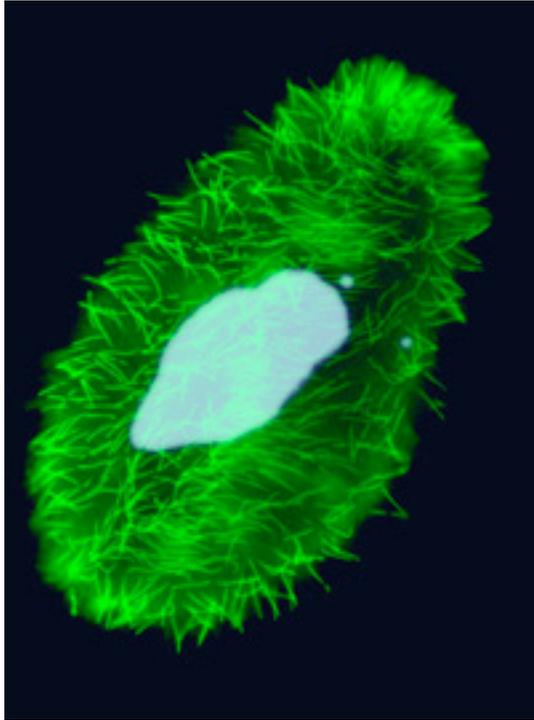


Paramecium tetraurelia somatic genome



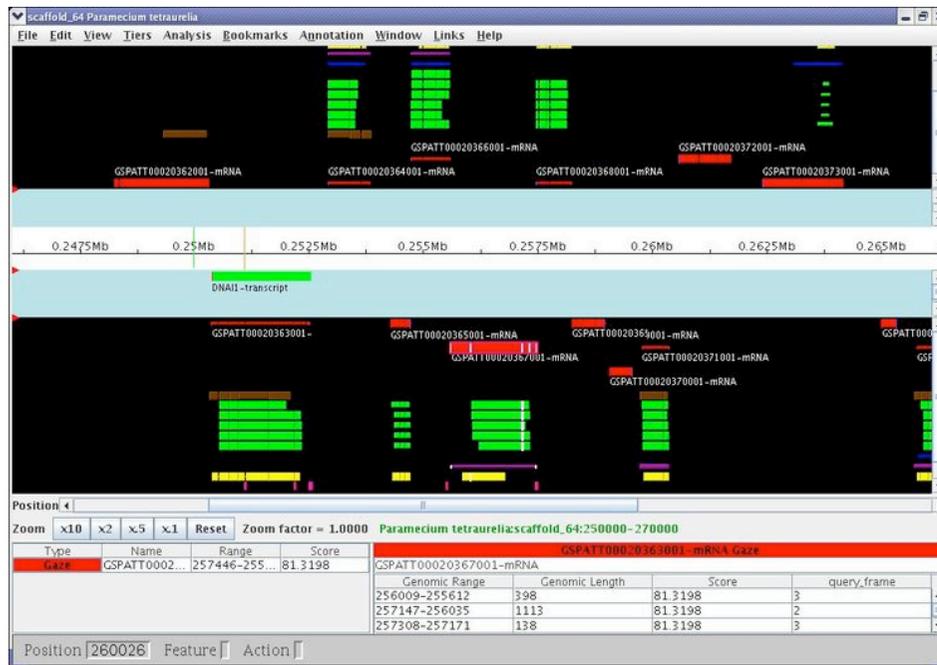
- 72 Mb
- 39,642 gene models
- 2.3 introns per gene
- < 15 Paramecium labs in the world
- ParameciumDB = 1 developer + PI

- at least 3 WGD; many gene families
- 12,026 pairs of paralogs from the most recent WGD, with same gene structure (information not used by the Genoscope annotation pipeline)

problematic genes

- 12,129 computationally identified potential errors (tagged)
 - Presence of an indel (assembly artefact)
 - Difference in gene size or structure between paralogs of recent whole genome duplication
- errors identified by biologists studying particular genes

non-generic ParameciumDB stuff

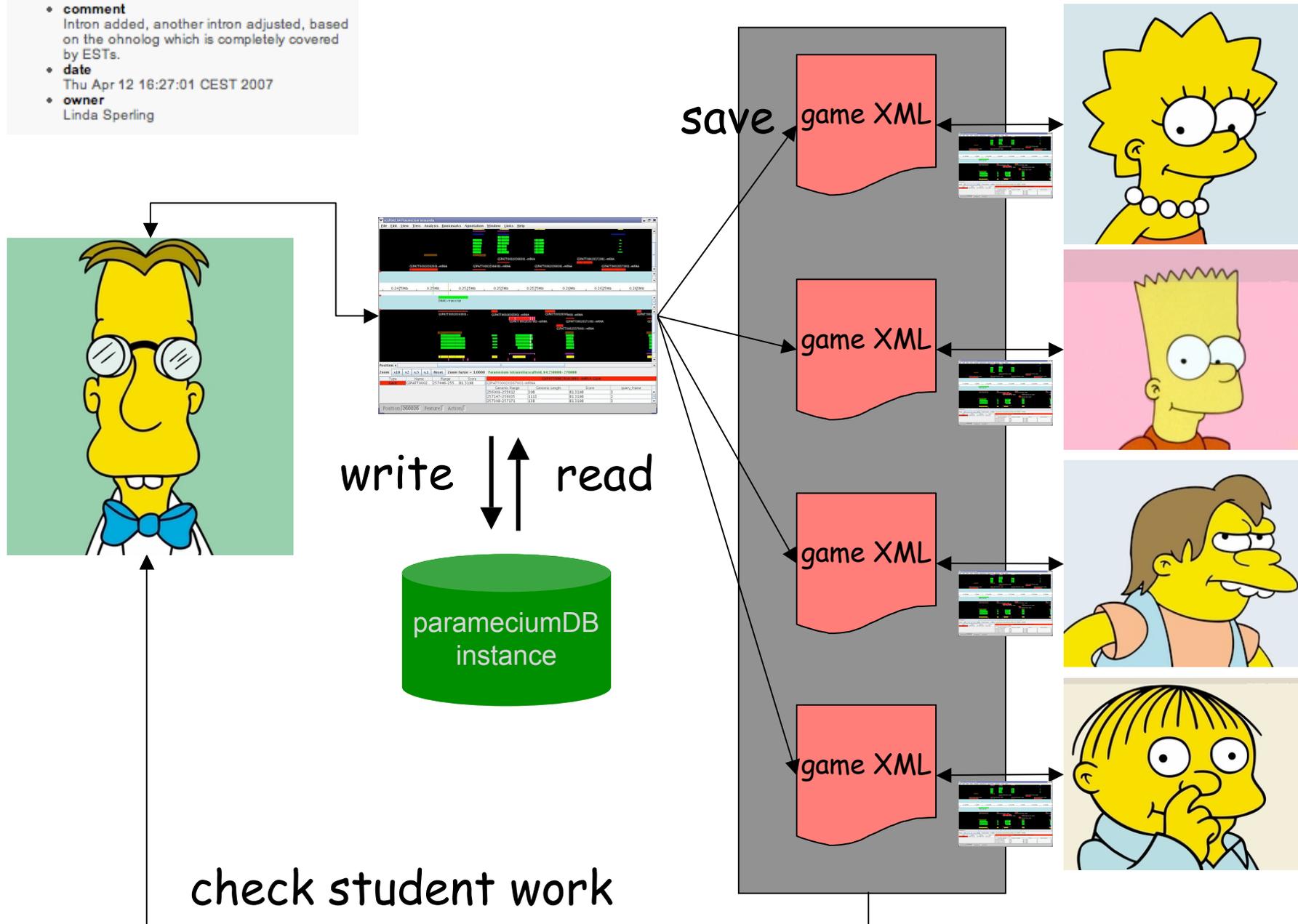


- temporary ID generated as soon as annot is created
- nightly script gives the « permanent » ID
- Genoscope annotations kept as evidence (black zone)
- annotators cannot modify or delete each others annotations

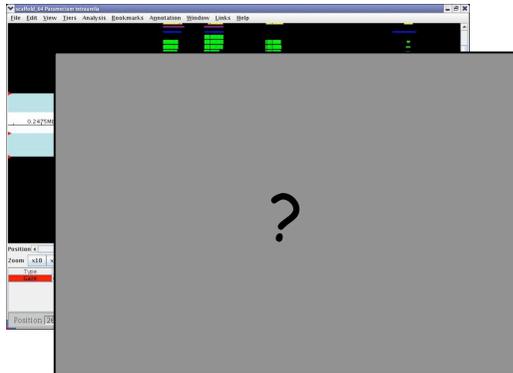
Classroom annotation

Properties

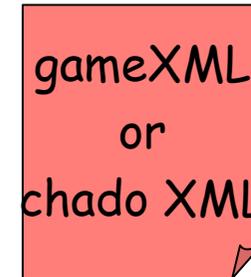
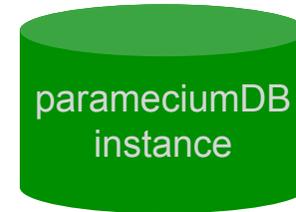
- **comment**
Intron added, another intron adjusted, based on the ohnolog which is completely covered by ESTs.
- **date**
Thu Apr 12 16:27:01 CEST 2007
- **owner**
Linda Sperling



adding functional annotation to Apollo ?



save



Add

- GO terms
- with evidence codes
- with publication references

Use

- phenote expertise to craft a plugin ?
- the improved GFF3 adaptor ? (obo-edit parsers)



credits



developers

Olivier Arnaiz

Scott Cain

Mark Gibson

Jonathan Crabtree

curators

Jean Cohen, CNRS Gif

Dean Fraga, Wooster College

Wei-Jen Chang, Hamilton College

