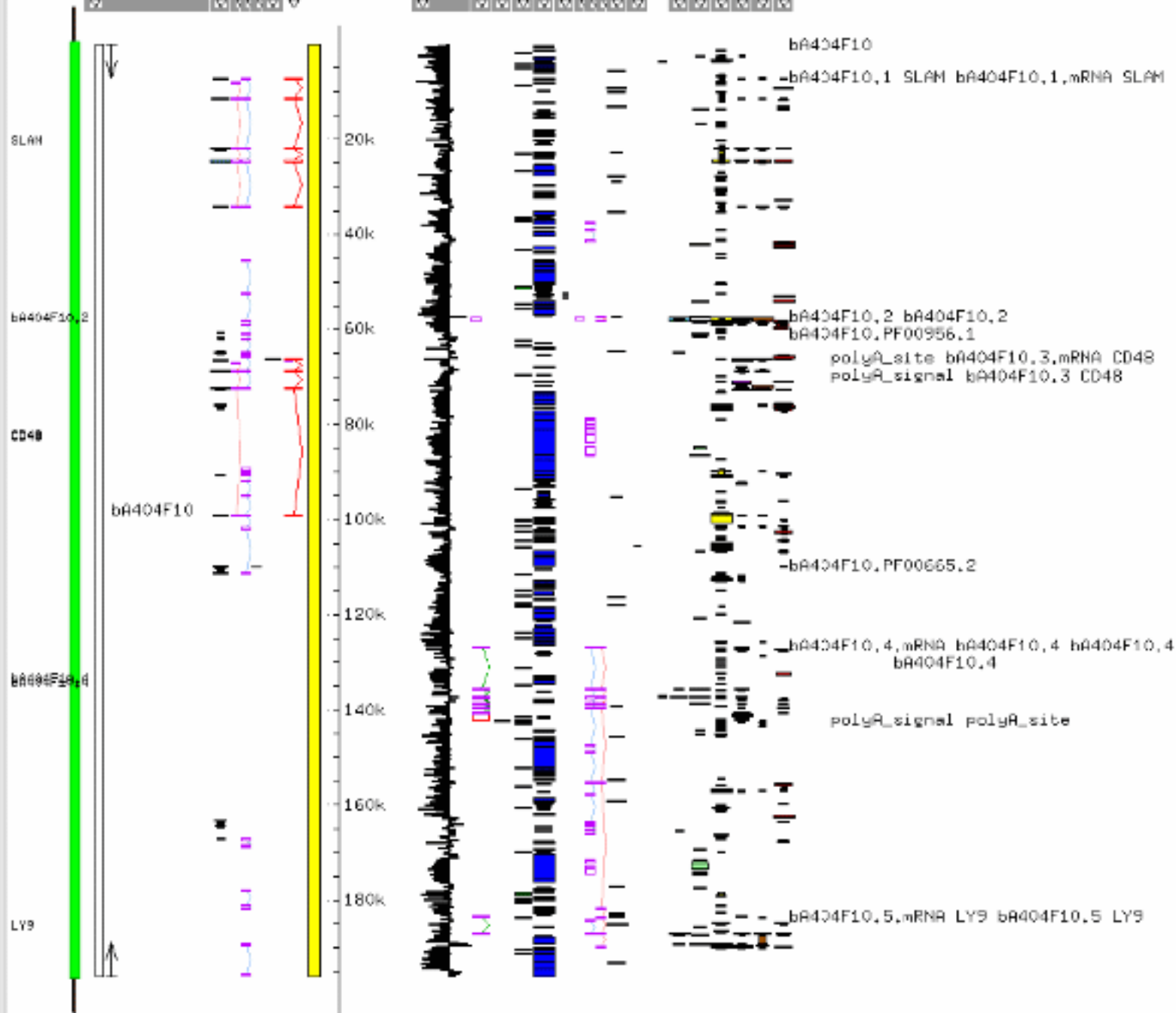


Rob Clack

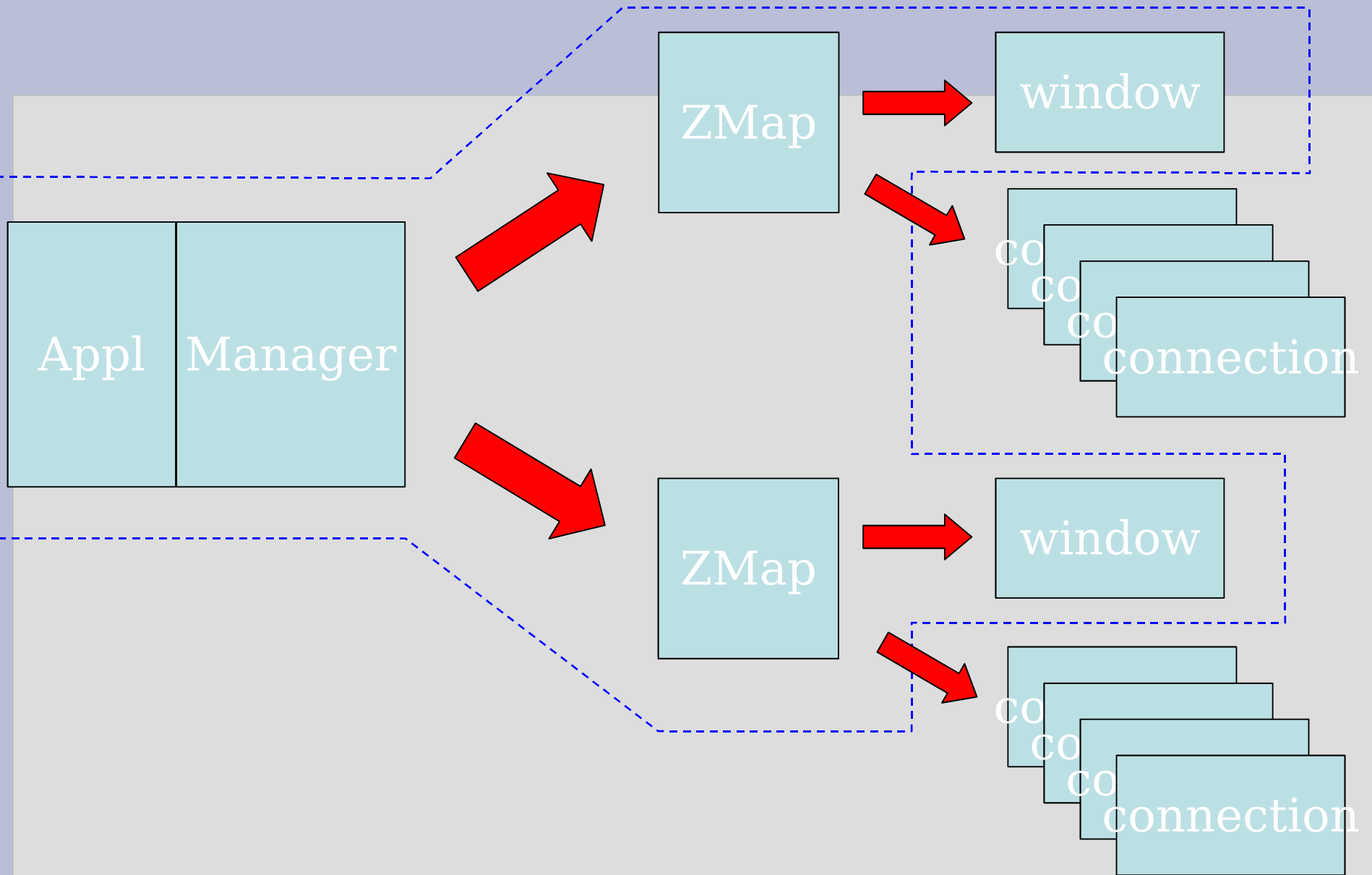
Wellcome Trust Sanger Institute  
Hinxton, near Cambridge

AceDB Development Team

NB text of talk is in 2 extra slides at the  
end



# ZMap and Threads



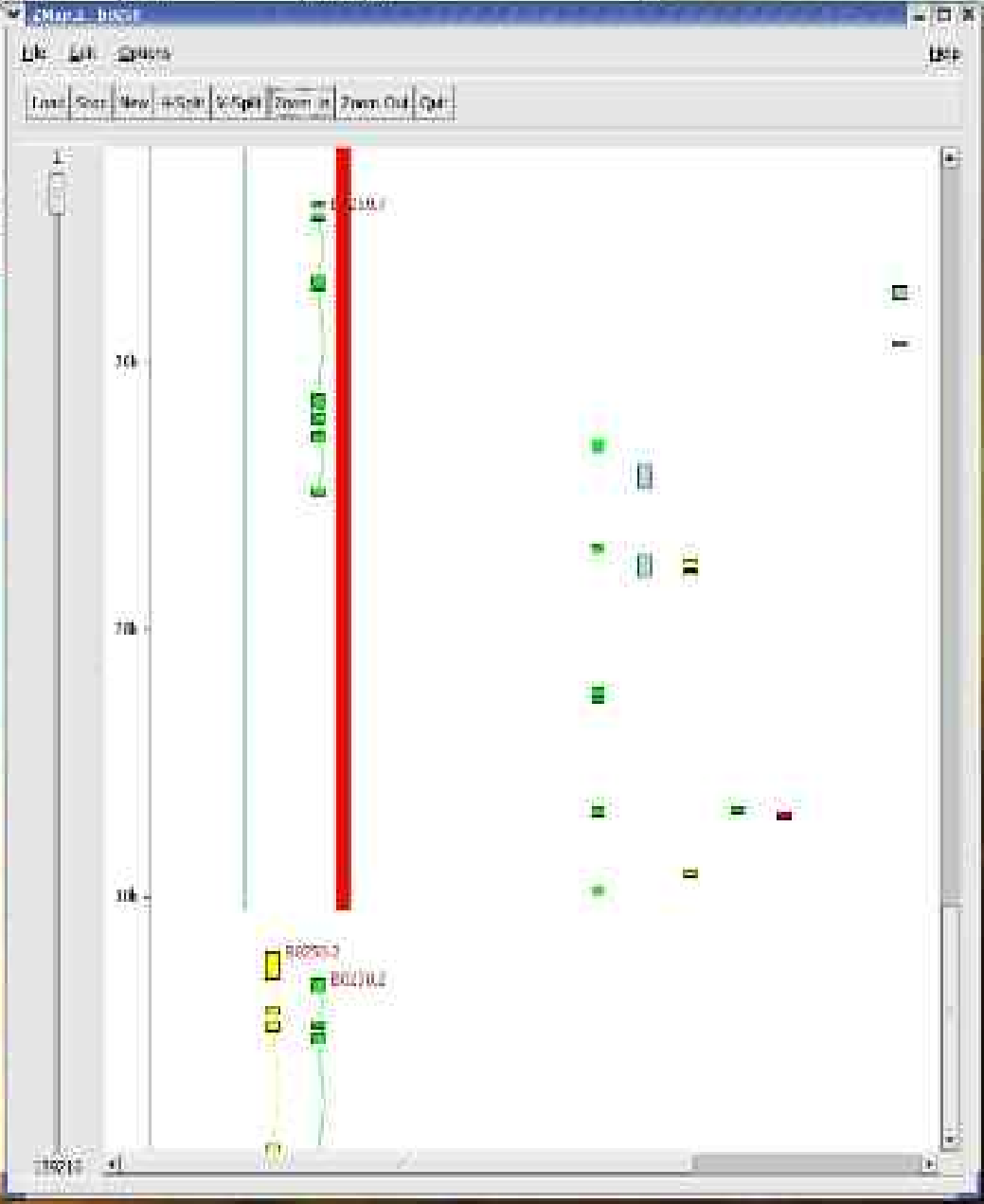
File Edit Options Help

View ZMap

Sequence: b0210 Create ZMap

Manage ZMaps

ZMap	Sequence	Status	Last Request
ZMap	b0210		



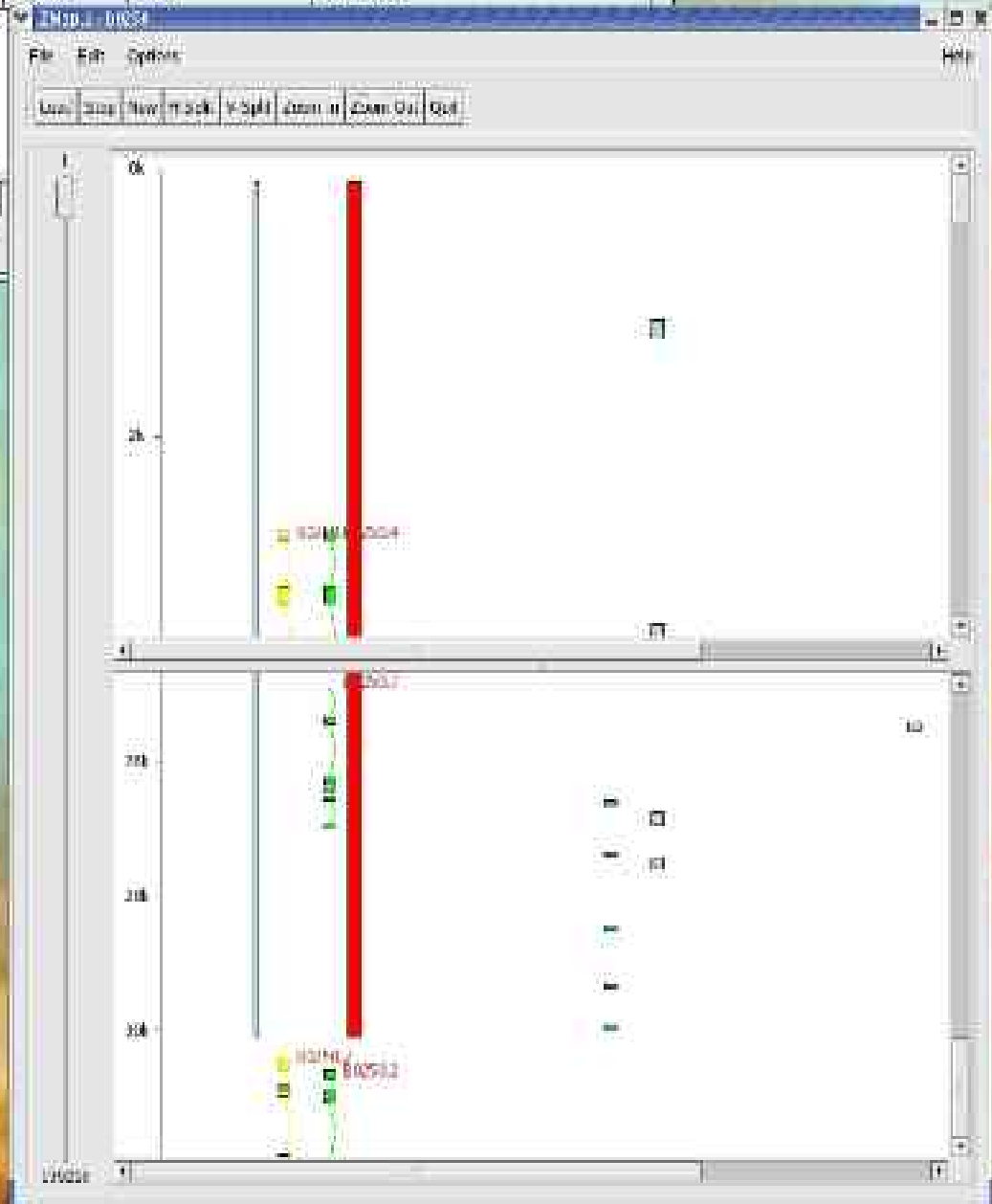
File Edit Options

New ZMap

Sequence: 10250

Manage ZMaps

ZMap	Sequence	Status	Last Received
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File Edit Options Help

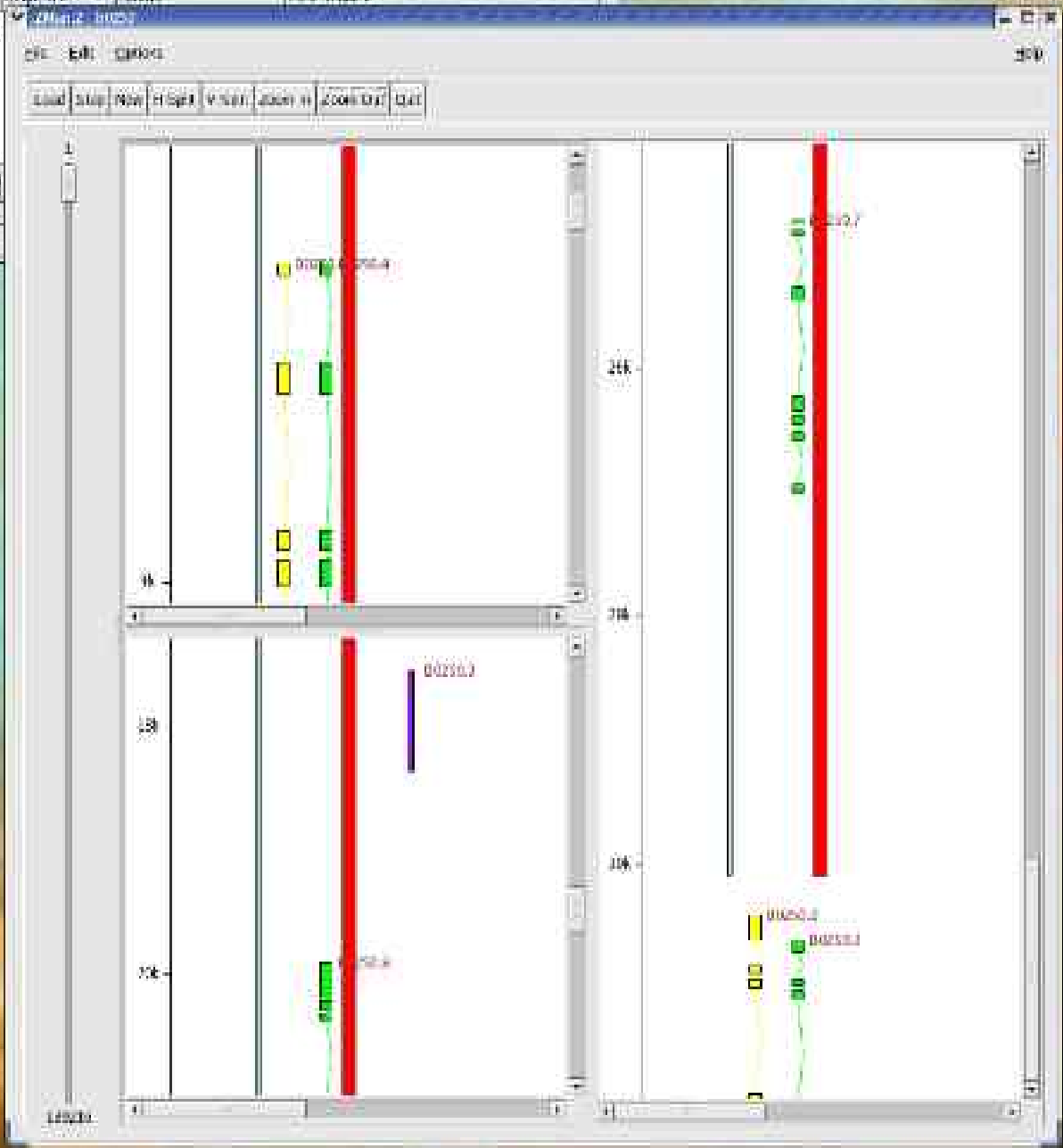
New ZMap

Sequence: 00000 [Create ZMap]

Break ZMap

ZMap	Sequence	Start	End	Label
ZMap				

Stop



# Zmap

- Multi-threaded standalone client
- Talks DAS2 and GFF
- Will talk GFF3
- Multiple views of a DNA sequence
- Parallel views of multiple sequences
- Independent zooming & scrolling

Acknowledgements: Ed Griffiths, Wellcome Trust Sanger Institute