

# Stay home . . . and contribute to Debian Med

Andreas Tille

Debian

Online, 29. August 2020

- 1 What is Debian Med?
- 2 COVID-19 hackathons
- 3 Single contributions to the first hackathon
- 4 Summary

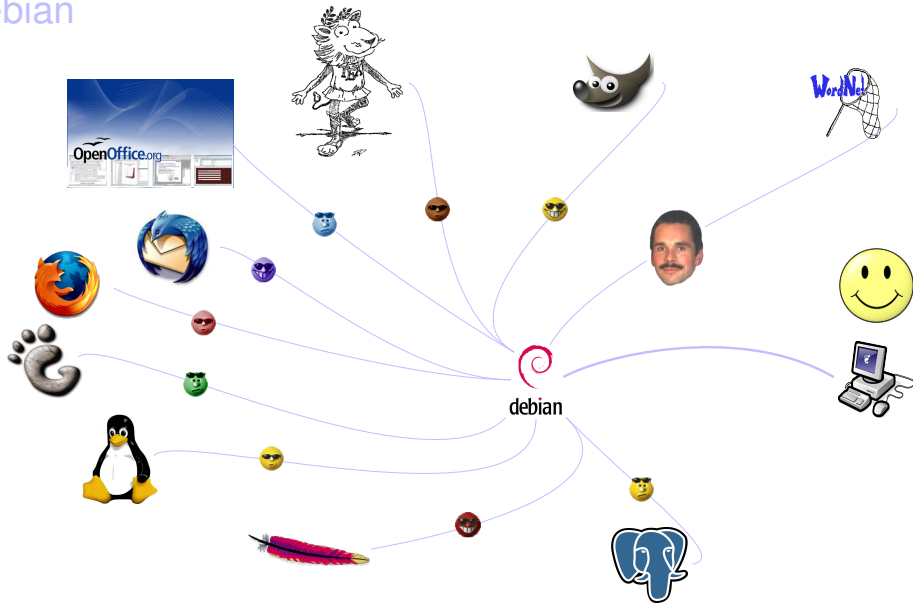
# Back in 2001 at DebConf 1



the first talk about the concept was prepared



# Debian



## Role of Blends to attract specific users



## Role of Blends to attract specific users

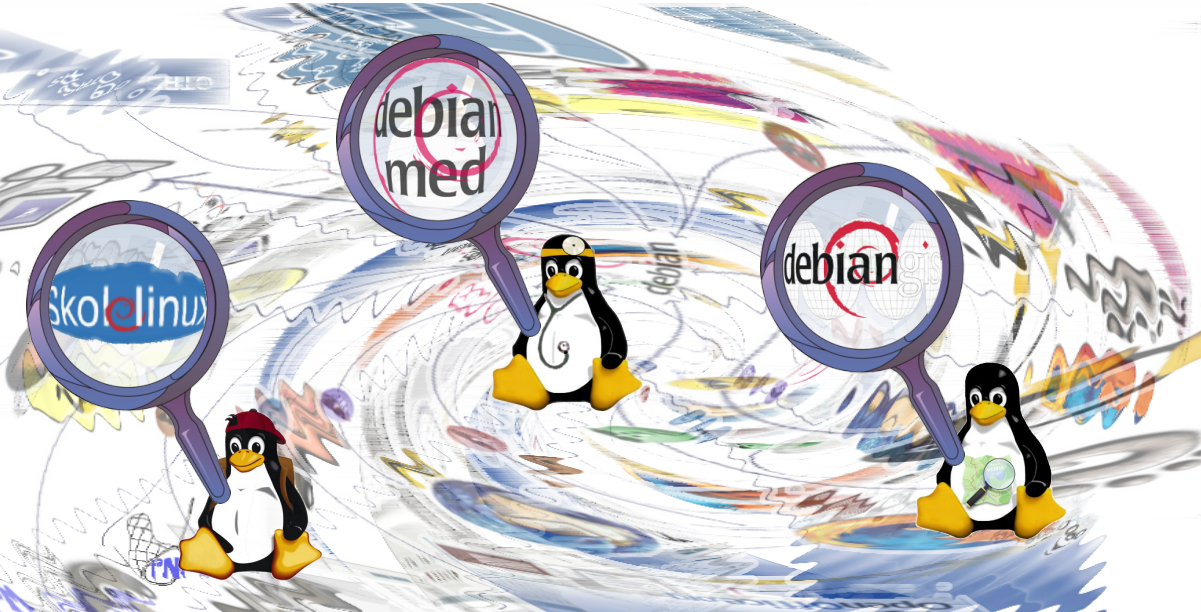


## Role of Blends to attract specific users

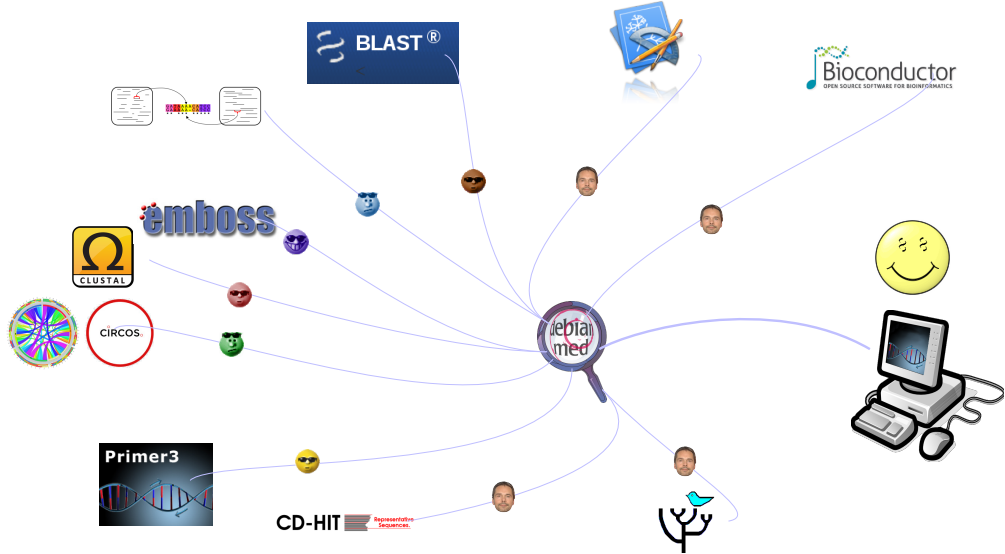




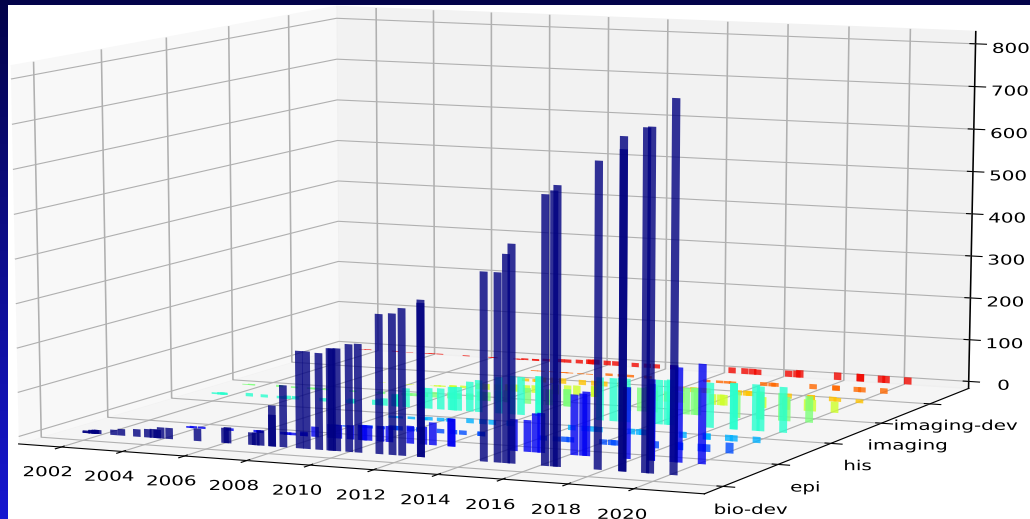
## Role of Blends to attract specific users



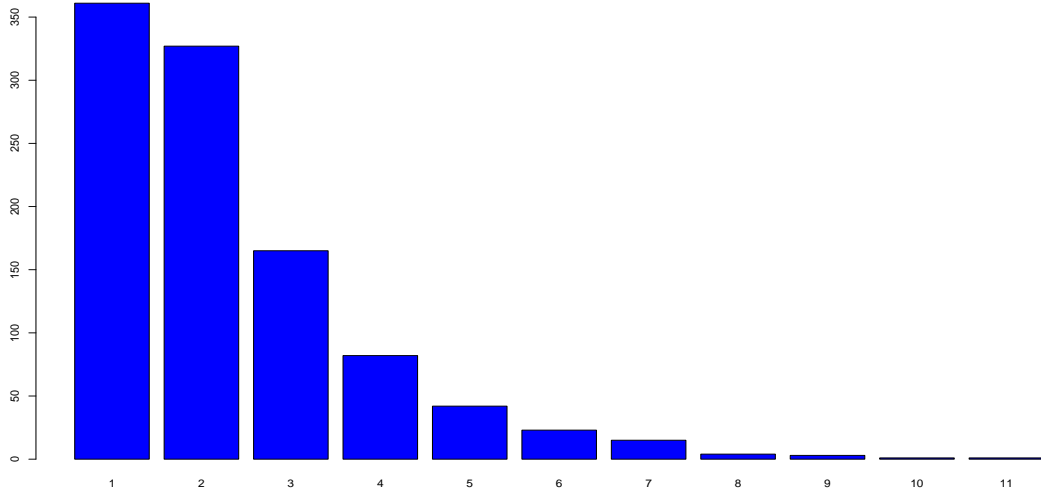
# Med-bio task of Debian Med



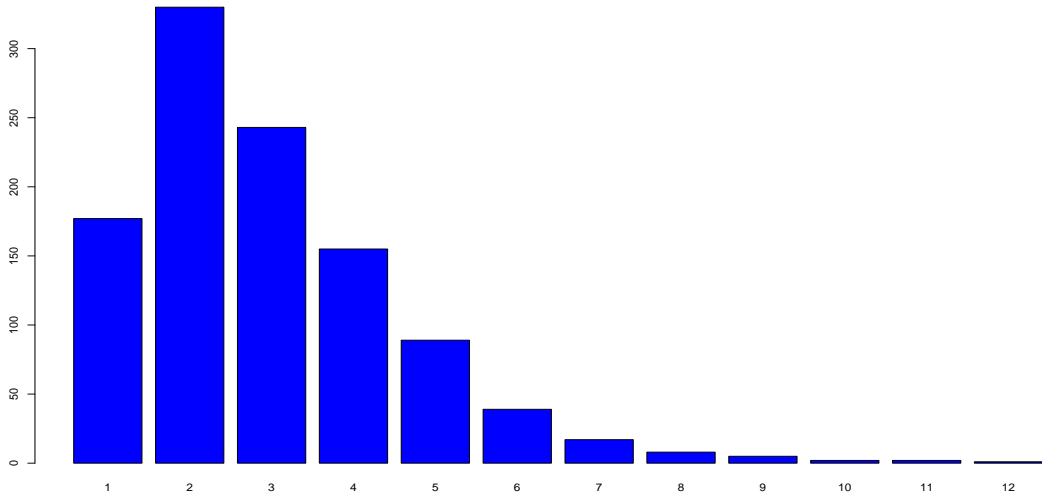
# Packages in selected tasks of Debian Med



# Maintainer per package relation in Debian Med in 2017



# Maintainer per package relation in Debian Med in today



# Debian Med has attracted one developer per year

According to a questionnaire in Wiki

- Debian Med has 42 DDs+DMs (not all active any more)
- 20 DDs *because* Debian Med exists;  
4 DDs before Debian Med started
- 10 out of the 20 above extended their activity to other fields in Debian
- 14 out of the 20 above are active in Debian Med

# Debian Med has attracted one developer per year

According to a questionnaire in Wiki

- Debian Med has 42 DDs+DMs (not all active any more)
- 20 DDs *because* Debian Med exists;  
4 DDs before Debian Med started
- 10 out of the 20 above extended their activity to other fields in Debian
- 14 out of the 20 above are active in Debian Med

# Debian Med has attracted one developer per year

According to a questionnaire in Wiki

- Debian Med has 42 DDs+DMs (not all active any more)
- 20 DDs *because* Debian Med exists;  
4 DDs before Debian Med started
- 10 out of the 20 above extended their activity to other fields in Debian
- 14 out of the 20 above are active in Debian Med



# Debian Med has attracted one developer per year

According to a questionnaire in Wiki

- Debian Med has 42 DDs+DMs (not all active any more)
- 20 DDs *because* Debian Med exists;  
4 DDs before Debian Med started
- 10 out of the 20 above extended their activity to other fields in Debian
- 14 out of the 20 above are active in Debian Med

# Not all tasks are appropriately covered

- **Bioinformatics: very good**
- Medical imaging: good
- Medical practice: there is something (gnumed, just lost freemedforms)
- Hospitals: close to nothing (fis-gtm)  
... besides a stable but unspecific OS

# Not all tasks are appropriately covered

- Bioinformatics: very good
- Medical imaging: good
- Medical practice: there is something (gnumed, just lost freemedforms)
- Hospitals: close to nothing (fis-gtm)  
... besides a stable but unspecific OS

# Not all tasks are appropriately covered

- Bioinformatics: very good
- Medical imaging: good
- Medical practice: there is something (gnumed, just lost freemedforms)
- Hospitals: close to nothing (fis-gtm)  
... besides a stable but unspecific OS

# Not all tasks are appropriately covered

- Bioinformatics: very good
- Medical imaging: good
- Medical practice: there is something (gnumed, just lost freemedforms)
- Hospitals: close to nothing (fis-gtm)  
... besides a stable but unspecific OS

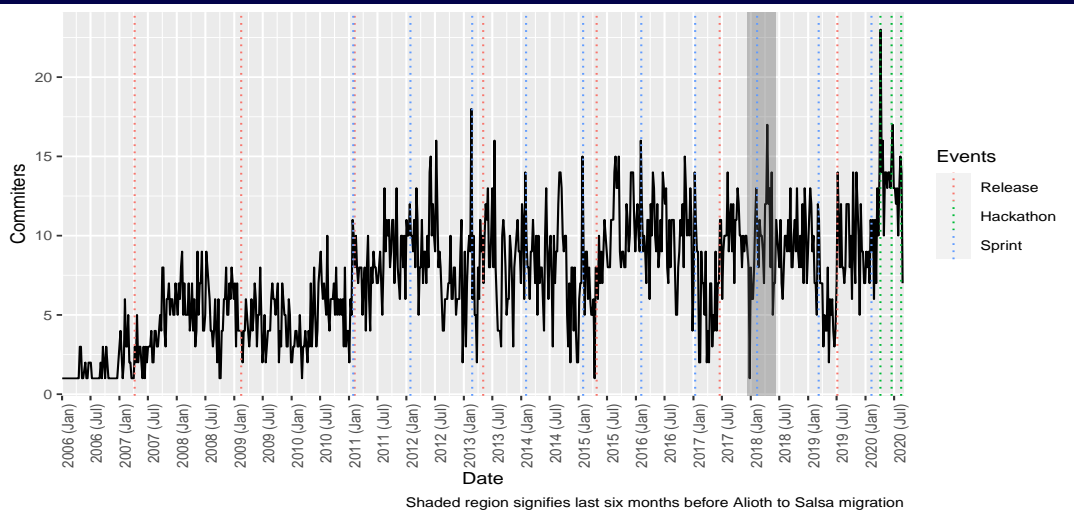
# Graphing the effect of COVID-19 hackathon

- Some graphs from team metrics based on weekly data
- Please note: R packages missing inside the graph since these are maintained in R packaging team

# Graphing the effect of COVID-19 hackathon

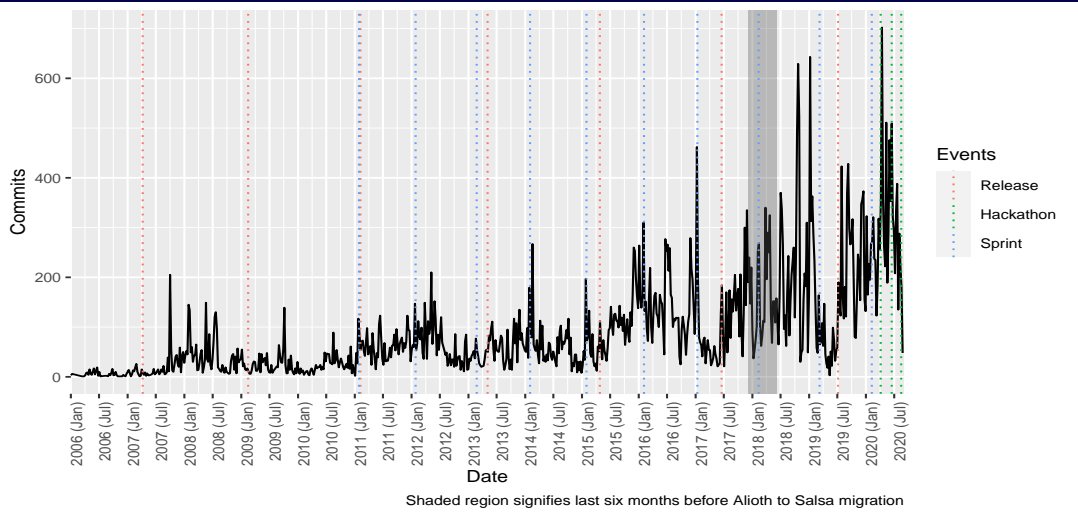
- Some graphs from team metrics based on weekly data
- Please note: R packages missing inside the graph since these are maintained in R packaging team

# Committers to Debian Med packages per week

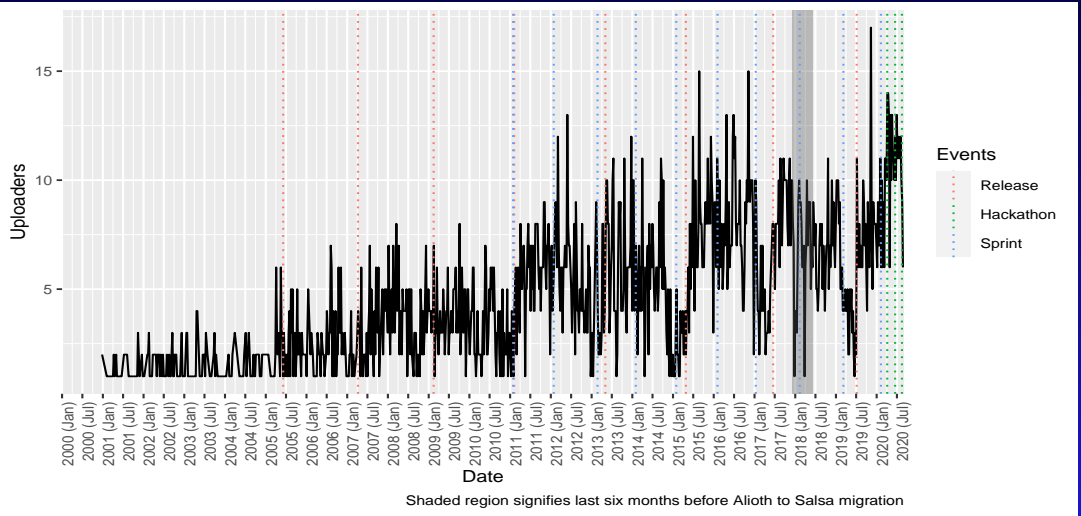




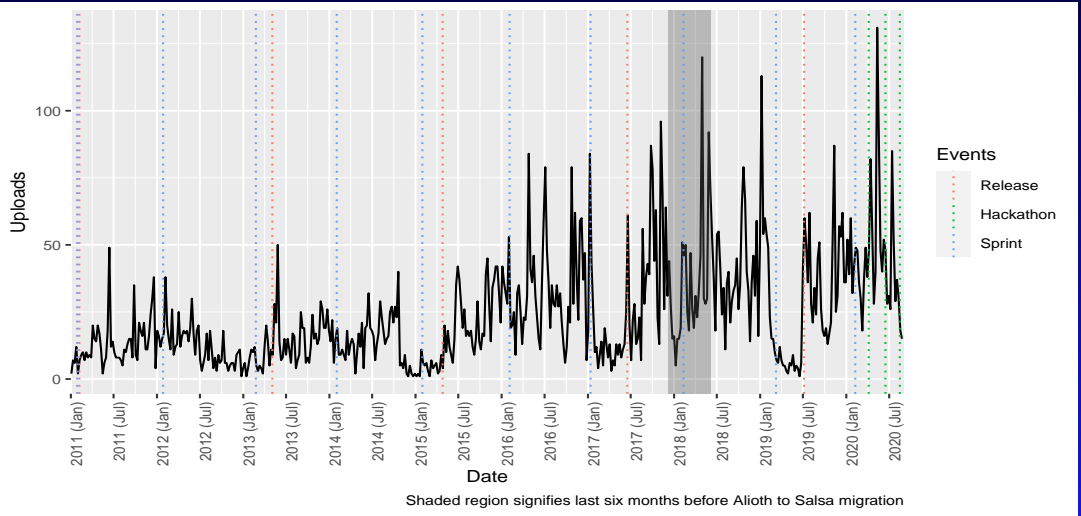
# Commits to Debian Med packages per week



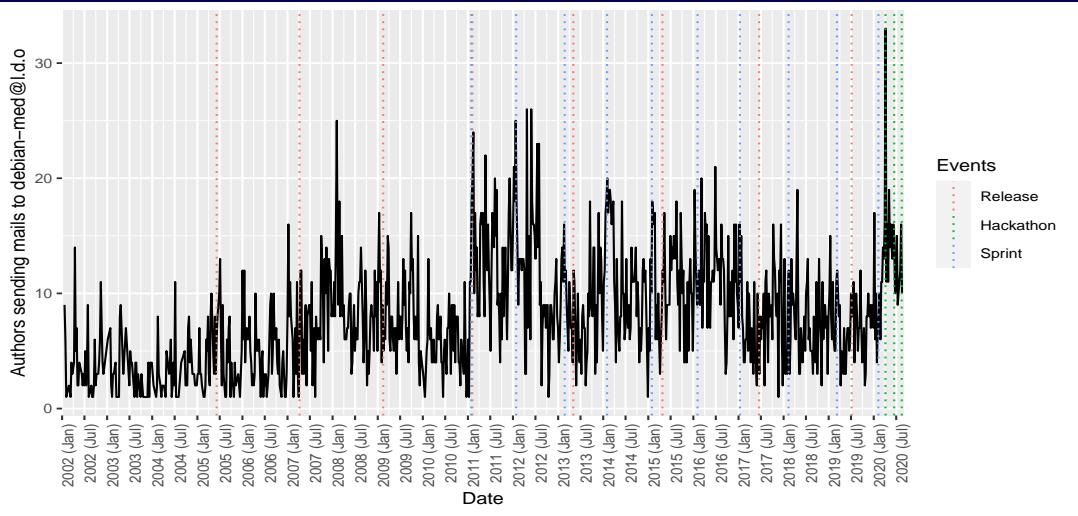
# Uploaders of Debian Med packages per week



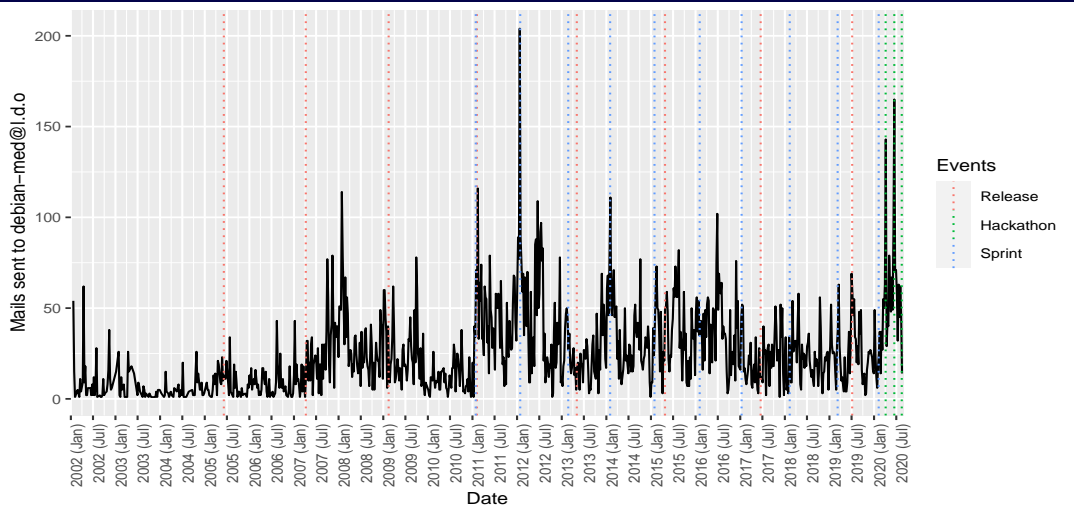
# Uploads of Debian Med packages per week



# Persons posting to debian-med@lists.debian.org



# Posts to debian-med@lists.debian.org



# Communication

- Daily jitsy meeting
- Mailinglist
- IRC
- Telegram

# Communication

- Daily jitsy meeting
- Mailinglist
- IRC
- Telegram

# Communication

- Daily jitsy meeting
- Mailinglist
- IRC
- Telegram



# Communication

- Daily jitsy meeting
- Mailinglist
- IRC
- Telegram

# Amazing ftpmaster support in first hackathon

- **Tons of kudos to ftpmaster for the great support!**

- Many packages in NEW queue were processed in less than 24 h!
- This was the most fun in my whole 22 year of Debian developer life
- It is extremely motivating to get such support
- To quote some understatement of Scott Kitterman:

```
<ScottK> I didn't do anything beyond taking some time off  
work so I would have more time to pick up the FTP Team end of  
getting the new packages in.
```

# Amazing ftpmaster support in first hackathon

- **Tons of kudos to ftpmaster for the great support!**
- Many packages in NEW queue were processed in less than 24 h!
- This was the most fun in my whole 22 year of Debian developer life
- It is extremely motivating to get such support
- To quote some understatement of Scott Kitterman:  
`<ScottK> I didn't do anything beyond taking some time off work so I would have more time to pick up the FTP Team end of getting the new packages in.`

# Amazing ftpmaster support in first hackathon

- **Tons of kudos to ftpmaster for the great support!**
- Many packages in NEW queue were processed in less than 24 h!
- This was the most fun in my whole 22 year of Debian developer life
- It is extremely motivating to get such support
- To quote some understatement of Scott Kitterman:  
`<ScottK> I didn't do anything beyond taking some time off work so I would have more time to pick up the FTP Team end of getting the new packages in.`

# Amazing ftpmaster support in first hackathon

- **Tons of kudos to ftpmaster for the great support!**
- Many packages in NEW queue were processed in less than 24 h!
- This was the most fun in my whole 22 year of Debian developer life
- It is extremely motivating to get such support
- To quote some understatement of Scott Kitterman:  
`<ScottK> I didn't do anything beyond taking some time off work so I would have more time to pick up the FTP Team end of getting the new packages in.`

# Amazing ftpmaster support in first hackathon

- **Tons of kudos to ftpmaster for the great support!**
- Many packages in NEW queue were processed in less than 24 h!
- This was the most fun in my whole 22 year of Debian developer life
- It is extremely motivating to get such support
- To quote some understatement of Scott Kitterman:  
`<ScottK> I didn't do anything beyond taking some time off  
work so I would have more time to pick up the FTP Team end of  
getting the new packages in.`

- Being tolerant to let Andreas Tille work all day even on weekends and holidays.  
**Thank you Katrin!**

# Liubov Chuprikova - Outreachy student last year

- scanned for the COVID/virology-related software, that is not in Debian, on Biohackathon wiki pages and in the scientific literature
- #942404: *discosnp*: flaky autopkgtest



# Liubov Chuprikova - Outreachy student last year

- scanned for the COVID/virology-related software, that is not in Debian, on Biohackathon wiki pages and in the scientific literature
- #942404: *discosnp*: flaky autopkgtest

# Malihe Asemani - former MoM student

- Learning packaging with package *fieldbioinformatics*
- Worked on package *arvados*

# Malihe Asemani - former MoM student

- Learning packaging with package *fieldbioinformatics*
- Worked on package *arvados*

# Rebecca N. Palmer - new to Debian Med

- *snakemake* updates and bug fixing (#955056)
- #953970: *python-boto*: autopkgtest failure with Python 3.8 as default
- joined daily video meetings

# Rebecca N. Palmer - new to Debian Med

- *snakemake* updates and bug fixing (#955056)
- #953970: *python-boto*: autopkgtest failure with Python 3.8 as default
- joined daily video meetings

# Rebecca N. Palmer - new to Debian Med

- *snakemake* updates and bug fixing (#955056)
- #953970: *python-boto*: autopkgtest failure with Python 3.8 as default
- joined daily video meetings

# Sao I Kuan

- Autopkgtests for packages *python-pyani*, *python-tinyalign*, *python-questplus* and *python-etelemetry*

- Packages uploaded to new in the sprint:

- *recan*
- *seirsplus*
- *idseq-bench*
- *insillicoseq*
- *smart-open*
- *ncbi-acc-download*

- Packages continued later

- *benten*
- *cwlformat*
- *dukpy*

- Quote:

Thank you for the opportunities, I really enjoyed them.

# Sao I Kuan

- Autopkgtests for packages *python-pyani*, *python-tinyalign*, *python-questplus* and *python-etelemetry*
- Packages uploaded to new in the sprint:

- *recan*
- *seirsplus*
- *idseq-bench*
- *insillicoseq*
- *smart-open*
- *ncbi-acc-download*

- Packages continued later

- *benten*
- *cwlformat*
- *dukpy*

- Quote:

Thank you for the opportunities, I really enjoyed them.



# Sao I Kuan

- Autopkgtests for packages *python-pyani*, *python-tinyalign*, *python-questplus* and *python-etelemetry*
- Packages uploaded to new in the sprint:

- *recan*
- *seirsplus*
- *idseq-bench*
- *insillicoseq*
- *smart-open*
- *ncbi-acc-download*

- Packages continued later

- *benten*
- *cwlformat*
- *dukpy*

- Quote:

Thank you for the opportunities, I really enjoyed them.

# Sao I Kuan

- Autopkgtests for packages *python-pyani*, *python-tinyalign*, *python-questplus* and *python-etelemetry*
- Packages uploaded to new in the sprint:

- *recan*
- *seirsplus*
- *idseq-bench*
- *insillicoseq*
- *smart-open*
- *ncbi-acc-download*

- Packages continued later

- *benten*
- *cwlformat*
- *dukpy*

- Quote:

Thank you for the opportunities, I really enjoyed them.

# Sao I Kuan

- Autopkgtests for packages *python-pyani*, *python-tinyalign*, *python-questplus* and *python-etelemetry*
- Packages uploaded to new in the sprint:

- *recan*
- *seirsplus*
- *idseq-bench*
- *insillicoseq*
- *smart-open*
- *ncbi-acc-download*

- Packages continued later

- *benten*
- *cwlformat*
- *dukpy*

- Quote:

Thank you for the opportunities, I really enjoyed them.

# Sao I Kuan

- Autopkgtests for packages *python-pyani*, *python-tinyalign*, *python-questplus* and *python-etelemetry*
- Packages uploaded to new in the sprint:

- *recan*
- *seirsplus*
- *idseq-bench*
- *insillicoseq*
- *smart-open*
- *ncbi-acc-download*

- Packages continued later

- *benten*
- *cwlformat*
- *dukpy*

- Quote:

Thank you for the opportunities, I really enjoyed them.

# Sao I Kuan

- Autopkgtests for packages *python-pyani*, *python-tinyalign*, *python-questplus* and *python-etelemetry*

- Packages uploaded to new in the sprint:

- *recan*
- *seirsplus*
- *idseq-bench*
- *insillicoseq*
- *smart-open*
- *ncbi-acc-download*

- Packages continued later

- *benten*
- *cwlformat*
- *dukpy*

- Quote:

Thank you for the opportunities, I really enjoyed them.

# Sao I Kuan

- Autopkgtests for packages *python-pyani*, *python-tinyalign*, *python-questplus* and *python-etelemetry*
- Packages uploaded to new in the sprint:

- *recan*
- *seirsplus*
- *idseq-bench*
- *insillicoseq*
- *smart-open*
- *ncbi-acc-download*

- Packages continued later

- *benten*
- *cwlformat*
- *dukpy*

- Quote:

Thank you for the opportunities, I really enjoyed them.

# Sao I Kuan

- Autopkgtests for packages *python-pyani*, *python-tinyalign*, *python-questplus* and *python-etelemetry*

- Packages uploaded to new in the sprint:

- *recan*
- *seirsplus*
- *idseq-bench*
- *insillicoseq*
- *smart-open*
- *ncbi-acc-download*

- Packages continued later

- *benten*
- *cwlformat*
- *dukpy*

- Quote:

Thank you for the opportunities, I really enjoyed them.

# Sao I Kuan

- Autopkgtests for packages *python-pyani*, *python-tinyalign*, *python-questplus* and *python-etelemetry*

- Packages uploaded to new in the sprint:

- *recan*
- *seirsplus*
- *idseq-bench*
- *insillicoseq*
- *smart-open*
- *ncbi-acc-download*

- Packages continued later

- *benten*
- *cwlformat*
- *dukpy*

- Quote:

Thank you for the opportunities, I really enjoyed them.



# Sao I Kuan

- Autopkgtests for packages *python-pyani*, *python-tinyalign*, *python-questplus* and *python-etelemetry*

- Packages uploaded to new in the sprint:

- *recan*
- *seirsplus*
- *idseq-bench*
- *insillicoseq*
- *smart-open*
- *ncbi-acc-download*

- Packages continued later

- *benten*
- *cwlformat*
- *dukpy*

- Quote:

Thank you for the opportunities, I really enjoyed them.

# Sao I Kuan

- Autopkgtests for packages *python-pyani*, *python-tinyalign*, *python-questplus* and *python-etelemetry*
- Packages uploaded to new in the sprint:

- *recan*
- *seirsplus*
- *idseq-bench*
- *insillicoseq*
- *smart-open*
- *ncbi-acc-download*

- Packages continued later

- *benten*
- *cwlformat*
- *dukpy*

- Quote:

Thank you for the opportunities, I really enjoyed them.

# Sao I Kuan

- Autopkgtests for packages *python-pyani*, *python-tinyalign*, *python-questplus* and *python-etelemetry*

- Packages uploaded to new in the sprint:

- *recan*
- *seirsplus*
- *idseq-bench*
- *insillicoseq*
- *smart-open*
- *ncbi-acc-download*

- Packages continued later

- *benten*
- *cwlformat*
- *dukpy*

- Quote:

Thank you for the opportunities, I really enjoyed them.

- *orthanc-python*

# Andreas Tille

- **New packages:** *augur*, *chip-seq*, *wtdbg2*, *r-cran-mediana*, *r-bioc-rgsepd*, *r-bioc-pwmenrich*, *r-cran-covid19us*, *r-bioc-mutationalpatterns*, *r-bioc-tcgabiolinks*, *r-bioc-rots*, as well as 36 preconditions for GNU R packages above
- Packages in progress *r-bioc-rcpi*, *r-cran-covid19*, *r-bioc-motifstack*
- Backports: *augur*, *chip-seq*
- Infrastructure
  - Fixed Ubuntu Thermometer page to display the latest Ubuntu releases
  - Importer for autopkgtest data in UDD
  - Checked excuses metadata for valuable data
- Licensing issues discussion with upstream
  - *trf* → **now free and in Debian**
  - *blat* unfortunately no progress
  - *r-cran-locfit* → free: enables prominent reverse dependencies in main
  - *gmap* → free
- Teaching

# Andreas Tille

- **New packages:** *augur*, *chip-seq*, *wtdbg2*, *r-cran-mediana*, *r-bioc-rgsepd*, *r-bioc-pwmenrich*, *r-cran-covid19us*, *r-bioc-mutationalpatterns*, *r-bioc-tcgabiolinks*, *r-bioc-rots*, as well as 36 preconditions for GNU R packages above
- **Packages in progress** *r-bioc-rcpi*, *r-cran-covid19*, *r-bioc-motifstack*
- **Backports:** *augur*, *chip-seq*
- **Infrastructure**
  - Fixed Ubuntu Thermometer page to display the latest Ubuntu releases
  - Importer for autopkgtest data in UDD
  - Checked excuses metadata for valuable data
- **Licensing issues discussion with upstream**
  - *trf* → **now free and in Debian**
  - *blat* unfortunately no progress
  - *r-cran-locfit* → free: enables prominent reverse dependencies in main
  - *gmap* → free
- **Teaching**

# Andreas Tille

- **New packages:** *augur*, *chip-seq*, *wtdbg2*, *r-cran-mediana*, *r-bioc-rgsepd*, *r-bioc-pwmenrich*, *r-cran-covid19us*, *r-bioc-mutationalpatterns*, *r-bioc-tcgabiolinks*, *r-bioc-rots*, as well as 36 preconditions for GNU R packages above
- **Packages in progress** *r-bioc-rcpi*, *r-cran-covid19*, *r-bioc-motifstack*
- **Backports:** *augur*, *chip-seq*
- **Infrastructure**
  - Fixed Ubuntu Thermometer page to display the latest Ubuntu releases
  - Importer for autopkgtest data in UDD
  - Checked excuses metadata for valuable data
- **Licensing issues discussion with upstream**
  - *trf* → **now free and in Debian**
  - *blat* unfortunately no progress
  - *r-cran-locfit* → free: enables prominent reverse dependencies in main
  - *gmap* → free
- **Teaching**

# Andreas Tille

- **New packages:** *augur*, *chip-seq*, *wtdbg2*, *r-cran-mediana*, *r-bioc-rgsepd*, *r-bioc-pwmenrich*, *r-cran-covid19us*, *r-bioc-mutationalpatterns*, *r-bioc-tcgabiolinks*, *r-bioc-rots*, as well as 36 preconditions for GNU R packages above
- **Packages in progress** *r-bioc-rcpi*, *r-cran-covid19*, *r-bioc-motifstack*
- **Backports:** *augur*, *chip-seq*
- **Infrastructure**
  - Fixed Ubuntu Thermometer page to display the latest Ubuntu releases
  - Importer for autopkgtest data in UDD
  - Checked excuses metadata for valuable data
- **Licensing issues discussion with upstream**
  - *trf* → **now free and in Debian**
  - *blat* unfortunately no progress
  - *r-cran-locfit* → free: enables prominent reverse dependencies in main
  - *gmap* → free
- **Teaching**



# Andreas Tille

- **New packages:** *augur*, *chip-seq*, *wtdbg2*, *r-cran-mediana*, *r-bioc-rgsepd*, *r-bioc-pwmenrich*, *r-cran-covid19us*, *r-bioc-mutationalpatterns*, *r-bioc-tcgabiolinks*, *r-bioc-rots*, as well as 36 preconditions for GNU R packages above
- **Packages in progress** *r-bioc-rcpi*, *r-cran-covid19*, *r-bioc-motifstack*
- **Backports:** *augur*, *chip-seq*
- **Infrastructure**
  - Fixed Ubuntu Thermometer page to display the latest Ubuntu releases
  - Importer for autopkgtest data in UDD
  - Checked excuses metadata for valuable data
- **Licensing issues discussion with upstream**
  - *trf* → **now free and in Debian**
  - *blat* unfortunately no progress
  - *r-cran-locfit* → free: enables prominent reverse dependencies in main
  - *gmap* → free
- **Teaching**

# Andreas Tille

- **New packages:** *augur*, *chip-seq*, *wtdbg2*, *r-cran-mediana*, *r-bioc-rgsepd*, *r-bioc-pwmenrich*, *r-cran-covid19us*, *r-bioc-mutationalpatterns*, *r-bioc-tcgabiolinks*, *r-bioc-rots*, as well as 36 preconditions for GNU R packages above
- **Packages in progress** *r-bioc-rcpi*, *r-cran-covid19*, *r-bioc-motifstack*
- **Backports:** *augur*, *chip-seq*
- **Infrastructure**
  - Fixed Ubuntu Thermometer page to display the latest Ubuntu releases
  - Importer for autopkgtest data in UDD
  - Checked excuses metadata for valuable data
- **Licensing issues discussion with upstream**
  - *trf* → **now free and in Debian**
  - *blat* unfortunately no progress
  - *r-cran-locfit* → free: enables prominent reverse dependencies in main
  - *gmap* → free
- **Teaching**

# Andreas Tille

- **New packages:** *augur*, *chip-seq*, *wtdbg2*, *r-cran-mediana*, *r-bioc-rgsepd*, *r-bioc-pwmenrich*, *r-cran-covid19us*, *r-bioc-mutationalpatterns*, *r-bioc-tcgabiolinks*, *r-bioc-rots*, as well as 36 preconditions for GNU R packages above
- **Packages in progress** *r-bioc-rcpi*, *r-cran-covid19*, *r-bioc-motifstack*
- **Backports:** *augur*, *chip-seq*
- **Infrastructure**
  - Fixed Ubuntu Thermometer page to display the latest Ubuntu releases
  - Importer for autopkgtest data in UDD
  - Checked excuses metadata for valuable data
- **Licensing issues discussion with upstream**
  - *trf* → **now free and in Debian**
  - *blat* unfortunately no progress
  - *r-cran-locfit* → free: enables prominent reverse dependencies in main
  - *gmap* → free
- **Teaching**

# Andreas Tille

- **New packages:** *augur*, *chip-seq*, *wtdbg2*, *r-cran-mediana*, *r-bioc-rgsepd*, *r-bioc-pwmenrich*, *r-cran-covid19us*, *r-bioc-mutationalpatterns*, *r-bioc-tcgabiolinks*, *r-bioc-rots*, as well as 36 preconditions for GNU R packages above
- **Packages in progress** *r-bioc-rcpi*, *r-cran-covid19*, *r-bioc-motifstack*
- **Backports:** *augur*, *chip-seq*
- **Infrastructure**
  - Fixed Ubuntu Thermometer page to display the latest Ubuntu releases
  - Importer for autopkgtest data in UDD
  - Checked excuses metadata for valuable data
- **Licensing issues discussion with upstream**
  - *trf* → **now free and in Debian**
  - *blat* unfortunately no progress
  - *r-cran-locfit* → free: enables prominent reverse dependencies in main
  - *gmap* → free
- **Teaching**

# Andreas Tille

- **New packages:** *augur*, *chip-seq*, *wtdbg2*, *r-cran-mediana*, *r-bioc-rgsepd*, *r-bioc-pwmenrich*, *r-cran-covid19us*, *r-bioc-mutationalpatterns*, *r-bioc-tcgabioblinks*, *r-bioc-rots*, as well as 36 preconditions for GNU R packages above
- **Packages in progress** *r-bioc-rcpi*, *r-cran-covid19*, *r-bioc-motifstack*
- **Backports:** *augur*, *chip-seq*
- **Infrastructure**
  - Fixed Ubuntu Thermometer page to display the latest Ubuntu releases
  - Importer for autopkgtest data in UDD
  - Checked excuses metadata for valuable data
- **Licensing issues discussion with upstream**
  - *trf* → **now free and in Debian**
  - *blat* unfortunately no progress
  - *r-cran-locfit* → free: enables prominent reverse dependencies in main
  - *gmap* → free
- **Teaching**

# Andreas Tille

- **New packages:** *augur*, *chip-seq*, *wtdbg2*, *r-cran-mediana*, *r-bioc-rgsepd*, *r-bioc-pwmenrich*, *r-cran-covid19us*, *r-bioc-mutationalpatterns*, *r-bioc-tcgabioblinks*, *r-bioc-rots*, as well as 36 preconditions for GNU R packages above
- **Packages in progress** *r-bioc-rcpi*, *r-cran-covid19*, *r-bioc-motifstack*
- **Backports:** *augur*, *chip-seq*
- **Infrastructure**
  - Fixed Ubuntu Thermometer page to display the latest Ubuntu releases
  - Importer for autopkgtest data in UDD
  - Checked excuses metadata for valuable data
- **Licensing issues discussion with upstream**
  - *trf* → **now free and in Debian**
  - *blat* unfortunately no progress
  - *r-cran-locfit* → free: enables prominent reverse dependencies in main
  - *gmap* → free
- **Teaching**

# Andreas Tille

- **New packages:** *augur*, *chip-seq*, *wtdbg2*, *r-cran-mediana*, *r-bioc-rgsepd*, *r-bioc-pwmenrich*, *r-cran-covid19us*, *r-bioc-mutationalpatterns*, *r-bioc-tcgabiolinks*, *r-bioc-rots*, as well as 36 preconditions for GNU R packages above
- **Packages in progress** *r-bioc-rcpi*, *r-cran-covid19*, *r-bioc-motifstack*
- **Backports:** *augur*, *chip-seq*
- **Infrastructure**
  - Fixed Ubuntu Thermometer page to display the latest Ubuntu releases
  - Importer for autopkgtest data in UDD
  - Checked excuses metadata for valuable data
- **Licensing issues discussion with upstream**
  - *trf* → **now free and in Debian**
  - *blat* unfortunately no progress
  - *r-cran-locfit* → free: enables prominent reverse dependencies in main
  - *gmap* → free
- **Teaching**

# Andreas Tille

- **New packages:** *augur*, *chip-seq*, *wtdbg2*, *r-cran-mediana*, *r-bioc-rgsepd*, *r-bioc-pwmenrich*, *r-cran-covid19us*, *r-bioc-mutationalpatterns*, *r-bioc-tcgabiolinks*, *r-bioc-rots*, as well as 36 preconditions for GNU R packages above
- **Packages in progress** *r-bioc-rcpi*, *r-cran-covid19*, *r-bioc-motifstack*
- **Backports:** *augur*, *chip-seq*
- **Infrastructure**
  - Fixed Ubuntu Thermometer page to display the latest Ubuntu releases
  - Importer for autopkgtest data in UDD
  - Checked excuses metadata for valuable data
- **Licensing issues discussion with upstream**
  - *trf* → **now free and in Debian**
  - *blat* unfortunately no progress
  - *r-cran-locfit* → free: enables prominent reverse dependencies in main
  - *gmap* → free
- **Teaching**



# Andreas Tille

- **New packages:** *augur*, *chip-seq*, *wtdbg2*, *r-cran-mediana*, *r-bioc-rgsepd*, *r-bioc-pwmenrich*, *r-cran-covid19us*, *r-bioc-mutationalpatterns*, *r-bioc-tcgabioblinks*, *r-bioc-rots*, as well as 36 preconditions for GNU R packages above
- **Packages in progress** *r-bioc-rcpi*, *r-cran-covid19*, *r-bioc-motifstack*
- **Backports:** *augur*, *chip-seq*
- **Infrastructure**
  - Fixed Ubuntu Thermometer page to display the latest Ubuntu releases
  - Importer for autopkgtest data in UDD
  - Checked excuses metadata for valuable data
- **Licensing issues discussion with upstream**
  - *trf* → **now free and in Debian**
  - *blat* unfortunately no progress
  - *r-cran-locfit* → free: enables prominent reverse dependencies in main
  - *gmap* → free
- **Teaching**

# Andrius Merkys - DebiChem

- *openmm* (High-performance molecular simulation library)
- *macromoleculebuilder* (only protein homology modelling tool in Debian)
- JS dependencies of streamlit: *node-cuint*, *node-xxhashjs*
- JS dependencies of shiny-server: *node-ip-address*, *node-stable*
- Quote

Congrats! And thank you for your tremendous efforts to coordinate the hackathon! :)

# Andrius Merkys - DebiChem

- *openmm* (High-performance molecular simulation library)
- *macromoleculebuilder* (only protein homology modelling tool in Debian)
- JS dependencies of streamlit: *node-cuint*, *node-xxhashjs*
- JS dependencies of shiny-server: *node-ip-address*, *node-stable*
- Quote

Congrats! And thank you for your tremendous efforts to coordinate the hackathon! :)

# Andrius Merkys - DebiChem

- *openmm* (High-performance molecular simulation library)
- *macromoleculebuilder* (only protein homology modelling tool in Debian)
- JS dependencies of streamlit: *node-cuint*, *node-xxhashjs*
- JS dependencies of shiny-server: *node-ip-address*, *node-stable*
- Quote

Congrats! And thank you for your tremendous efforts to coordinate the hackathon! :)

# Andrius Merkys - DebiChem

- *openmm* (High-performance molecular simulation library)
- *macromoleculebuilder* (only protein homology modelling tool in Debian)
- JS dependencies of streamlit: *node-cuint*, *node-xxhashjs*
- JS dependencies of shiny-server: *node-ip-address*, *node-stable*
- Quote

Congrats! And thank you for your tremendous efforts to coordinate the hackathon! :)

# Andrius Merkys - DebiChem

- *openmm* (High-performance molecular simulation library)
- *macromoleculebuilder* (only protein homology modelling tool in Debian)
- JS dependencies of streamlit: *node-cuint*, *node-xxhashjs*
- JS dependencies of shiny-server: *node-ip-address*, *node-stable*
- Quote

Congrats! And thank you for your tremendous efforts to coordinate the hackathon! :)

# Antoni Villalonga - new in Debian Med

- *sprai* (Python2 to Python3 #943280)
- *harvest-tools* (Python2 to Python3 #943055)
- *kmer* (Python2 to Python3 #936802, #958840)
- *kissplice* (Python2 to Python3 #936798)
- Remained active in second sprint in June

# Antoni Villalonga - new in Debian Med

- *sprai* (Python2 to Python3 #943280)
- *harvest-tools* (Python2 to Python3 #943055)
- *kmer* (Python2 to Python3 #936802, #958840)
- *kissplice* (Python2 to Python3 #936798)
- Remained active in second sprint in June



# Antoni Villalonga - new in Debian Med

- *sprai* (Python2 to Python3 #943280)
- *harvest-tools* (Python2 to Python3 #943055)
- *kmer* (Python2 to Python3 #936802, #958840)
- *kissplice* (Python2 to Python3 #936798)
- Remained active in second sprint in June

# Antoni Villalonga - new in Debian Med

- *sprai* (Python2 to Python3 #943280)
- *harvest-tools* (Python2 to Python3 #943055)
- *kmer* (Python2 to Python3 #936802, #958840)
- *kissplice* (Python2 to Python3 #936798)
- Remained active in second sprint in June

# Antoni Villalonga - new in Debian Med

- *sprai* (Python2 to Python3 #943280)
- *harvest-tools* (Python2 to Python3 #943055)
- *kmer* (Python2 to Python3 #936802, #958840)
- *kissplice* (Python2 to Python3 #936798)
- Remained active in second sprint in June

- List of possibly COVID-19 relevant packages
- General QA work to spot issues in relevant Debian Med packages
- For instance spot non-functional watch files (like python-deeptools) by comparing Debian and upstream version
- Non-technical work

- List of possibly COVID-19 relevant packages
- General QA work to spot issues in relevant Debian Med packages
- For instance spot non-functional watch files (like python-deeptools) by comparing Debian and upstream version
- Non-technical work

- List of possibly COVID-19 relevant packages
- General QA work to spot issues in relevant Debian Med packages
- For instance spot non-functional watch files (like python-deeptools) by comparing Debian and upstream version
- Non-technical work

- List of possibly COVID-19 relevant packages
- General QA work to spot issues in relevant Debian Med packages
- For instance spot non-functional watch files (like python-deeptools) by comparing Debian and upstream version
- Non-technical work

# Dylan Aïssi

- *r-cran-isoband*
- Bug fixing
  - #942469 of *r-cran-rmarkdown*,
  - #943550 of *r-cran-rmarkdown*
  - #955640 of *r-cran-uwot*
  - #954813 of *r-cran-rlang*
  - #955167 of *r-cran-sf*
- Thanks a lot to Dylan for stepping in for all those *r-{bioconductor,cran}-\** packages which I left alone since the COVID-19 effort started



# Dylan Aïssi

- *r-cran-isoband*
- **Bug fixing**
  - #942469 of *r-cran-rmarkdown*,
  - #943550 of *r-cran-rmarkdown*
  - #955640 of *r-cran-uwot*
  - #954813 of *r-cran-rlang*
  - #955167 of *r-cran-sf*
- Thanks a lot to Dylan for stepping in for all those *r-{bioconductor,cran}-\** packages which I left alone since the COVID-19 effort started

# Dylan Aïssi

- *r-cran-isoband*
- **Bug fixing**
  - #942469 of *r-cran-rmarkdown*,
  - #943550 of *r-cran-rmarkdown*
  - #955640 of *r-cran-uwot*
  - #954813 of *r-cran-rlang*
  - #955167 of *r-cran-sf*
- Thanks a lot to Dylan for stepping in for all those *r- $\{bioconductor, cran\}$ -\** packages which I left alone since the COVID-19 effort started

# Emmanuel Arias - new in Debian Med

- ITP *idseq-dag*

# Étienne Mollier - new in Debian Med

- *prinseq-lite* as well as its dependencies
- WIP: *virusseeker-virome*
- WIP: *repeatmasker* (licensing issues)
- Helped moving forward licensing discussion with Tandem Repeats Finder upstream
- Lots of RC bugfixes (Python2 to Python3 migration, gcc-10) as well as #952757 of *mypy*
- Joined all video meetings

# Étienne Mollier - new in Debian Med

- *prinseq-lite* as well as its dependencies
- **WIP:** *virusseeker-virome*
- WIP: *repeatmasker* (licensing issues)
- Helped moving forward licensing discussion with Tandem Repeats Finder upstream
- Lots of RC bugfixes (Python2 to Python3 migration, gcc-10) as well as #952757 of *mypy*
- Joined all video meetings

# Étienne Mollier - new in Debian Med

- *prinseq-lite* as well as its dependencies
- **WIP:** *virusseeker-virome*
- **WIP:** *repeatmasker* (licensing issues)
- Helped moving forward licensing discussion with Tandem Repeats Finder upstream
- Lots of RC bugfixes (Python2 to Python3 migration, gcc-10) as well as #952757 of *mypy*
- Joined all video meetings

# Étienne Mollier - new in Debian Med

- *prinseq-lite* as well as its dependencies
- **WIP:** *virusseeker-virome*
- **WIP:** *repeatmasker* (licensing issues)
- **Helped moving forward licensing discussion with Tandem Repeats Finder upstream**
- Lots of RC bugfixes (Python2 to Python3 migration, gcc-10) as well as #952757 of *mypy*
- Joined all video meetings

# Étienne Mollier - new in Debian Med

- *prinseq-lite* as well as its dependencies
- **WIP:** *virusseeker-virome*
- **WIP:** *repeatmasker* (licensing issues)
- Helped moving forward licensing discussion with Tandem Repeats Finder upstream
- Lots of RC bugfixes (Python2 to Python3 migration, gcc-10) as well as #952757 of *mypy*
- Joined all video meetings



# Étienne Mollier - new in Debian Med

- *prinseq-lite* as well as its dependencies
- WIP: *virusseeker-virome*
- WIP: *repeatmasker* (licensing issues)
- Helped moving forward licensing discussion with Tandem Repeats Finder upstream
- Lots of RC bugfixes (Python2 to Python3 migration, gcc-10) as well as #952757 of *mypy*
- Joined all video meetings

# Hamid - friend from DebConf19

- Fixes for *minimap2*
- #956136: *nanopolish*: FTBFS (undefined references)

# Hamid - friend from DebConf19

- Fixes for *minimap2*
- #956136: *nanopolish*: FTBFS (undefined references)

# Jun Aruga - Redhat, Fedora MedicalSig, Sprint participant

- Create spreadsheet with COVID-19 relevant software used in workflows showing what is available in Redhat, Debian and Conda
- Extremely helpful as todo list and to coordinate work
- General discussion about Nanopore workflows

# Jun Aruga - Redhat, Fedora MedicalSig, Sprint participant

- Create spreadsheet with COVID-19 relevant software used in workflows showing what is available in Redhat, Debian and Conda
- Extremely helpful as todo list and to coordinate work
- General discussion about Nanopore workflows

# Jun Aruga - Redhat, Fedora MedicalSig, Sprint participant

- Create spreadsheet with COVID-19 relevant software used in workflows showing what is available in Redhat, Debian and Conda
- Extremely helpful as todo list and to coordinate work
- General discussion about Nanopore workflows

# Michael R. Crusoe - became DD soon after Hackathon

- Communication and reports to COVID-19 Biohackathon of world wide bioinformatics projects where Debian Med participated in
- Created Git repository on Salsa as well as Wiki pages
- Assembled the final report about the hackathon
- *routine-update*
- Bug #955566: *khmer*: autopkgtest regression: undefined references

# Michael R. Crusoe - became DD soon after Hackathon

- Communication and reports to COVID-19 Biohackathon of world wide bioinformatics projects where Debian Med participated in
- Created Git repository on Salsa as well as Wiki pages
- Assembled the final report about the hackathon
- *routine-update*
- Bug #955566: *khmer*: autopkgtest regression: undefined references



# Michael R. Crusoe - became DD soon after Hackathon

- Communication and reports to COVID-19 Biohackathon of world wide bioinformatics projects where Debian Med participated in
- Created Git repository on Salsa as well as Wiki pages
- Assembled the final report about the hackathon
- *routine-update*
- Bug #955566: *khmer*: autopkgtest regression: undefined references

# Michael R. Crusoe - became DD soon after Hackathon

- Communication and reports to COVID-19 Biohackathon of world wide bioinformatics projects where Debian Med participated in
- Created Git repository on Salsa as well as Wiki pages
- Assembled the final report about the hackathon
- *routine-update*
- Bug #955566: *khmer*: autopkgtest regression: undefined references

# Michael R. Crusoe - became DD soon after Hackathon

- Communication and reports to COVID-19 Biohackathon of world wide bioinformatics projects where Debian Med participated in
- Created Git repository on Salsa as well as Wiki pages
- Assembled the final report about the hackathon
- *routine-update*
- Bug #955566: *khmer*: autopkgtest regression: undefined references

# Nilesh Patra - GSoC student

- *parasail* new package helping several reverse depends
- Autopkgtest and fixes for *r-bioc-demixt*
- Joined all video meetings
- Lots of further contributions after the sprint
- Became DM meanwhile
- Quote:

Thanks a lot for these efforts, and congratulations on getting your talk selected!

# Nilesh Patra - GSoC student

- *parasail* new package helping several reverse depends
- Autopkgtest and fixes for *r-bioc-demixt*
- Joined all video meetings
- Lots of further contributions after the sprint
- Became DM meanwhile
- Quote:

Thanks a lot for these efforts, and congratulations on getting your talk selected!

# Nilesh Patra - GSoC student

- *parasail* new package helping several reverse depends
- Autopkgtest and fixes for *r-bioc-demixt*
- Joined all video meetings
- Lots of further contributions after the sprint
- Became DM meanwhile
- Quote:

Thanks a lot for these efforts, and congratulations on getting your talk selected!

# Nilesh Patra - GSoC student

- *parasail* new package helping several reverse depends
- Autopkgtest and fixes for *r-bioc-demixt*
- Joined all video meetings
- Lots of further contributions after the sprint
- Became DM meanwhile
- Quote:

Thanks a lot for these efforts, and congratulations on getting your talk selected!

# Nilesh Patra - GSoC student

- *parasail* new package helping several reverse depends
- Autopkgtest and fixes for *r-bioc-demixt*
- Joined all video meetings
- Lots of further contributions after the sprint
- Became DM meanwhile
- Quote:

Thanks a lot for these efforts, and congratulations on getting your talk selected!



# Nilesh Patra - GSoC student

- *parasail* new package helping several reverse depends
- Autopkgtest and fixes for *r-bioc-demixt*
- Joined all video meetings
- Lots of further contributions after the sprint
- Became DM meanwhile
- Quote:

Thanks a lot for these efforts, and congratulations on getting your talk selected!

# Olek Wojnar - new in Debian Med

- Arranged expedited NEW review with ftpmaster team. Documented process in email and on wiki.
- Introducing, guiding and sponsoring newcomers.
- Initiate *bazel* packaging team
- Opening the option to package *tensorflow* which enables lots of other COVID-19 relevant packages
- *Thanks a lot Olek, for your great work!*

# Olek Wojnar - new in Debian Med

- Arranged expedited NEW review with ftpmaster team. Documented process in email and on wiki.
- Introducing, guiding and sponsoring newcomers.
- Initiate *bazel* packaging team
- Opening the option to package *tensorflow* which enables lots of other COVID-19 relevant packages
- *Thanks a lot Olek, for your great work!*

# Olek Wojnar - new in Debian Med

- Arranged expedited NEW review with ftpmaster team. Documented process in email and on wiki.
- Introducing, guiding and sponsoring newcomers.
- Initiate *bazel* packaging team
- Opening the option to package *tensorflow* which enables lots of other COVID-19 relevant packages
- *Thanks a lot Olek, for your great work!*

# Olek Wojnar - new in Debian Med

- Arranged expedited NEW review with ftpmaster team. Documented process in email and on wiki.
- Introducing, guiding and sponsoring newcomers.
- Initiate *bazel* packaging team
- Opening the option to package *tensorflow* which enables lots of other COVID-19 relevant packages
- *Thanks a lot Olek, for your great work!*

# Olek Wojnar - new in Debian Med

- Arranged expedited NEW review with ftpmaster team. Documented process in email and on wiki.
- Introducing, guiding and sponsoring newcomers.
- Initiate *bazel* packaging team
- Opening the option to package *tensorflow* which enables lots of other COVID-19 relevant packages
- *Thanks a lot Olek, for your great work!*

# Pierre Gruet - new in Debian Med

- Wrote tests for *sumaclust* and its close relatives *sumatra* and *sumalibs*
- Closed bugs:
  - #952093 of *sumaclust* (FTBFS)
  - #954262 of *sumaclust*: fails to migrate to testing for too long
  - #956232 of *sumaclust*: Last sequence of input is skipped on arm64
- Several Java dependencies of *snpeff*
- Kept on working in the team fixing Java dependencies

# Pierre Gruet - new in Debian Med

- Wrote tests for *sumaclust* and its close relatives *sumatra* and *sumalibs*
- Closed bugs:
  - #952093 of *sumaclust* (FTBFS)
  - #954262 of *sumaclust*: fails to migrate to testing for too long
  - #956232 of *sumaclust*: Last sequence of input is skipped on arm64
- Several Java dependencies of *snpeff*
- Kept on working in the team fixing Java dependencies



# Pierre Gruet - new in Debian Med

- Wrote tests for *sumaclust* and its close relatives *sumatra* and *sumalibs*
- Closed bugs:
  - #952093 of *sumaclust* (FTBFS)
  - #954262 of *sumaclust*: fails to migrate to testing for too long
  - #956232 of *sumaclust*: Last sequence of input is skipped on arm64
- Several Java dependencies of *snpeff*
- Kept on working in the team fixing Java dependencies

# Pierre Gruet - new in Debian Med

- Wrote tests for *sumaclust* and its close relatives *sumatra* and *sumalibs*
- Closed bugs:
  - #952093 of *sumaclust* (FTBFS)
  - #954262 of *sumaclust*: fails to migrate to testing for too long
  - #956232 of *sumaclust*: Last sequence of input is skipped on arm64
- Several Java dependencies of *snpeff*
- Kept on working in the team fixing Java dependencies

# Pierre Gruet - new in Debian Med

- Wrote tests for *sumaclust* and its close relatives *sumatra* and *sumalibs*
- Closed bugs:
  - #952093 of *sumaclust* (FTBFS)
  - #954262 of *sumaclust*: fails to migrate to testing for too long
  - #956232 of *sumaclust*: Last sequence of input is skipped on arm64
- Several Java dependencies of *snpeff*
- Kept on working in the team fixing Java dependencies

# Pierre Gruet - new in Debian Med

- Wrote tests for *sumaclust* and its close relatives *sumatra* and *sumalibs*
- Closed bugs:
  - #952093 of *sumaclust* (FTBFS)
  - #954262 of *sumaclust*: fails to migrate to testing for too long
  - #956232 of *sumaclust*: Last sequence of input is skipped on arm64
- Several Java dependencies of *snpeff*
- Kept on working in the team fixing Java dependencies

# Pierre Gruet - new in Debian Med

- Wrote tests for *sumaclust* and its close relatives *sumatra* and *sumalibs*
- Closed bugs:
  - #952093 of *sumaclust* (FTBFS)
  - #954262 of *sumaclust*: fails to migrate to testing for too long
  - #956232 of *sumaclust*: Last sequence of input is skipped on arm64
- Several Java dependencies of *snpeff*
- Kept on working in the team fixing Java dependencies

# Pranav Ballaney - GSoC student

- New package *trinculo*
- New package *r-bioc-htsfilter*
- #954511: *bioperl-run* FTBFS: `dh_auto_test`: error
- Several autopkgtests
- Joined video meetings

# Pranav Ballaney - GSoC student

- New package *trinculo*
- New package *r-bioc-htsfilter*
- #954511: *bioperl-run* FTBFS: `dh_auto_test`: error
- Several autopkgtests
- Joined video meetings

# Pranav Ballaney - GSoC student

- New package *trinculo*
- New package *r-bioc-htsfilter*
- #954511: *bioperl-run* FTBFS: `dh_auto_test`: error
- Several autopkgtests
- Joined video meetings



# Pranav Ballaney - GSoC student

- New package *trinculo*
- New package *r-bioc-htsfilter*
- #954511: *bioperl-run* FTBFS: `dh_auto_test`: error
- Several autopkgtests
- Joined video meetings

# Pranav Ballaney - GSoC student

- New package *trinculo*
- New package *r-bioc-htsfilter*
- #954511: *bioperl-run* FTBFS: `dh_auto_test`: error
- Several autopkgtests
- Joined video meetings

- Working down a huge list of new packages as ftpmaster rewarding our work to become effective in less than 24 hours.

- Restructuring source *orthanc*:  
Packages *liborthancframework-dev* and *liborthancframework1* are now pending in the NEW queue
- *orthanc-gdcm*
- Progressively update the other *orthanc* plugins so as to remove the source code of Orthanc out of the source packages

- Restructuring source *orthanc*:  
Packages *liborthancframework-dev* and *liborthancframework1* are now pending in the NEW queue
- *orthanc-gdcm*
- Progressively update the other *orthanc* plugins so as to remove the source code of Orthanc out of the source packages

- Restructuring source *orthanc*:  
Packages *liborthancframework-dev* and *liborthancframework1* are now pending in the NEW queue
- *orthanc-gdcm*
- Progressively update the other *orthanc* plugins so as to remove the source code of Orthanc out of the source packages

# Shayan Doust - former MoM student

- Came back short after our first sprint from a forced break
- Lots of contributions since May 2020
- Became DM now

# Shayan Doust - former MoM student

- Came back short after our first sprint from a forced break
- Lots of contributions since May 2020
- Became DM now



# Shayan Doust - former MoM student

- Came back short after our first sprint from a forced break
- Lots of contributions since May 2020
- Became DM now

- **Contacts to some upstreams**
- Analyse workflows and the work that needs to be done
- Requests transition from packaging towards executing these workflows and provide tutorials

- Contacts to some upstreams
- Analyse workflows and the work that needs to be done
- Requests transition from packaging towards executing these workflows and provide tutorials

- Contacts to some upstreams
- Analyse workflows and the work that needs to be done
- Requests transition from packaging towards executing these workflows and provide tutorials

- Fix #950311: *fastqc*: **FAIL** strings in output - what does this mean?
- Fix #952603: *python-tinylalign*: license of buildwheels.sh is CC0

- Fix #950311: *fastqc*: **FAIL** strings in output - what does this mean?
- Fix #952603: *python-tinylalign*: license of buildwheels.sh is CC0

# Effect of COVID-19 on the Debian Med project

- The Debian Med project became a totally new drive
- It is even more fun to work in this project
- Everybody is kindly invited to share this fun with us and join the project

# Effect of COVID-19 on the Debian Med project

- The Debian Med project became a totally new drive
- It is even more fun to work in this project
- Everybody is kindly invited to share this fun with us and join the project



# Effect of COVID-19 on the Debian Med project

- The Debian Med project became a totally new drive
- It is even more fun to work in this project
- Everybody is kindly invited to share this fun with us and join the project

# Effect of COVID-19 on my own work inside the project

- My work shifted from packaging way stronger to mentoring and organising
- Its even more fun than before to see all those skilled developers doing stuff I could never approach myself
- Thanks a lot to all who contributed

# Effect of COVID-19 on my own work inside the project

- My work shifted from packaging way stronger to mentoring and organising
- Its even more fun than before to see all those skilled developers doing stuff I could never approach myself
- Thanks a lot to all who contributed

# Effect of COVID-19 on my own work inside the project

- My work shifted from packaging way stronger to mentoring and organising
- Its even more fun than before to see all those skilled developers doing stuff I could never approach myself
- Thanks a lot to all who contributed

This talk is available at  
<http://people.debian.org/~tille/talks/>



Andreas Tille <tille@debian.org>