The Debian-Med project

Andreas Tille

Debian

LSM, Amiens 2007

Structure

- What is Debian-Med
 - Motivation
 - Community
 - Why Debian
- 2 Realisation
 - Available packages
 - Techniques
- Status
 - Experiences
 - Debian-Med for service providers
 - Prospectus

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- Some subareas well covered
- Medical data processing more than just practice and patient management
- Preclinical research of microbiology and genetics as well as medical imaging
- Pool of existing free medical software

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- Unreasonable effort to install upstream programs
- No interest in administration
- Interest reduced onto free medical software
- Easy usage
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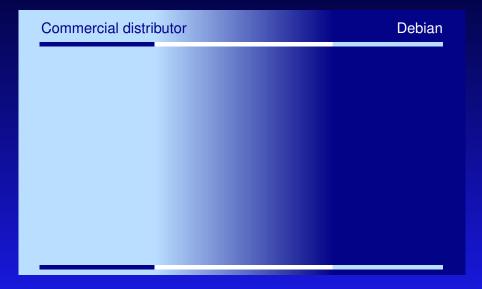
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Company	Structure	Organisation
Employees	Persons	Volunteers

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Customising Debian

- Debian > 10000 packages
- Focus on medical subset of those packages
- Packaging and integrating other medical software
- Easy installation and configuration
- Maintaining a general infrastructure for medical users
- General overview about free medical software
- Propagate the idea of Free Software in medicine
- Completely integrated into Debian no fork

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Basic ideas

Do not make a separate distribution but make Debian fit for medical care

No development of medical software - just smooth integration of third-party software

Debian-Developer = missing link between upstream author and user

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- Flexible, not bound on commercial interest
- Strict rules (policy) glue all things together
- Common interest of each individual developer:
 Get the best operating system for himself.
- Some developers work in the field of medicine
- In contrast to employees of companies every single Debian developer has the freedom and ability to realize his vision
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- BioPython

 Python tools for development of applications for computational molecular biology which address the needs of current and future work in bioinformatics.
- BioSQUID Library of C code functions for sequence analysis including a number of small utility programs to convert, show statistics, manipulate and do other functions on sequence files.
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<u>Boxshade</u> Rendering graphics of protein or DNA sequence alignments (output of alignment programs like ClustalW) to enable incorporation into text processing software.

<u>ClustalW</u> Simultaneous alignment of many nucleotide or amino acid sequences. ClustalW recognises which format is being used and whether the sequences are nucleic acid (DNA/RNA) or amino acid (proteins). It outputs alignments in various formats such as the PHYLIP one.

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- <u>fastDNAml</u> Attempt to solve the same problem as DNAML (from PhyLip), but to do so faster and using less memory, so that larger trees and/or more bootstrap replicates become tractable.
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Packages medical imaging

- CTN Central Test Node: DICOM implementation which was designed to be used at the RSNA (Radiological Society of North America) annual meetings to foster cooperative demonstrations. The goal was to provide a centralized implementation that facilitated vendor participation based on the evolving DICOM standard.
- <u>CTSim</u> Interactive computed tomography simulator. CTSim has very educational trace modes for viewing the data collection simulation as well as the reconstruction.
- DCMTK DICOM-toolkit: collection of libraries and applications implementing large parts the DICOM standard for medical image communication. It includes software for examining, constructing and converting DICOM image files, handling offline media, sending and receiving images over a network connection, . . .

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MedCon Medical Image Conversion provides a flexible command-line utility and a neat graphical front-end. The supported formats are: Acr/Nema 2.0, Analyze (SPM), Concorde, DICOM 3.0, Ecat/Matrix 6.4, InterFile3.3, GIF and raw/binary data. The library (libmdc) can be used by other programs for import and export and is extendable for other formats.

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 - Ensures compliance of all dependencies
 - Clean upgrades
 - Easy handling of security updates
 - Basis of modern GNU/Linux distributions

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- Installation of "meta-packages" for certain tasks
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- Adapted configuration (optional)
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Role based user menus

User in role med gets additional menu



- Good overview about relevant software
- Every package features own entry
- Other users are not affected

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- 3 Status
 - Experiences
 - Debian-Med for service providers
 - Prospectus

- Debian-Med is a practice management system itself
- Is only interesting for doctors
- Not interesting for mikro-biologists / medical physicists
- Should be installed by health care professionals
- Debian-Maintainer are programming software for doctors
- Debian-Med does not need supporter
- 7) Can be used on SuSE Linux
- Medical software can not be free
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 - Software free of charge
 - Merits for
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