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Improvements and new features in the 7th major release of the **Bio-Linux** distro

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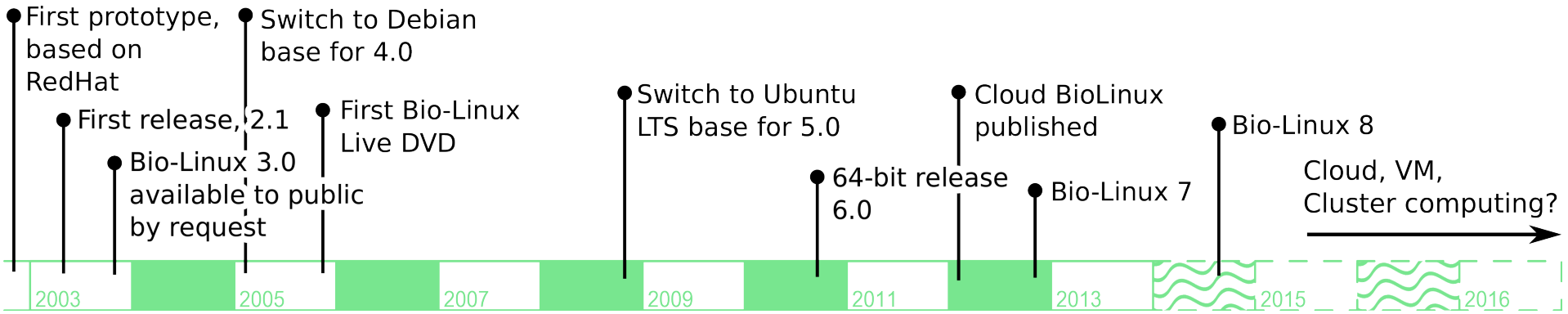
Bio-Linux

Contents

- History of Bio-Linux?
- Who uses it?
- What's new in Version 7?
- What are we planning for the future?

A quick history of Bio-Linux

- Started for a specific group of users
- Single system image, no packages
- EMBOSS + STADEN “killer apps”



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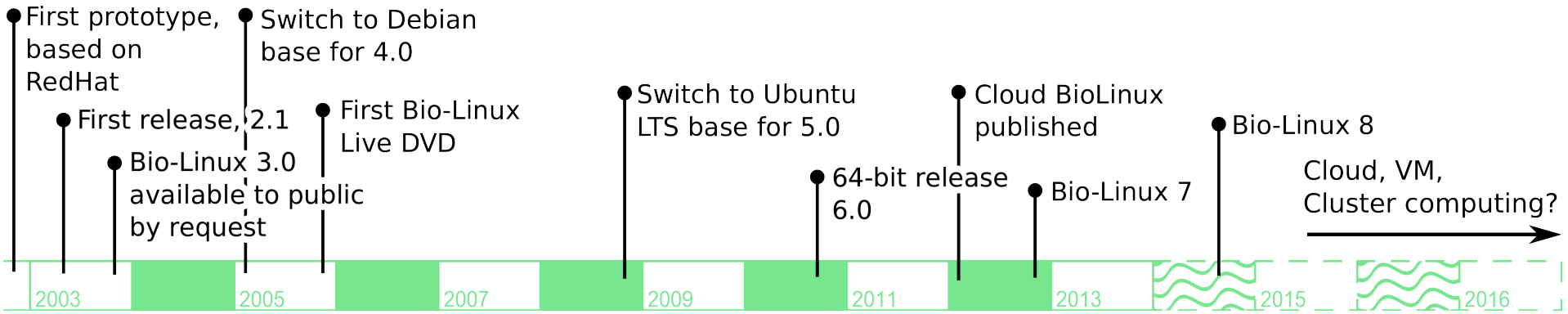
A quick history of Bio-Linux

- Since 2008 a customised Ubuntu image
- Close links with Debian Med



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Developer Interactions

Developer Community

debian med

Cloud BioLinux

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Known users of Bio-Linux

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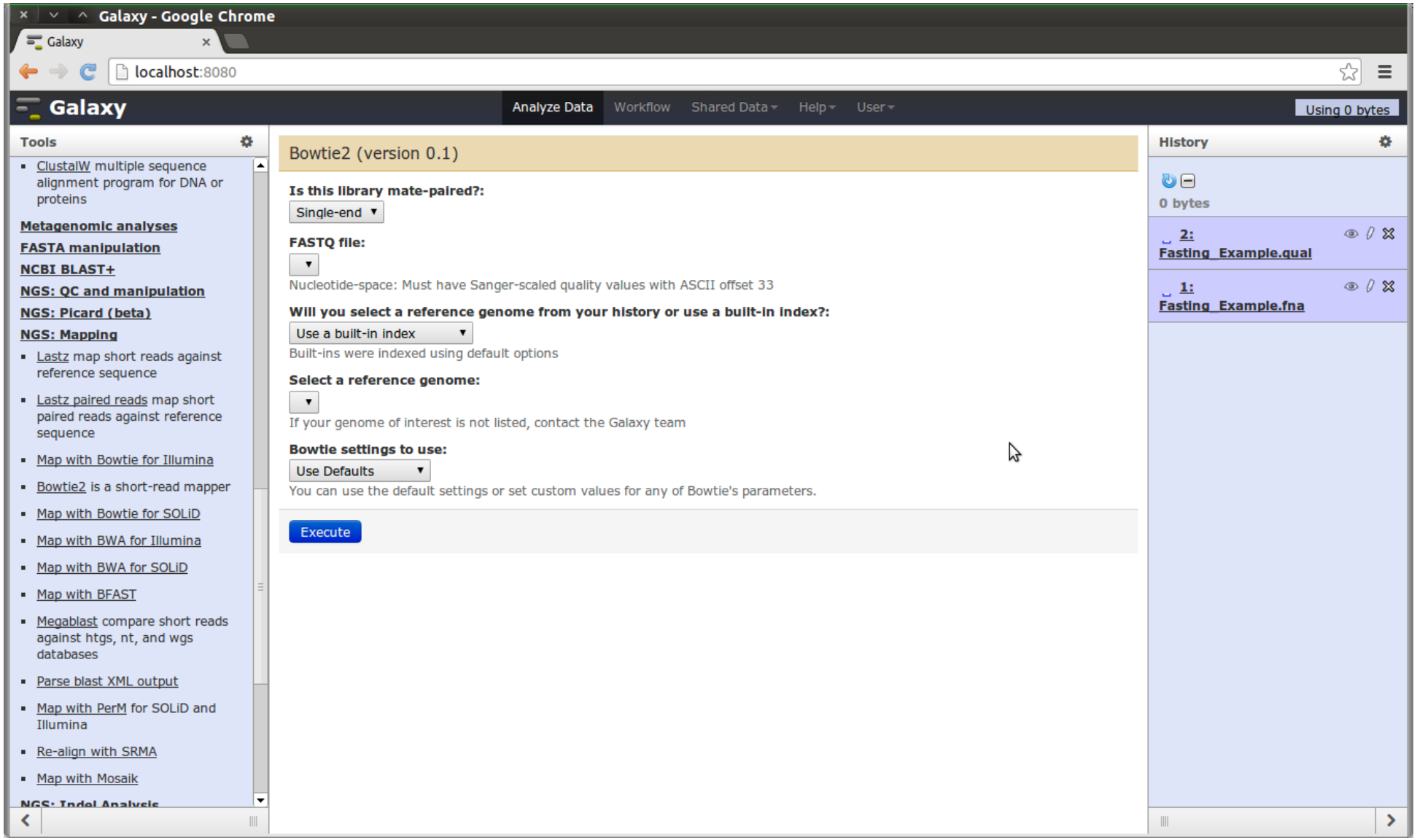
What goes on Bio-Linux?

- Must be freely redistributable, ideally FOSS
- Marker gene analysis, metagenomics pipelines
- General conversion and formatting tools
- Things that are already packaged (Debian Med)
- Things that NERC users ask for
- Things that make the system more user-friendly
- Priority is to make things better for existing users than to find new ones

New in version 7



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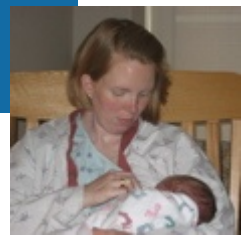
New in version 7

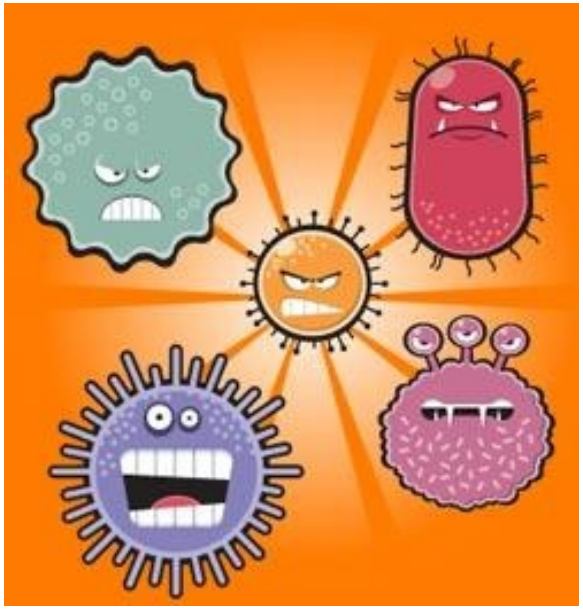
mothur



Quantitative Insights Into Microbial Ecology

qiime

AmpliconNoise



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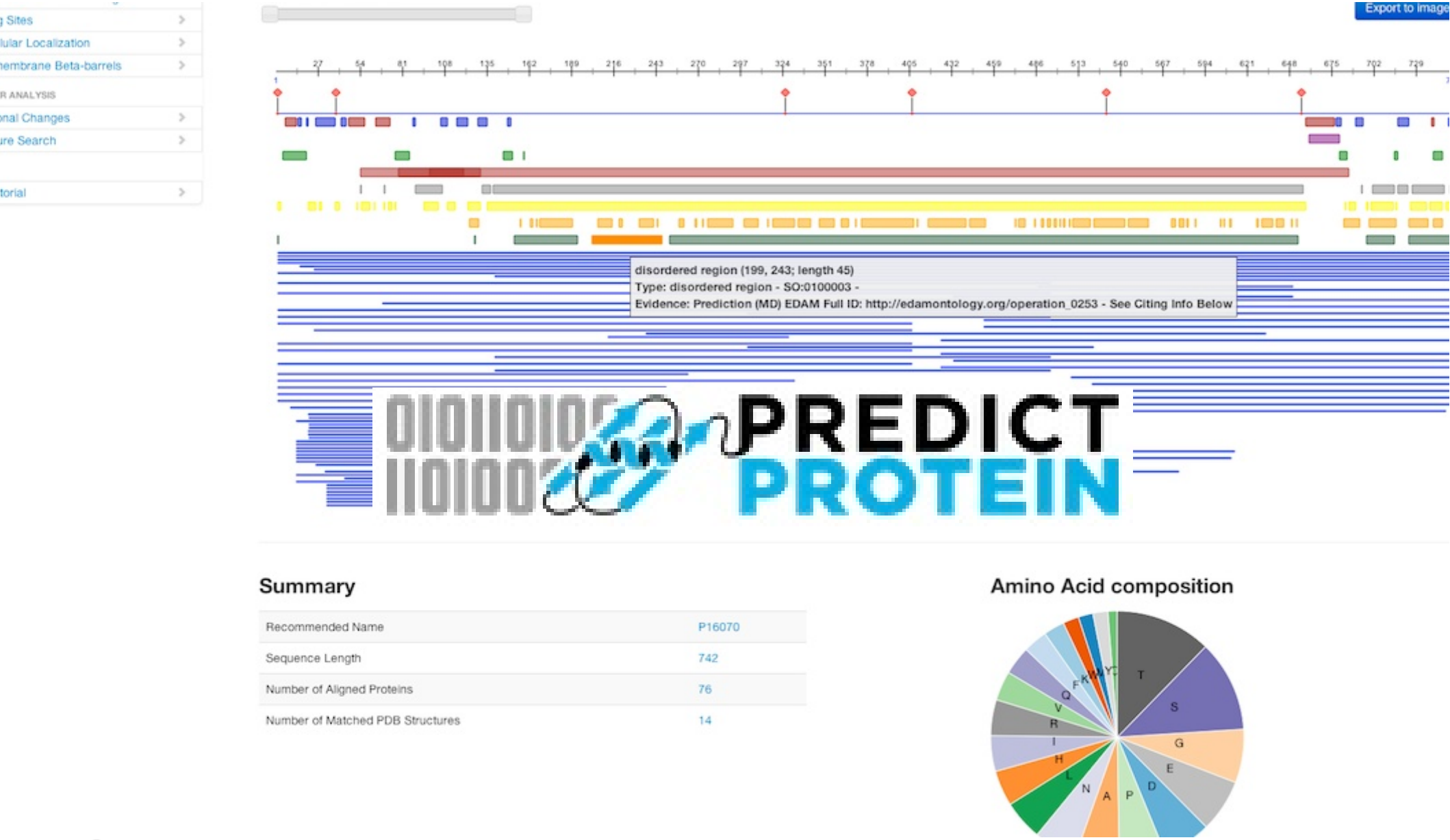
New in version 7



Summary

Recommended Name	P16070
Sequence Length	742
Number of Aligned Proteins	76
Number of Matched PDB Structures	14

Amino Acid composition

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New in version 7

- Also...
  - FastQC – nextgen quality assessment
  - Bowtie-Bio tools
  - Several NGS assemblers
  - and of course latest EMBOSS + STADEN (gap5)

Teaching on Bio-Linux

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Teaching and Outreach

→ environmentalomics.org

elixir-europe.org ←

Future

- Continue to do what we're good at
- More developer time wanted (always!)
- More tutorial/course material
- More focus on VM/Cloud

Acknowledgements

- Current NEBC team
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