

# Cibiv Beamer Template

INFORMATIVE SUBTITLE

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April 17, 2017

Center for Integrative Bioinformatics Vienna



**CIBIV**  
Center for Integrative Bioinformatics Vienna

- ▶ The theme works with `pdflatex` and standard font

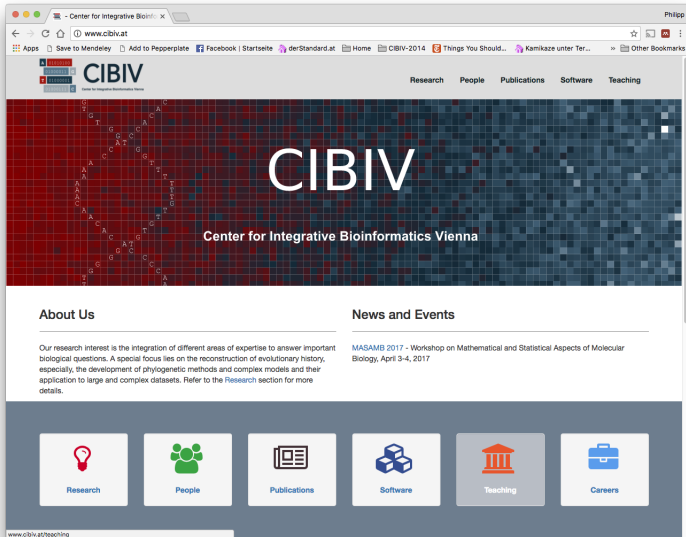
# Requirements

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

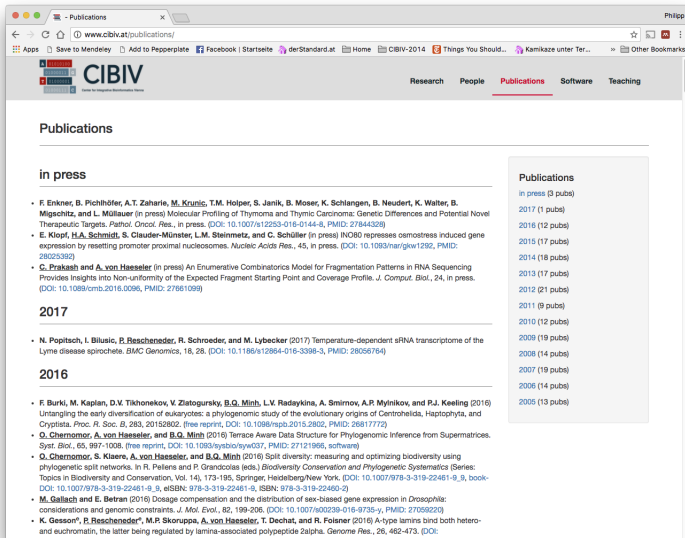
**Defining sections gives you this**

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# Figures (with handout option)



# Figures (with handout option)



The screenshot shows a web browser window displaying the CIBIV Publications page. The browser's address bar shows the URL [www.cibiv.at/publications/](http://www.cibiv.at/publications/). The CIBIV logo is prominently displayed at the top left of the page content, with the tagline "Center for Integrative Bioinformatics Vienna" below it. A navigation bar at the top right includes links for Research, People, Publications (which is highlighted), Software, and Teaching. The main content area is titled "Publications" and is divided into three sections: "in press", "2017", and "2016". Each section contains a list of publications with author names, titles, and links to the full text or abstract. A sidebar on the right side of the page, titled "Publications", provides a summary of the number of publications for each year, ranging from 2005 to 2017, with a total of 13 publications in 2005 and 1 pub in 2017.

**Publications**

**in press**

- F. Enkner, B. Pichthöfer, A.T. Zaharie, **M. Krunić**, T.M. Holper, S. Janik, B. Moser, K. Schlangen, B. Neudert, K. Walter, B. Milschitz, 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 osmolarity induced gene expression by resetting promoter proximal nucleosomes. *Nucleic Acids Res.*, 45, in press. (DOI: 10.1093/nar/gkw1292, PMID: 28025392)
- 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: 27661099)

**2017**

- N. Popitsch, I. Bilusic, **P. Rescheneder**, R. Schroeder, and M. Lybecker (2017) Temperature-dependent sRNA transcriptome of the Lyme disease spirochete. *BMC Genomics*, 18, 28. (DOI: 10.1186/s12864-016-3398-3, PMID: 28056764)

**2016**

- F. Burki, M. Kaplan, D.V. Tikhonov, V. Ziatogursky, **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, 20152602. (free reprint, DOI: 10.1098/rspb.2015.2602, PMID: 26817772)
- Q. Chermakov**, **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/ytw037, PMID: 27121956, software)
- Q. Chermakov**, S. Klaere, **A. von Haeseler**, and **B.Q. Minh** (2016) Split diversity: measuring and optimizing biodiversity using phylogenetic split networks. In R. Peltens 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\_book-6, DOI: 10.1007/978-3-319-22461-9\_8, 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<sup>a</sup>, **P. Rescheneder**<sup>a</sup>, M.P. Skoruppa, **A. von Haeseler**, T. Dechat, and R. Foisner (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 pub)

2016 (12 pubs)

2015 (17 pubs)

2014 (16 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)

## 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 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 tree

- **Sequence evolution** model the substitution process, allow dependence between sites, 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. ...

A	01010100
	01000011
T	01000001
	01000111

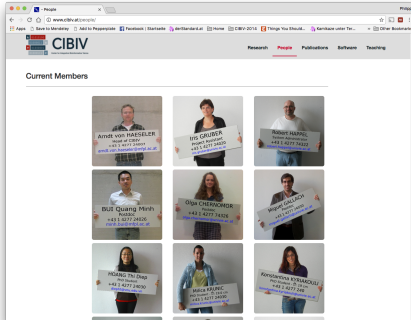


it is necessary to  
this sequence that  
seem to be an



**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
- ...

# Blocks

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

## Default

Block content.

## Default

Block content.

## Alert

Block content.

## Alert

Block content.

## Example

Block content.

## Example

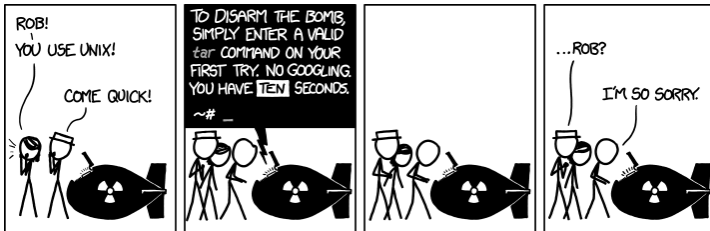
Block content.

## Command line blocks / figure placeholder

```
$ 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
```



Here is text with a reference in the footer<sup>1</sup>  
Some references to showcase [**Nguyen2015**]  
**Minh2013**

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<sup>1</sup>Minh2013.

Not part of numbering

