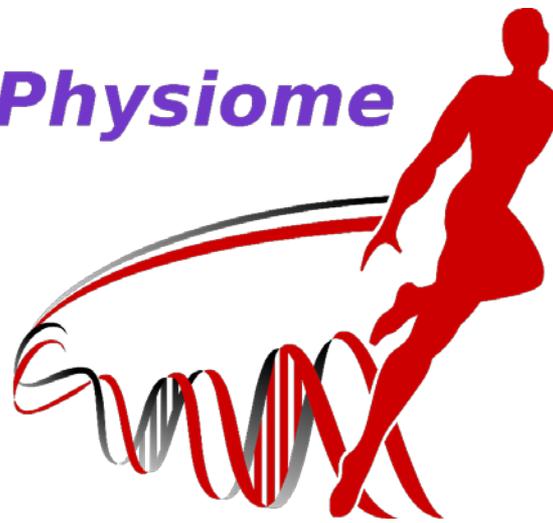


Physiome



Physiome: encouraging reproducibly FAIR computational modelling

David Nickerson, Tommy Yu,
Soroush Safaei, Peter Hunter

<https://doi.org/10.17608/k6.auckland.7040321>



**AUCKLAND
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FAIR guiding principles for scientific data

<https://doi.org/10.1038/sdata.2016.18>

FAIRsharing.org
standards, databases, policies

<http://fairsharing.org/>

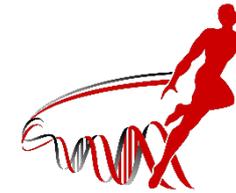
Findable



<http://fairdomhub.org/>

Accessible

Interoperable



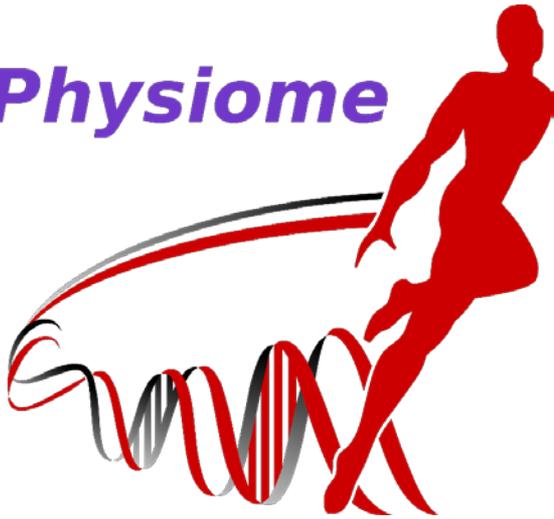
<https://models.physiomeproject.org/>

Reusable

FAIR Metrics

<http://fairmetrics.org/>

Physiome



Physiome papers describe the details of mathematical models and computational simulations associated with a 'primary' experimental/modelling paper that has been accepted to a peer-reviewed physiology, bioengineering or biophysics journal.

journal.physiomeproject.org

The purpose of *Physiome* is to encourage the reproducibility and reuse of models by providing citation credit for papers that describe and document curated and annotated models. The journal will assist authors in making suitable submissions available in the Physiome encoding standards.

Open access with **low cost**.

The Physiome Journal data repository

Secure <https://physiome.figshare.com>

figshare My data search on figshare Browse Upload David Nickerson



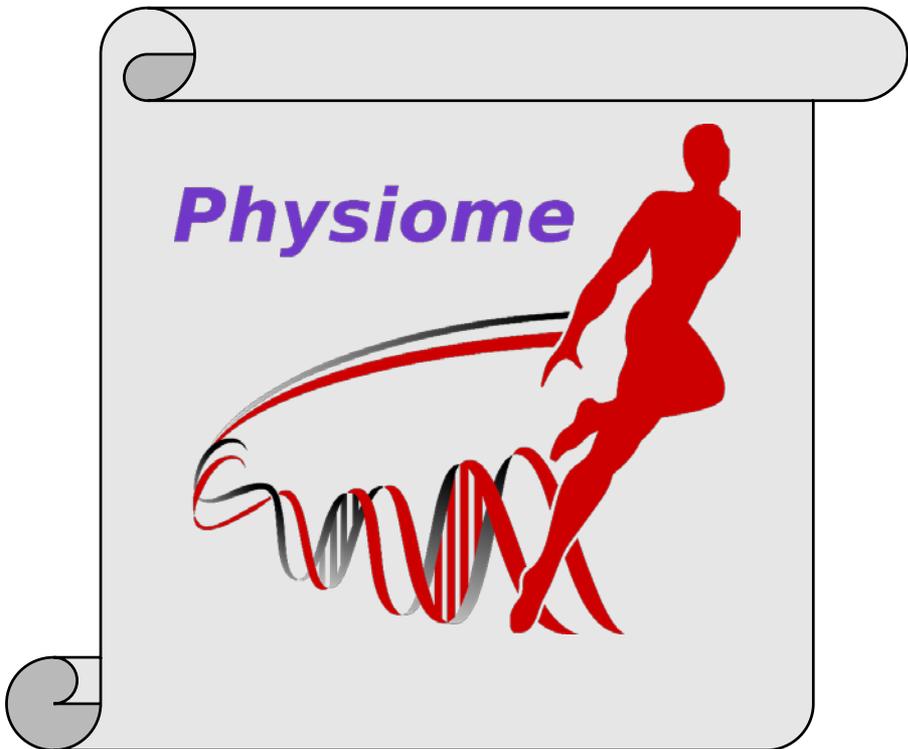
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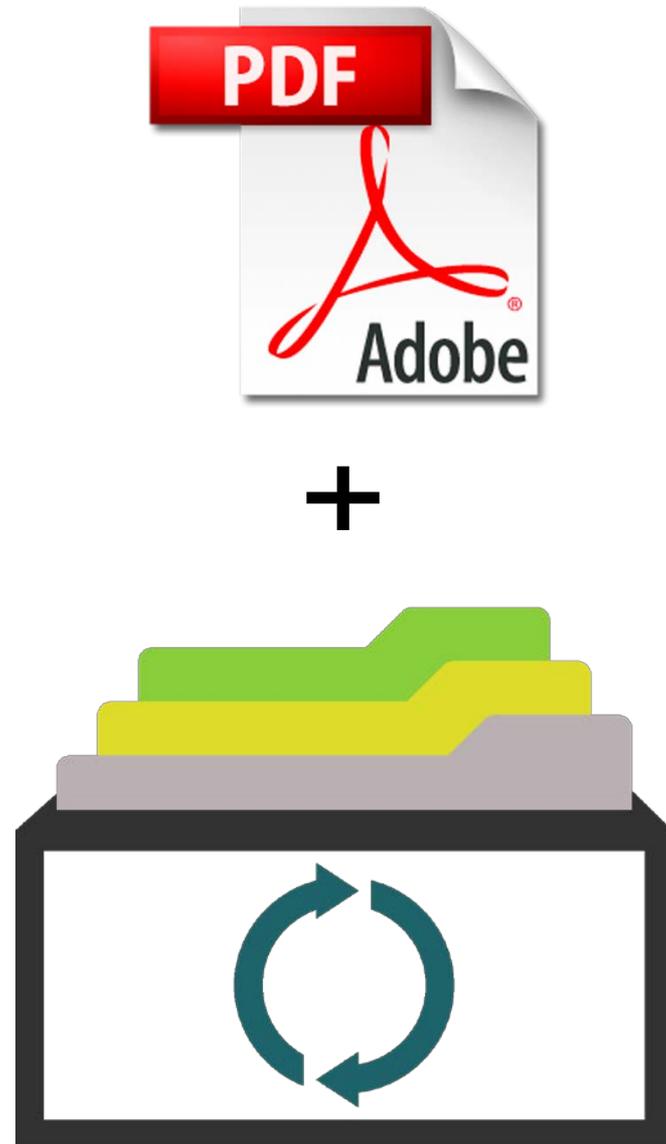
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COLLECTION DATASET

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=





Core Standards

Standards for Knowledge Representation

BioPAX



Standards for Visual Representation



Standards for Models and their Analyses



Associated Standards
Used by core standards

Projects



Infrastructure

BioModels.net
qualifiers



Controlled
Vocabularies



<http://co.mbine.org/>

Meeting in Boston this October: http://co.mbine.org/events/COMBINE_2018

Encouraging collaboration and reuse

- Track and recognise contributions

Metrics to demonstrate impact

- people get credit for making models FAIR
- e.g. altmetric donut

The Colours of the Donut

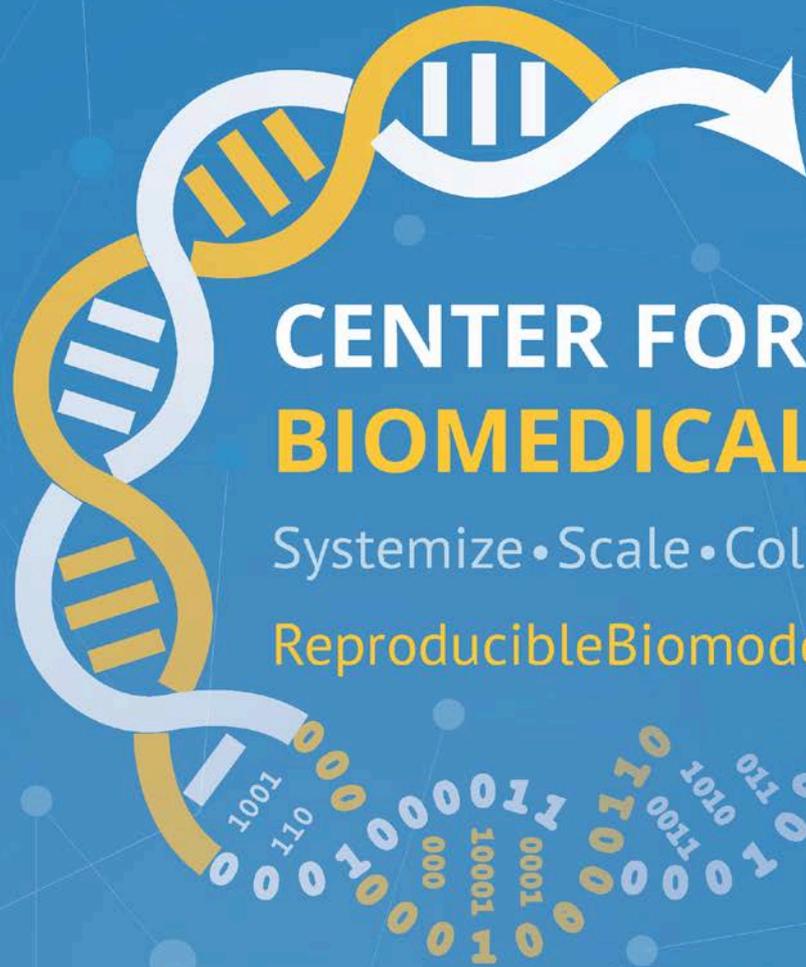
- | | |
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| Twitter | Faculty1000 |
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| Facebook | Youtube |
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| Wikipedia | |



<http://www.springersource.com/an-introduction-to-altmetric-data-what-can-you-see/>

Encouraging collaboration and reuse

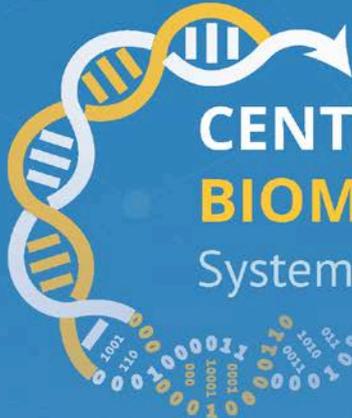
- Track and recognise contributions
- Needs to be easy
- Harmonising annotations
- “Rules” for how we construct models
- Reproducibility is key!



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Systemize • Scale • Collaborate • Reuse • Reproduce

ReproducibleBiomodels.org



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TECHNOLOGY DEVELOPMENT

- Data discovery & integration
- Scalable model building
- Reproducible simulation
- Reproducible visualization
- Mining simulation results
- Model provenance

AUTHOR & JOURNAL SERVICES

- Technical guidance
- Technology customization
- Model annotation
- Pre-publication model review
- Simulation results repository
- Online simulation & visualization

EDUCATION & OUTREACH

- Scalable modeling
- Reuse & reproducibility
- Ontologies & standards

REPRODUCIBLEBIOMODELS.ORG • INFO@REPRODUCIBLEBIOMODELS.ORG

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Current state of *Physiome*

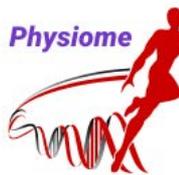
- Soft launch at IUPS World Congress
- <https://journal.physiomeproject.org>
- <https://physiome.figshare.com>
- Aiming for “first volume” end of 2018
- Submission site available soon after

Acknowledgements

- *Physiome* management board: Denis Noble, Walter Boron, Stig Omholt, Andrew McCulloch, Peter Hunter
- Jim Bassingthwaighte, Dan Beard, many others



Aotearoa Foundation





Key enabling technologies

- Unique, persistent, and resolvable identifiers
- Tools to encourage collaboration and reuse
- Metrics to demonstrate impact



Identifiers

- Standard formats which provide identifier assignment



Identifiers

- Standard formats which provide identifier assignment
- Repositories adding:
 - persistence
 - versioning
 - resolvability

Physiome Model Repository (PMR)

<https://models.physiomeproject.org>



Models Home Expos

You are here: Home / Protein M

Protein Modules

25D
HH potassium ion channel r

25D
HH sodium ion channel moc

28F
A kinetic model of Na+/H+

290
A kinetic model of Cl-/HCO3-

293
A kinetic model of V-type H

294
A kinetic model of Na+/K+

295
A kinetic model of Na+/HCO3-

Chang, Fujita, 1999

A kinetic model of the thiaz

Eskandari, Wright, Loo,

Kinetics of the Reverse Mod

Mackenzie, Loo, Panayoto

Biophysical Characteristics o

Mode

You are here: Home / Exposures / SED-ML example / vanderpol.cellml

View Wizard Exposure Root Sharing

Na+ vanderpol.cellml

Annotation by David Nickerson — last modified Sep 27, 2017 09:19 AM — History

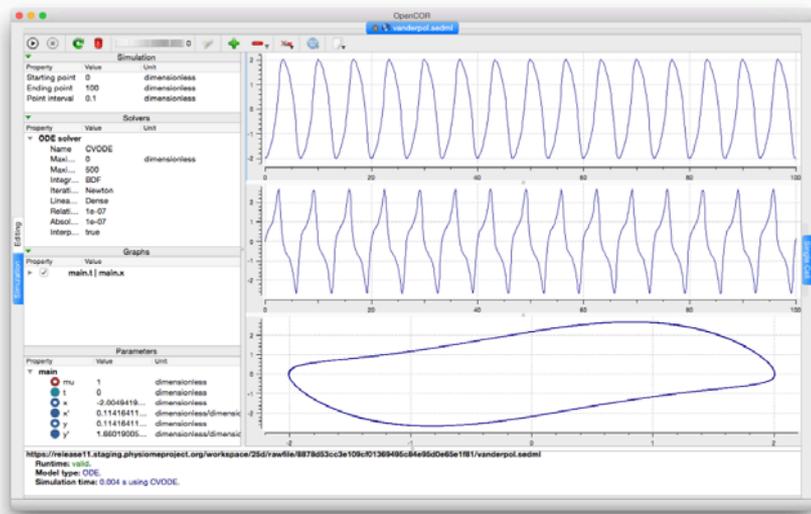
Description: Van der Pol oscillator

A kinetic model used in the *Create and run a simple CellML model: editing and simulation* section of the tutorial, the classical Van der Pol oscillator is the first model described in the tutorial. The simulation experiment for this model described in the tutorial can be obtained by loading the corresponding SED-ML document into OpenCOR and executing the simulation. The results of which are shown below. A rendering of the mathematical model itself is available here.

Work:

This wo model a models

- NHI
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A screenshot illustrating the results when the associated SED-ML document is loaded into OpenCOR and the simulation executed.

This can be reproduced directly from the repository by choosing the **Launch with OpenCOR** link from the *Views Available*.

Source

Derived from workspace SED-ML example at changeset 5257320c5ba4.

Collaboration

To begin collaborating on this work, please use your git client and issue this command:

```
git clone https://models.physio
```

Downloads

- Download This File
- Complete Archive as .tgz
- COMBINE Archive

Views Available

- Documentation
- Model Metadata
- Model Curation
- Mathematics
- Generated Code
- Cite this model
- Source View
- Launch with OpenCOR

Tools

- Compare...
- CombineArchive Web

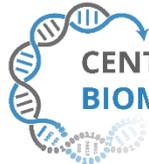
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Identifiers

- Standard formats which provide identifier assignment
- Repositories adding:
 - persistence
 - versioning
 - resolvability
- Annotations



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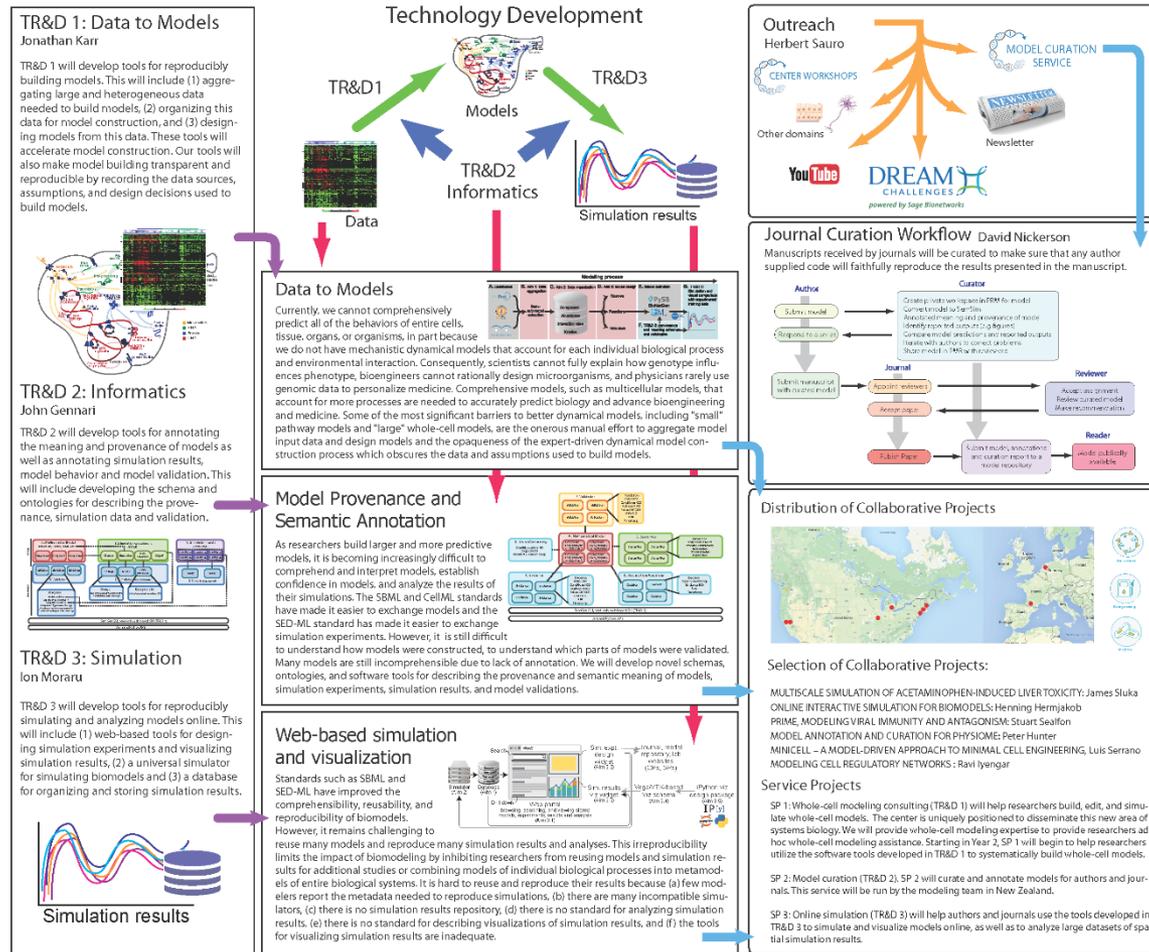
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Introduction

The Center for Reproducible Biomedical Modeling is a new technology development center with funded by the National Institute of Biomedical Imaging and Bioengineering with contributions from the National Institute of General Medical Sciences. The long-term goal of the center is to enable comprehensive predictive models of biological systems, such as whole-cell models, that could help physicians personalize therapy and help bioengineers rationally design microorganisms. Achieving this goal requires procedures for systematically, scalably, and reproducibly building, simulating, verifying, and applying models.

Herbert M Sauro: University of Washington, Bioengineering
Michael L Blinov: UConn Health, Cell Analysis and Modeling
Dan Cook: University of Washington, Health Informatics
John H Gennari: University of Washington, Health Informatics
Arthur P Goldberg: Mt Sinai, Genetics and Genomic Sciences
Jonathan R Karr: Mount Sinai, Genetics and Genomic Sciences
Ion I Moraru: UConn Health, Cell Analysis and Modeling
David P Nickerson: Auckland Bioengineering Institute
Jim C Schaff: UConn Health, Cell Analysis and Modeling



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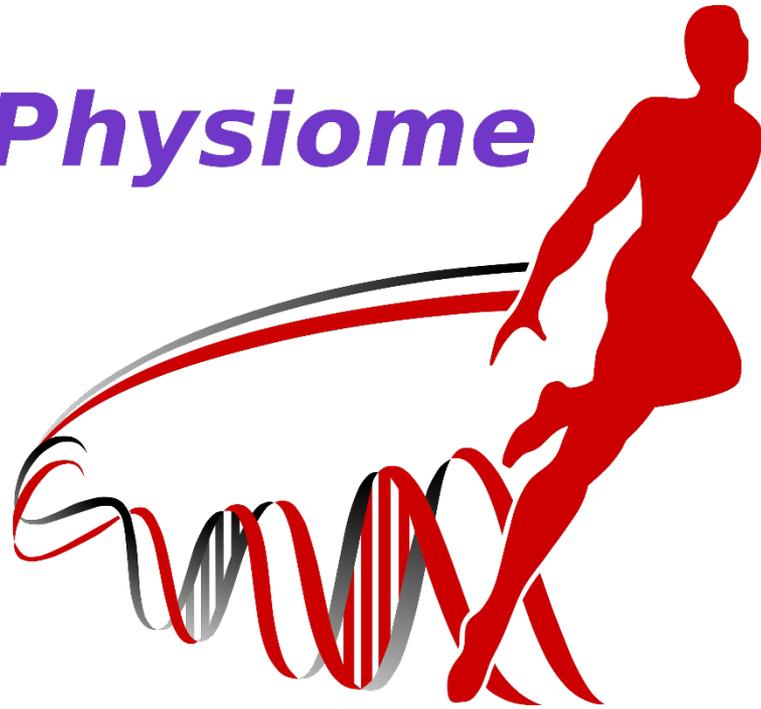


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Exciting News: ShareLaTeX is Joining Overleaf

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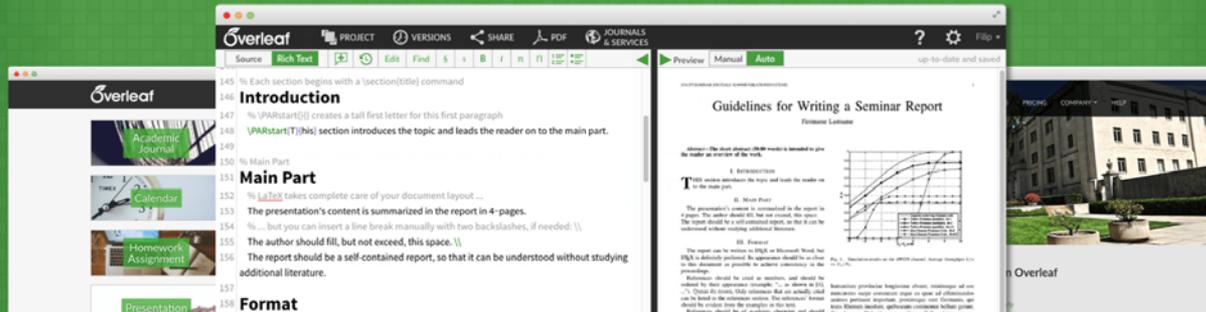
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