

Custom Debian Distributions

Making Debian the distribution of choice for specific work fields

Andreas Tille

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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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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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- 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
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- CDDs are working as a looking glass onto Debian package pool

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Special applications







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Tasks files

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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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

Further usage of tasks files

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Bugs overview

Zusammenfassung

Bugs des Pakets: **all**

Alle Bugs: **126**

Unerledigte Bugs: **61**

Erledigte Bugs: **65**

Bugs Übersicht

Unerledigte Bugs

aeskulap (1)

489371	aeskulap : [INTL:pt] Updated Portuguese translation for package messages	wishlist
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arb (1)

364908	Please build arb for powerpc	wishlist
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bioperl (1)

266921	bioperl: AlignO::next_aln does not return multiple alignments for bl2seq	normal
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cimg-dev (3)

363199	Spelling mistake in package description	minor
399846	[Cimg]: Please update to 1.2.8	normal
460024	cimg-dev: Please update dependencies to libftw3-3	important

ctsim (3)







462189	wxwindows2.4 is scheduled to be removed	serious
488286	ctsim: please switch to libftw3-dev	wishlist
488287	ctsim: still depends on xlibmesa-glx-dev	minor

cycle (3)

422878	cycle: Cycle failed to export to iCal	normal
433759	cycle: Specific french characters as password lead to crash	normal
444776	typo	normal

Support Debian Description Translation project

DDTP Statistiken

						
adun.app	✓	✓	✓	✓	✗	✓
aeskulap	✓	✓	✓	✗	✓	✓
altree	✓	✗	✗	✗	✗	✓
amap-align	✓	✗	✓	✗	✗	✓
amide	✓	✓	✓	✗	✓	✓
autodock	✓	✗	✗	✗	✗	✓
autogrid	✓	✗	✗	✗	✗	✓
biococoa.app	✓	✗	✗	✗	✗	✓
biomode	✓	✓	✓	✗	✓	✓
bioperl	✓	✗	✓	✗	✗	✓
biosquid	✓	✓	✓	✗	✗	✓
blast2	✓	✓	✓	✗	✓	✓
boxshade	✓	✓	✓	✗	✗	✓
chemtool	✓	✓	✓	✗	✓	✓
cimg-dev	✓	✓	✓	✗	✗	✓
cl-pubmed	✓	✓	✓	✗	✗	✓
ctn	✓	✓	✓	✓	✗	✓
ctn-dev	✓	✓	✓	✗	✗	✓
ctsim	✓	✓	✓	✓	✗	✓
cycle	✓	✓	✓	✗	✓	✓

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



AMIDE (Amide's a Medical Image Data Examiner - Amide ist ein Untersucher medizinischer Bilddaten) ist ein Werkzeug zur Anzeige und Analyse von medizinischen Bilddatensätzen. Seine Fähigkeiten umfassen die simultane Behandlung von mehreren, aus einer Vielzahl von Dateiformaten importierten, Datensätzen, Bildzusammenführungen, dreidimensionales Zeichnen von Interessensregionen und deren Analyse, Volumenberechnung und Ausrichtung an starren Körpern.

Give experts a chance to provide proper translations

unübersetzt



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 imágenes médicas. Sus funcionalidades incluyen el manejo simultáneo de múltiples conjuntos de datos importados desde distintos formatos de archivo, la fusión de imágenes, el dibujado y análisis de regiones de interés en 3 dimensiones, el dibujado de volúmenes y el alineado de cuerpos rígidos.

Watching upstream

informazioni

Sviluppatori, visitate la nostra

QA report

newer upstream available (14)

package	repository	archive	bugs	upstream
altree (alphy, altree, altree-examples, libcutils-perl)	1.0.1-3 (1.1.0-1)			1.1.0
biojava (libbiojava-doc, libbiojava-java)	1.4pre1-1			20020823
cluster3 [non-free]	1.27-0.1			1.39
fact++	1.1.8-1 (1.1.11-1)			1.1.11
gdcmm (\${python:Provides}, libgdcmm-dev, libgdcmm-tools, libgdcmm2, libgdcmm2-dbg, libgdcmm2-dev, libvtkgdcmm, libvtkgdcmm-dev, libvtkgdcmm-tools, python-gdcmm, python-vtkgdcmm)	2.0.6			2.0.6patch1
gnumed-server	0v8-1			9-rc1
imagej [contrib]	1.40a-1 (1.41c-1)			1.41c
libgenome (libgenome-1.3-0, libgenome-1.3-0-dev, libgenome- 1.3-dev)	1.3.1-1			2.2.0
libmems (libmems-1.6-1, libmems-1.6-1-dev, libmems-1.6-dev)	1.6.0-1			2.2.0
libsaml (\${python:Provides}, libsbml-dev, libsbml-java, libsbml-perl, libsbml3, libsbml3-dev, libsbml3-doc, libsbml3-examples, libsbml3-java, libsbml3-java-doc, libsbml3-octave, libsbml3-perl, libsbml3-perl-doc, libsbml3-ruby, libsbml3-ruby1.8, python-sbml, python- sbml3, python-sbml3-doc)	3.0.0beta2-1 (3.1.1-1)			3.1.1
meme [non-free]	3.0.13-1			3.5.0
murasaki	1.3-1			1.35c
treemap	0.7-1.2 (0.7.2-1)			0.7.2
vista (libvista-2-1, libvista-2-dev, vista-tools)	2.1.7-1			2.2.1

Putting QA info into CDD frame

wise (wise, wise-doc)	2.4.1-5	2.4.1-3		2.4.1
new and incoming (1)				
package	repository	archive	bugs	upstream
infernall	0.81-1 (0.81-2)	0.81-1 (new)		0.81
packages with strange versions in the repository (1)				
package	repository	archive	bugs	upstream
aeskulap	0.2.2b1-2 (0.2.2b1-3)	0.2.2b1-1		0.2.2-beta1
work in progress (22)				
package	repository	archive	bugs	upstream
bioimagesuite (bioimagesuite, bioimagesuite-data, libbioimagesuite2)	(2.0-1)			Missing (copyright info)
dialign-t-doc [non-free]	0.2.2-1	0.2.2-1		NotFound (copyright info)
ecell (ecell, ecell-doc)	(3.1.100-2)			3.1.106rc2
emboss-kaptain (embassy-domainatrix-kaptain, emboss-kaptain)	(0.98-1)			0.98
gamgi (gamgi, gamgi-dat, gamgi-doc)	(0.13.1-1)			0.13.2
gbrowse	(1.68-1)			1.68
gbrowse-karyotype	(cvs20071113-1)			Missing (copyright info)
haploview [contrib]	(4.0-1)			4.0
kalign	2.03-2 (2.03-3)	2.03-1	2	Invalid (copyright info)

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Additional fields

Prospective packages

Depends: *not yet existing package name*

Homepage: *Homepage of project*

Responsible: *Future maintainer (optional)*

License: *License of software to package*

WNPP: *Bug number (optional)*

Pkg-URL: *URL to unofficial package*

Pkg-Description: *Description of prospective package*

Tasks pages

Biology

Debian Med micro-biology packages

This meta package will install Debian packages related to molecular biology, structural biology and bioinformatics for use in life sciences.

[Translate description](#)

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
- Red: The project is not (yet) available as a Debian package

Debian Med Biology packages

Official Debian packages

Adun.app

Molekularsimulator für GNUstep
<http://diana.imim.es/Adun>

Maintainer: Debian-Med Packaging Team

Version: 0.8.2

License: DFSG free

Official Debian package -

Fix translated description

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

Altree

Programm zur Phylogenie-basierten Analyse
<http://claire.bardel.free.fr/>

Maintainer: Debian-Med Packaging Team

Version: 1.0.1

License: DFSG free

Official Debian package -

Fix translated description

Diese Software wurde für Phylogenie-basierte Analyse entworfen. Zum Einen ermöglicht sie die Entdeckung einer Beziehung zwischen einem untersuchten Gen und einer Krankheit, zum Anderen wird eine Hypothese über die Anfälligkeit möglich.

Amap-align

Multiple Alignments durch Sequenz-»annealing« bei Proteinen
<http://bio.math.berkeley.edu/amac/>

Maintainer: Debian-Med Packaging Team

Version: 2.2

License: DFSG free

Official Debian package -

Fix translated description

AMAP ist ein Kommandozeilenwerkzeug, um mehrfache Alignments von peptidischen Sequenzen durchzuführen. Es verwendet »Posterior-Dekodierung«, ein Alignment durch Sequenz-annealing, anstelle der traditionellen fortschreitenden Alignmentmethoden. Es ist das einzige Alignmentprogramm, das erlaubt, den Empfindlichkeit-/Genauigkeits-Kompromiss zu kontrollieren. Die Software basiert auf dem Quellcode von ProbCons, verwendet aber metrische Alignmentgenauigkeit (alignment metric accuracy) und beseitigt die Konsistenz-Transformation.

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

Unofficial packages

that are useful in epidemiological research.

[Translate description](#)

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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](#)

[Links to other tasks](#)

[Index of all tasks](#)
[Biology](#)

Epigrass

Wissenschaftliches Werkzeug für Simulationen und Szenarioanalyse im epidemiologischen Beziehungsnetz
<http://epigrass.sourceforge.net/>
Maintainer: Debian-Med Packaging Team

Version: 1.5.1

License: DFSG free

Official Debian package -
Fix translated description

Epigrass ist eine Software für die Visualisierung, Analyse und Simulation von epidemischen Prozessen in georeferenzierten Netzen.

EpiGrass kann mit GRASS GIS interagieren, von wo es Karten und ähnliche geografische Informationen übernehmen kann. Trotzdem ist für die Nutzung der meisten Features von EpiGrass die Installation von GRASS GIS nicht erforderlich.

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

Netepi-analysis

network-enabled tools for epidemiology and public health practice
<http://www.netepi.org/>
Responsible: Andreas Tille

License: free

Unofficial Debian package

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 programmatic 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
<http://www.netepi.org/>
Responsible: Andreas Tille

License: free

Unofficial Debian package

NetEpi, which is short for "Network-enabled Epidemiology", is a collaborative project to create a suite of free, open source

To do: prospective packages

Debian packages not available

Bioimagesuite

integrated image analysis software suite

<http://www.bioimagesuite.org/>

License: GPL

Debian package not available

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 intergrated 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 <http://research.yale.edu/bioimagesuite/forum/index.php?board=12.0>

Blox

medical imaging and visualization program

<http://sourceforge.net/projects/blox/>

License: GPL

Debian package not available

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 (<http://pnj.med.jhu.edu/methods/morph.htm>).

Brainvisa

image processing factory for MR images

<http://brainvisa.info/>

License: Free? (CeCill License)

Debian package not available

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.

Conquest-dicom-server

Full featured DICOM server

License: Public domain

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

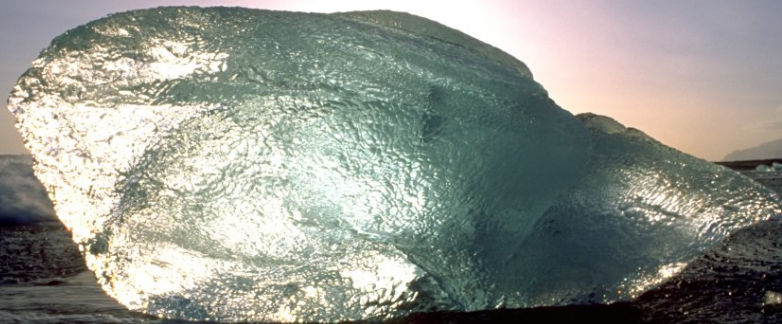
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This talk is available at



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

Andreas Tille <tille@debian.org>