Custom **Debian** Distributions
Making Debian the distribution of choice for specific work fields

*Andreas Tille*

*Debian Conference 8*

Mar del Plata, August 12, 2008
Overview

1. Symbiosis between experts and developers
   - Short intro CDD
   - Missing link upstream developer – user

2. Used techniques
   - Using cdd-dev
   - Web tools
   - Prospective packages and to do list

3. Future
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3. Future
Reminder: Basic goal of CDDs

- Debian > 22,000 packages
- Users interested in *subset*
- Groups of specialised users
- Easy installation and configuration
- While *Debian* stays general support specialists as well
- **No derivative** from Debian

*Basic idea: Do not make a separate distribution but make Debian fit for special purpose instead*
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Looking from outside

- Doctor and friend of mine:
  “Debian developers == ‘secret society’” 😊
- We know we are everything but secret
- At least one feature of secrecy: concealment
  - Concealment inside advertising noise of proprietary products
  - Concealment by disunity

→ Breaking the secret by advertising complete solutions
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Upstream - Debian Developer - User

- Tie a solid network of Debian developers, upstream developers (“developing experts”) and users
- Rationale: Experts in this field need help in build system / packaging
- Upstream anticipates enhancements of build system and security audit
- Finally support upstream developers to become Debian maintainers
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Attracting people by providing interesting techniques

- Acceptance of new methods higher if the techniques provided are convincing enough
- Simple ways to categorise packages (“tasks files”)
- Internationalised web pages displaying relevant packages
- Key documentation feature
- Promoting software that builds a complete working environment
- Rise user interest by providing ready to install software in the context of their work field

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Upstream developers often weak in advertising

- Just put stuff on a simple web page
- The better ones use repository like Savannah, SourceForge, ...
- Debian tries to provide a simple access for the user
- Just make sure it is not hidden like a needle in a haystack amongst other packages
- CDDs are working as a looking glass onto Debian package pool
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3 Future
Similar to `debian/control`

Task: *taskname*
Description: *Shortdescription*
   *Longdescription*

Depends: *some dependant packages*
Recommends: *some recommended packages*
Suggests: *some suggested packages*
Verify availability of Depends / Recommends

Turn Depends into Recommends

Packages unavailable in main will be turned into Suggests

Create proper debian/control file to build valid metapackages

Create tasksel control file <CDD>-tasks.desc
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- Create proper `debian/control` file to build valid metapackages
- Create `tasksel control file <CDD>-tasks.desc`
Symbiosis between experts and developers

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Future
Further usage of tasks files

- Debian Edu uses information to build installation media
- Debian Med has developed several web tools
  - Bugs overview
  - Description translation (DDTP) status
  - QA features
  - Tasks overview
- Tasks overview is factorised for all CDDs
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# Bugs overview

Bugs Übersicht

## Unerledigte Bugs

<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
<th>Severity</th>
</tr>
</thead>
<tbody>
<tr>
<td>aeskulap</td>
<td>aeskulap : [NTL:pt] Updated Portuguese translation for package messages</td>
<td>wishlist</td>
</tr>
<tr>
<td>arb</td>
<td>Please build arb for powerpc</td>
<td>wishlist</td>
</tr>
<tr>
<td>bioperl</td>
<td>bioperl: AlignIO::next_aln does not return multiple alignments for bl2seq</td>
<td>normal</td>
</tr>
<tr>
<td>cimg-dev</td>
<td>Spelling mistake in package description</td>
<td>minor</td>
</tr>
<tr>
<td></td>
<td>[Cimg]: Please update to 1.2.8</td>
<td>normal</td>
</tr>
<tr>
<td></td>
<td>cimg-dev: Please update dependencies to libfftw3-3</td>
<td>important</td>
</tr>
<tr>
<td>ctsim</td>
<td>wxwindows2.4 is scheduled to be removed</td>
<td>serious</td>
</tr>
<tr>
<td></td>
<td>ctsim: please switch to libfftw3-dev</td>
<td>wishlist</td>
</tr>
<tr>
<td></td>
<td>ctsim: still depends on xlibmesa-gl-dev</td>
<td>minor</td>
</tr>
<tr>
<td>cycle</td>
<td>cycle: Cycle failed to export to iCal</td>
<td>normal</td>
</tr>
<tr>
<td></td>
<td>cycle: Specific french characters as password lead to crash</td>
<td>normal</td>
</tr>
<tr>
<td></td>
<td>typo</td>
<td>normal</td>
</tr>
</tbody>
</table>
## Support Debian Description Translation project

### DDTP Statistiken

<table>
<thead>
<tr>
<th>Package</th>
<th>DE</th>
<th>ES</th>
<th>FR</th>
<th>IT</th>
<th>JA</th>
<th>BR</th>
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<tr>
<td>adun.app</td>
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<td>✔️</td>
<td>✔️</td>
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<tr>
<td>altree</td>
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<td>▼️</td>
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<td>biococoa.app</td>
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<td>chemtool</td>
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<td>▼️</td>
<td>▼️</td>
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<tr>
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<tr>
<td>ctn</td>
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</tr>
<tr>
<td>cycle</td>
<td>✔️</td>
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Users deserve translated descriptions

Programme pour l'imagerie médicale
AMIDE (AMIDE's a Medical Image Data Examiner) est un outil pour la visualisation et l'analyse de jeux de données d'imagerie médicale. On peut noter parmi ses fonctionnalités la prise en charge simultanée de données importées de fichiers aux formats divers, la fusion d'images, la définition de régions d'intérêt tridimensionnelles, le rendu des volumes et l'alignement de structures solides.

software para imagens médicas
AMIDE: (Amide's a Medical Imaging Data Examiner -- Amide é um examinador de dados de imagens médicas)
O AMIDE é uma ferramenta para visualização e análise de conjuntos de dados de imagens médicas. Suas potencialidades incluem o manuseio simultâneo de múltiplos conjuntos de dados importados de uma variedade de formatos de arquivos, fusão de imagens, desenho e análise de área de interesse em 3D, renderização de volume e alinhamento de corpo rígido.

Software für medizinische Bildverarbeitung
Give experts a chance to provide proper translations

unübersetzt
Bitte folge dem unten angegebenen Link, um eine erste Übersetzung einzugeben:
http://ddtp.debian.net/ddtss/index.cgi//it/translate/amide

医学画像用ソフトウェア
AMIDE: (Amide's a Medical Imaging Data Examiner)
AMIDE は医学画像データセットの閲覧および分析用ツールです。
各種ファイルフォーマットからインポートされた複数のデータセットの
同時操作、画像の合成、興味のある画像や分析の三次元領域化、
体積レンダリング、そして剛体の配列が可能です。

programa de imágenes médicas
AMIDE: («Amide's a Medical Imaging Data Examiner», Amide es un examinador
de datos de imágenes médicas)
AMIDE es una herramienta para visualizar y analizar conjuntos de datos de
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múltiples conjuntos de datos importados desde distintos formatos de
archivo, la fusión de imágenes, el dibujo y análisis de regiones de
interés en 3 dimensiones, el dibujo de volúmenes y el alineado de cuerpos
rígidos.

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## Watching upstream

### Custom Debian Distributions

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<th>repository</th>
<th>archive</th>
<th>bugs</th>
<th>upstream</th>
</tr>
</thead>
<tbody>
<tr>
<td>altree</td>
<td>1.0.1-3 (1.1.0-1)</td>
<td></td>
<td></td>
<td>1.1.0</td>
</tr>
<tr>
<td>(alphy, altree, altree-examples, libcutils-perl)</td>
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<tr>
<td>biojava</td>
<td>1.4pre1-1</td>
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<td>20020823</td>
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<td>(libbiojava-doc, libbiojava-java)</td>
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<td></td>
<td></td>
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</tr>
<tr>
<td>cluster3 [non-free]</td>
<td>1.27-0.1</td>
<td></td>
<td></td>
<td>1.39</td>
</tr>
<tr>
<td>fact++</td>
<td>1.16-1 (1.11-1)</td>
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<td>1.11</td>
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<tr>
<td>gdcm</td>
<td>2.0.6</td>
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<td>2.0.6patch1</td>
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<tr>
<td>(${python-Provides}, libgdcm-dev, libgdcm-tools, libgdcm2, libgdcm2-dbg, libgdcm2-dev, libvtkgdcm, libvtkgdcm-dev, libvtkgdcm-tools, python-gdcm, python-vtkgdcm)</td>
<td></td>
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<td></td>
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</tr>
<tr>
<td>gnunet-server</td>
<td>0v8-1</td>
<td></td>
<td></td>
<td>9-rc1</td>
</tr>
<tr>
<td>image [contrib]</td>
<td>1.40a-1 (1.41c-1)</td>
<td></td>
<td></td>
<td>1.41c</td>
</tr>
<tr>
<td>libgenome</td>
<td>1.3.1-1</td>
<td></td>
<td></td>
<td>2.2.0</td>
</tr>
<tr>
<td>(libgenome-1.3-0, libgenome-1.3-0-dev, libgenome-1.3-dev)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>libmems</td>
<td>1.5.0-1</td>
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<td>2.2.0</td>
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<tr>
<td>(libmems-1.6-1, libmems-1.6-1-dev, libmems-1.6-dev)</td>
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<tr>
<td>libsbml</td>
<td>3.0.0beta2-1</td>
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<td></td>
<td>3.1.1</td>
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<tr>
<td>(${python-Provides}, libsbml-dev, libsbml-java, libsbml-perl, libsbml3, libsbml3-dev, libsbml3-doc, libsbml3-examples, libsbml3-java, libsbml3-java-doc, libsbml3-occt, libsbml3-perl, libsbml3-perl-doc, libsbml3-ruby, libsbml3-ruby1.8, python-sbml, python-sbml3, python-sbml3-doc)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>meme [non-free]</td>
<td>3.0.13-1</td>
<td></td>
<td></td>
<td>3.5.0</td>
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<tr>
<td>murasaki</td>
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<td></td>
<td>1.35c</td>
</tr>
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<td>treeplot</td>
<td>0.7.1.2</td>
<td></td>
<td></td>
<td>0.7.2</td>
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<tr>
<td>(libvista-2, libvista-2-dev, vista-tools)</td>
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<td></td>
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<tr>
<td>vista</td>
<td>2.1.7-1</td>
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<td></td>
<td>2.2.1</td>
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</tbody>
</table>
## Putting QA info into CDD frame

<table>
<thead>
<tr>
<th>Package</th>
<th>Repository</th>
<th>Archive</th>
<th>Bugs</th>
<th>Upstream</th>
</tr>
</thead>
<tbody>
<tr>
<td>wise (wise, wise-doc)</td>
<td>2.4.1-5</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>new and incoming (1)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>package</td>
<td>repository</td>
<td>archive</td>
<td>bugs</td>
<td>upstream</td>
</tr>
<tr>
<td>infernal</td>
<td>0.81-1 (0.81-2)</td>
<td>0.81-1 (new)</td>
<td></td>
<td>0.81</td>
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<tr>
<td>packages with strange versions in the repository (1)</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>package</td>
<td>repository</td>
<td>archive</td>
<td>bugs</td>
<td>upstream</td>
</tr>
<tr>
<td>aeskulap</td>
<td>0.2.2b1-2 (0.2.2b1-3)</td>
<td>0.2.2b1-1</td>
<td></td>
<td>0.2.2-beta1</td>
</tr>
<tr>
<td>work in progress (22)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>package</td>
<td>repository</td>
<td>archive</td>
<td>bugs</td>
<td>upstream</td>
</tr>
<tr>
<td>bioimagesuite</td>
<td>(2.0-1)</td>
<td></td>
<td></td>
<td>Missing (copyright info)</td>
</tr>
<tr>
<td>(bioimagesuite, bioimagesuite-data, libbioimagesuite2)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>dialign-t-doc [non-free]</td>
<td>0.2.2-1</td>
<td>0.2.2-1</td>
<td></td>
<td>NotFound (copyright info)</td>
</tr>
<tr>
<td>ecell (ecell, ecell-doc)</td>
<td>(3.1.100-2)</td>
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<td></td>
<td>3.1.106rc2</td>
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<tr>
<td>emboss-kaptain</td>
<td>(0.98-1)</td>
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<td></td>
<td>0.98</td>
</tr>
<tr>
<td>(embassy-domainatrix-kaptain, emboss-kaptain)</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>gamgi (gamgi, gamgi-dat, gamgi-doc)</td>
<td>(0.13.1-1)</td>
<td></td>
<td></td>
<td>0.13.2</td>
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<tr>
<td>gbrowse</td>
<td>(1.68-1)</td>
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<td>1.68</td>
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<tr>
<td>gbrowse-karyotype</td>
<td>(cvs20071113-1)</td>
<td></td>
<td></td>
<td>Missing (copyright info)</td>
</tr>
<tr>
<td>haploview [contrib]</td>
<td>(4.0-1)</td>
<td></td>
<td></td>
<td>4.0</td>
</tr>
<tr>
<td>kalign</td>
<td>2.03-2 (2.03-3)</td>
<td>2.03-1</td>
<td></td>
<td>Invalid (copyright info)</td>
</tr>
</tbody>
</table>
Symbiosis between experts and developers
- Short intro CDD
- Missing link upstream developer – user

Used techniques
- Using \texttt{cdd-dev}
- Web tools
- Prospective packages and to do list

Future
### Prospective packages

<table>
<thead>
<tr>
<th>Field</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Depends</td>
<td><em>not yet existing package name</em></td>
</tr>
<tr>
<td>Homepage</td>
<td><em>Homepage of project</em></td>
</tr>
<tr>
<td>Responsible</td>
<td><em>Future maintainer (optional)</em></td>
</tr>
<tr>
<td>License</td>
<td><em>License of software to package</em></td>
</tr>
<tr>
<td>WNPP</td>
<td><em>Bug number (optional)</em></td>
</tr>
<tr>
<td>Pkg-URL</td>
<td><em>URL to unofficial package</em></td>
</tr>
<tr>
<td>Pkg-Description</td>
<td><em>Description of prospective package</em></td>
</tr>
</tbody>
</table>

---

*Andreas Tille  (Debian Conference 8)  Custom Debian Distributions  Mar del Plata, August 12, 2008*
Debian Med Biology packages

Official Debian packages

**Adun.app**
Molekularsimulator für GNUstep
http://diana.imim.es/Adun
Maintainer: Debian-Med Packaging Team

Dies ist ein neues, erweiterbares Molekularsimulationsprogramm, das auch Analysefähigkeiten und Datenverwaltung beinhaltet.

**Amap-align**
Multiple Alignments durch Sequenz-»annealing« bei Proteinen
http://bio.math.berkeley.edu/emap/
Maintainer: Debian-Med Packaging Team


Das Java-Visualisierungswerkzeug von AMAP 2.2 ist noch nicht als Debian-Paket erstellt.

**Amap-align**
Multiple Alignments durch Sequenz-»annealing« bei Proteinen
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Maintainer: Debian-Med Packaging Team


Das Java-Visualisierungswerkzeug von AMAP 2.2 ist noch nicht als Debian-Paket erstellt.
Unofficial packages

The list to the right includes various software projects which are of some interest to the Debian Med Project. Currently, only a few of them are available as Debian packages. It is our goal, however, to include all software in Debian Med which can sensibly add to a high quality Custom Debian Distribution.

For a better overview of the project's availability as a Debian package, each head row has a color code according to this scheme:

- Green: The project is available as an official Debian package
- Yellow: The project is available as an unofficial Debian package

If you discover a project which looks like a good candidate for Debian Med to you, or if you have prepared an unofficial Debian package, please do not hesitate to send a description of that project to the Debian Med mailing list.

---

**Epigrass**

*Wissenschaftliches Werkzeug für Simulationen und Szenanalyse im epidemiologischen Beziehungsnetz*


**Maintainer:** Debian-Med Packaging Team


---

**Experimental or unofficial Debian packages, projects with packaging stuff in SVN**

**Netepi-analysis**

*network-enabled tools for epidemiology and public health practice*


**License:** free

**Responsible:** Andreas Tille

NetEpi, which is short for "Network-enabled Epidemiology", is a collaborative project to create a suite of free, open source software tools for epidemiology and public health practice. Anyone with an interest in population health epidemiology or public health informatics is encouraged to examine the prototype tools and to consider contributing to their further development. Contributions which involve formal and/or informal testing of the tools in a wide range of circumstances and environments are particularly welcome, as is assistance with design, programming and documentation tasks. This is a tool for conducting epidemiological analysis of data sets, both large and small, either through a Web browser interface, or via a programmable interface. In many respects it is similar to the analysis facilities included in the Epi Info suite, except that NetEpi Analysis is designed to be installed on servers and accessed remotely via Web browsers, although it can also be installed on individual desktop or laptop computers.

The software was developed by New South Wales Department of Health.

---

**Netepi-collection**

*network-enabled tools for epidemiology and public health practice*


**License:** free

**Responsible:** Andreas Tille

NetEpi, which is short for "Network-enabled Epidemiology", is a collaborative project to create a suite of free, open source
### Debian packages not available

<table>
<thead>
<tr>
<th>Package</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Bioimagesuite</strong></td>
<td>Integrated image analysis software suite. Bioimage Suite has extensive capabilities for both neuro/cardiac and abdominal image analysis and state of the art visualization. Many packages are available that are highly extensible, and provide functionality for image visualization and registration, surface editing, cardiac 4D multi-slice editing, diffusion tensor image processing, mouse segmentation and registration, and much more. It can be integrated with other biomedical image processing software, such as FSL and SPM. This site provides information, downloads, documentation, and other resources for users of the software. Bioimage Suite was developed at Yale University and has been extensively used at different labs at Yale since 2004. There is a forum at Bioimage Suite site for discussion of compiling it from source and packaging issues at <a href="http://research.yale.edu/bioimagesuite/forum/index.php?board=12.0">http://research.yale.edu/bioimagesuite/forum/index.php?board=12.0</a></td>
</tr>
<tr>
<td><strong>Blox</strong></td>
<td>Medical imaging and visualization program. The purpose of the project is to develop a quantitative medical imaging and visualization program for use on brain MR, DTI and MRS data. It is a joint project of the Kennedy Krieger Institute and the Johns Hopkins University, Psychiatric Neuroimaging Lab (<a href="http://pni.med.jhu.edu/methods/morph.htm">http://pni.med.jhu.edu/methods/morph.htm</a>).</td>
</tr>
<tr>
<td><strong>Brainvisa</strong></td>
<td>Image processing factory for MR images. BrainVISA is a software, which embodies an image processing factory. A simple control panel allows the user to trigger some sequences of treatments on series of images. These treatments are performed by calls to command lines provided by different laboratories. These command lines, hence, are the building blocks on which are built the assembly lines of the factory. BrainVISA is distributed with a toolbox of building blocks dedicated to the segmentation of T1-weighted MR images. The product of the main assembly line made up from this toolbox is the following: grey/white classification for Voxel Based Morphometry, Meshes of each hemisphere surface for visualization purpose, Spherical meshes of each hemisphere white matter surface, a graph of the cortical folds, a labeling of the cortical folds according to a nomenclature of the main sulci.</td>
</tr>
<tr>
<td><strong>Conquest-dicom-server</strong></td>
<td>Full featured PACS server that provides the ability to handle DICOM images and radiology data. Supports DICOMDIR, DICOMSOP, and DICOMSPPA protocols.</td>
</tr>
</tbody>
</table>
Try to establish technique

- **Further enhancements**
  - Make projects like DebiChem and Debian-Accessibility using the framework
  - Try to bring back external projects to Debian by providing attractive tools
Try to establish technique

- Further enhancements
- Make projects like DebiChem and Debian-Accessibility using the framework
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Try to establish technique

- Further enhancements
- Make projects like DebiChem and Debian-Accessibility using the framework
- Try to bring back external projects to Debian by providing attractive tools
This talk is available at

http://people.debian.org/~tille/talks/

Andreas Tille <tille@debian.org>