

CIBIV BEAMER TEMPLATE

INFORMATIVE SUBTITLE

John/Jane Doe

February 8, 2017

Center for Integrative Bioinformatics Vienna



CIBIV
Center for Integrative Bioinformatics Vienna

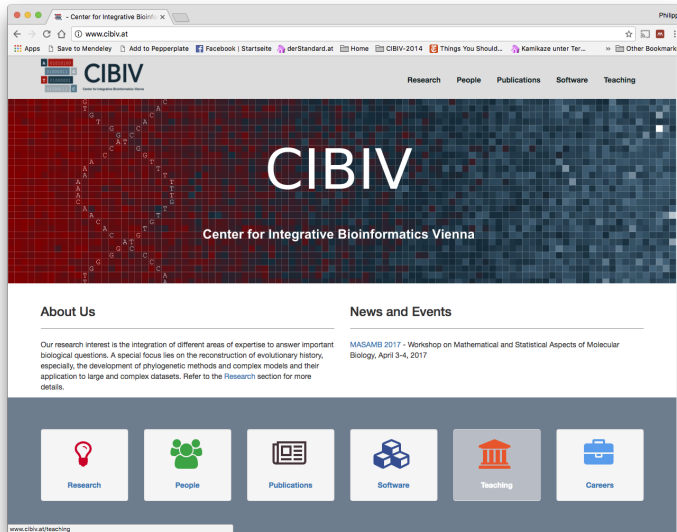
- ▶ The theme works with pdflatex and standard font

REQUIREMENTS

- ▶ The theme works with pdflatex and standard font
- ▶ However, I would **recommend** installing **FiraFont** (<http://mozilla.github.io/Fira/>) and using LuaLatex for compiling

DEFINING SECTIONS GIVES YOU THIS

FIGURES (WITH HANDOUT OPTION)



FIGURES (WITH HANDOUT OPTION)

The screenshot shows a web browser window with the URL www.cibiv.at/publications/. The page features the CIBIV logo and navigation links for Research, People, Publications (highlighted), Software, and Teaching. The main content is divided into three sections: 'in press', '2017', and '2016', each containing a list of publications with author names, titles, and DOIs. A sidebar on the right titled 'Publications' provides a summary of the publication counts for each year.

Publications

in press

- F. Enkner, B. Pichlhöfer, A.T. Zaharie, M. Krunić, T.M. Holper, S. Janik, B. Moser, K. Schlangen, B. Neudert, K. Walter, B. Migschitz, and L. Mülbauer (in press) Molecular Profiling of Thymoma and Thymic Carcinoma: Genetic Differences and Potential Novel Therapeutic Targets. *Pathol. Oncol. Res.*, in press. (DOI: 10.1007/s12253-016-0144-8, PMID: 27844328)
- E. Klopff, H.A. Schmidt, S. Clauder-Münster, L.M. Steinmetz, and C. Schüller (in press) INO80 represses osmotic stress induced gene expression by resetting promoter proximal nucleosomes. *Nucleic Acids Res.*, 45, in press. (DOI: 10.1093/nar/gkw1292, PMID: 26825392)
- C. Prakash and A. von Haeseler (in press) An Enumerative Combinatorics Model for Fragmentation Patterns in RNA Sequencing Provides Insights into Non-uniformity of the Expected Fragment Starting Point and Coverage Profile. *J. Comput. Biol.*, 24, in press. (DOI: 10.1089/cmb.2016.0096, PMID: 27961099)

2017

- N. Popitsch, I. Bilusic, B. Rescheneder, R. Schroeder, and M. Lybecker (2017) Temperature-dependent sRNA transcriptome of the Lyme disease spirochete. *BMC Genomics*, 18, 28. (DOI: 10.1186/s12964-016-3396-3, PMID: 28056764)

2016

- F. Burki, M. Kaplan, D.V. Tikhonov, V. Zlatogursky, B.Q. Minh, L.V. Radaykina, A. Smirnov, A.P. Mylnikov, and P.J. Keeling (2016) Untangling the early diversification of eukaryotes: a phylogenomic study of the evolutionary origins of Centrohelida, Haptophyta, and Cryptista. *Proc. R. Soc. B*, 283, 20152802. (free reprint, DOI: 10.1098/rspb.2015.2802, PMID: 26817772)
- O. Chermomor, A. von Haeseler, and B.Q. Minh (2016) Terrace Aware Data Structure for Phylogenomic Inference from Supermatrices. *Syst. Biol.*, 65, 997-1008. (free reprint, DOI: 10.1093/sysbio/syw037, PMID: 27121966, software)
- O. Chermomor, S. Klaere, A. von Haeseler, and B.Q. Minh (2016) Split diversity: measuring and optimizing biodiversity using phylogenetic split networks. In R. Pelens and P. Grandcolas (eds.) *Biodiversity Conservation and Phylogenetic Systematics (Series: Topics in Biodiversity and Conservation, Vol. 14)*, 173-195. Springer, Heidelberg/New York. (DOI: 10.1007/978-3-319-22461-9_9, book-DOI: 10.1007/978-3-319-22461-9_9, eISBN: 978-3-319-22461-9, ISBN: 978-3-319-22460-2)
- M. Gallach and E. Betran (2016) Dosage compensation and the distribution of sex-biased gene expression in *Drosophila*: considerations and genomic constraints. *J. Mol. Evol.*, 82, 199-206. (DOI: 10.1007/s00239-016-9735-y, PMID: 27059220)
- K. Gesson, B. Rescheneder, M.P. Skoruppa, A. von Haeseler, T. Dechat, and R. Foianer (2016) A-type lamins bind both hetero- and euchromatin, the latter being regulated by lamina-associated polypeptide 2alpha. *Genome Res.*, 26, 462-473. (DOI: 10.1101/060000)

Publications

in press (3 pubs)

2017 (1 pubs)

2016 (12 pubs)

2015 (17 pubs)

2014 (18 pubs)

2013 (17 pubs)

2012 (21 pubs)

2011 (9 pubs)

2010 (12 pubs)

2009 (19 pubs)

2008 (14 pubs)

2007 (19 pubs)

2006 (14 pubs)

2005 (13 pubs)

- ▶ **Alignments** Statistics of sequence alignment (i.e. mcmcalign). Recently we have extended this approach to reconstruct an alignment and a phylogenetic tree simultaneously.
- ▶ **Sequence evolution** To understand sequence evolution it is necessary to model the substitution process. We are working on models sequence that allow dependencies among sequence sites (Markov fields seem to be an appropriate tool). We are developing test statistics to select the "best" model, to detect groups of sequence that evolve differently from the rest of a gene family, say. ...

PICTURE OVERLAY (ABSOLUTE POSITION)

- **Alignments** Statistics of sequence alignment (i.e. mcmcalgn). Recently we have extended this approach to reconstruct an alignment and a phylogenetic
- **Sequence evolution** to model the sequence the fields seem to be an appropriate way. We are developing test statistics to select the "best" model, to detect groups of sequence that evolve differently from the rest of a gene family, say. ...

A	01010100
	01000011
T	01000001
	01000111

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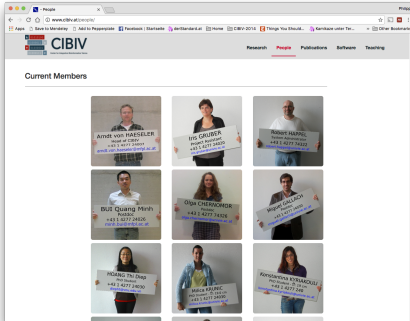
Center for Integrative Bioinformatics Vienna

on it is necessary
models
sites (Markov

ing test

Table 1: Largest cities in the world

City	Population
Mexico City	20,116,842
Shanghai	19,210,000
Peking	15,796,450
Istanbul	14,160,467



- ▶ Arndt
- ▶ Iris
- ▶ Robert
- ▶ Minh
- ▶ Olga
- ▶ Miguel
- ▶ ...

Three different block environments are pre-defined and may be styled with an optional background color.

Default

Block content.

Default

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Alert

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Alert

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Example

Block content.

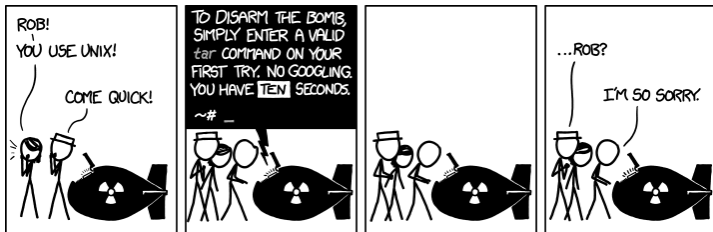
Example

Block content.

```
$ tar cvf archive_name.tar dirname/  
$ tar xvf archive_name.tar  
$ tar -cjf - /directory/to/archive/ | wc -c
```

COMMAND LINE BLOCKS / FIGURE PLACEHOLDER

```
$ tar cvf archive_name.tar dirname/  
$ tar xvf archive_name.tar  
$ tar -cjf - /directory/to/archive/ | wc -c
```



REFERENCES

Here is text with a reference in the footer¹

Some references to showcase [2]

Bui Quang Minh, Minh Anh Thi Nguyen, and Arndt Von Haeseler. “Ultrafast approximation for phylogenetic bootstrap”. In: *Molecular Biology and Evolution* 30.5 (2013), pp. 1188–1195. ISSN: 07374038. DOI: 10.1093/molbev/mst024

¹Bui Quang Minh, Minh Anh Thi Nguyen, and Arndt Von Haeseler. “Ultrafast approximation for phylogenetic bootstrap”. In: *Molecular Biology and Evolution* 30.5 (2013), pp. 1188–1195. ISSN: 07374038. DOI: 10.1093/molbev/mst024.

Not part of numbering

REFERENCES



Bui Quang Minh, Minh Anh Thi Nguyen, and Arndt Von Haeseler. “Ultrafast approximation for phylogenetic bootstrap”. In: *Molecular Biology and Evolution* 30.5 (2013), pp. 1188–1195. ISSN: 07374038. DOI: 10.1093/molbev/mst024.



Lam Tung Nguyen et al. “IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies”. In: *Molecular Biology and Evolution* 32.1 (2015), pp. 268–274. ISSN: 15371719. DOI: 10.1093/molbev/msu300.