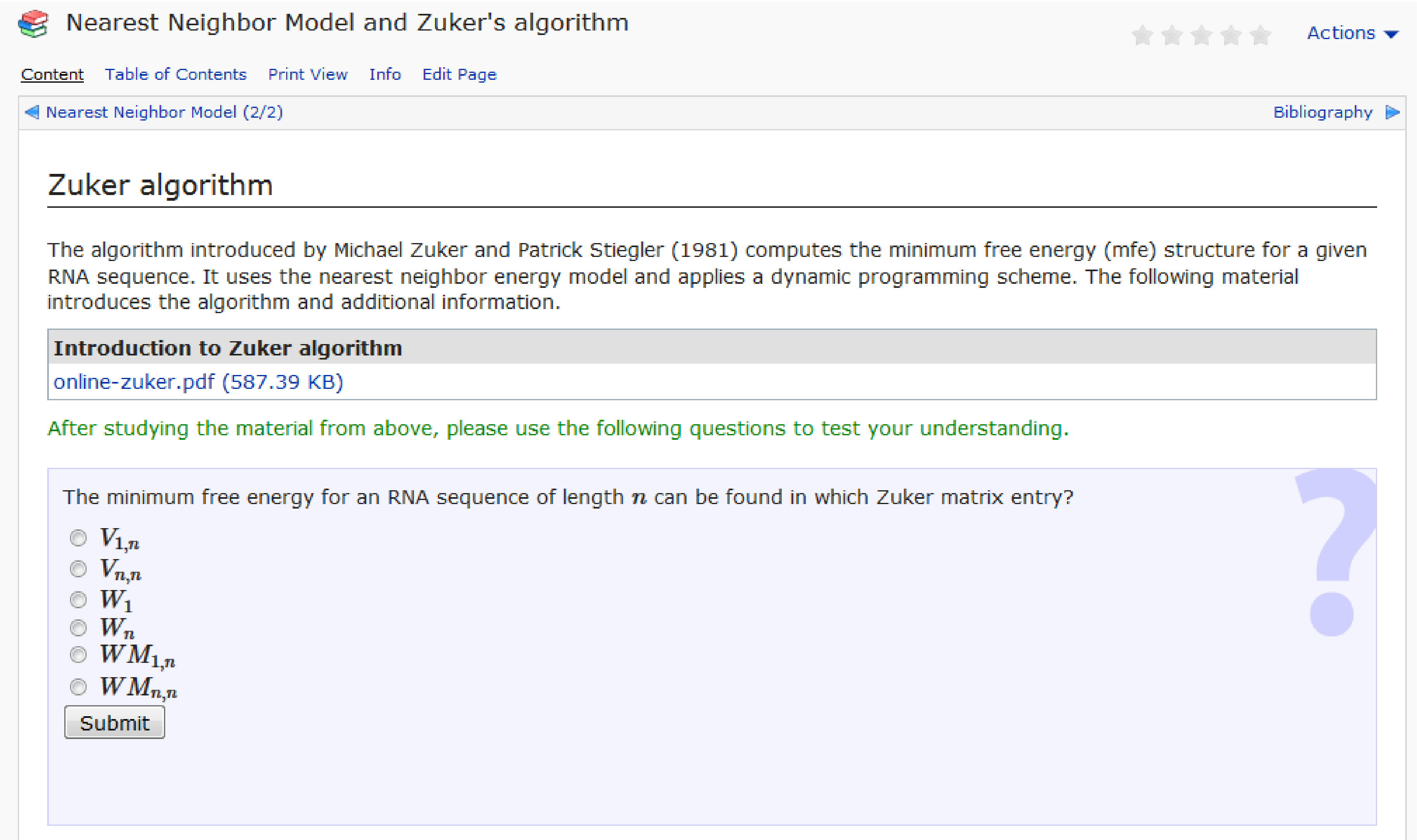
- Blended learning = mix presence + e-learning
- Flipped classroom
  - Lecture content via selfstudy
  - Lecture = discussion meeting

- Advantageous:
  - E-Learning modules + learning self control
  - Enforced proof of learning progress

Our E-Learning modules

- E-Learning modules
  - Content (slides, text, pics, video, …)
  - Self tests
  - Linking to additional material
- Usable for
  - Bachelor/Master courses
  - PhD specialization support
  - Promotion of **YOUR** algorithm

Example



Zuker algorithm

The algorithm introduced by Michael Zuker and Patrick Stiegler (1981) computes the minimum free energy (mfe) structure for a given RNA sequence. It uses the nearest neighbor energy model and applies a dynamic programming scheme. The following material introduces the algorithm and additional information.

Introduction to Zuker algorithm
online-zuker.pdf (587.39 KB)

After studying the material from above, please use the following questions to test your understanding.

The minimum free energy for an RNA sequence of length n can be found in which Zuker matrix entry?

○ $V_{1,n}$
○ $V_{n,n}$
○ W_1
○ W_n
○ $WM_{1,n}$
○ $WM_{n,n}$

What I would like to have …

- Course = combination of „normal“ lectures and flipped classroom events

- Collection of Bioinf E-Learning modules
- Public
- Collaboration + external contributions/use
  - Contribution to our stuff
  - Access to external stuff

Thanks