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**WC***langdocumentation*

**Release 0.0.1**

**Karr Lab**

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This package defines *wc\_lang*, a data-driven language for concisely describing WC models.

Whole-cell (WC) models are comprehensive computational models of all of the biochemical activity inside individual cells [Karr et al., 2015; Macklin et al., 2014]. WC models have great potential to enable bioengineers to rationally design microorganisms for industrial and medical applications and to enable physicians to personalize medical therapy [Carrera and Covert, 2015]. Please see [WholeCell.org](http://WholeCell.org) for more information about WC modeling, including perspectives, reviews, and tutorials.

### References

- Carrera J & Covert MW. (2015). Why Build Whole-Cell Models? *Trends in Cell Biology*, 25(12), 719-722. DOI: [10.1016/j.tcb.2015.09.004](https://doi.org/10.1016/j.tcb.2015.09.004)
- Karr JR, Takahashi K & Funahashi A. (2015). The principles of whole-cell modeling. *Current Opinion in Microbiology*, 27, 18-24. DOI: [10.1016/j.mib.2015.06.004](https://doi.org/10.1016/j.mib.2015.06.004)
- Macklin DN, Ruggero NA & Covert MW. (2014). The future of whole-cell modeling. *Current Opinion in Biotechnology*, 28, 111-115. DOI: [10.1016/j.copbio.2014.01.012](https://doi.org/10.1016/j.copbio.2014.01.012)



## 1.1 Installation

### 1.1.1 Prerequisites

- Python
- Pip

### 1.1.2 Latest release from PyPI

Run the following command to install the latest version from PyPI:

```
wc_lang
```

### 1.1.3 Latest revision from GitHub

Run the following command to install the latest version from GitHub:

```
pip install git+https://github.com/KarrLab/wc_utils.git#egg=wc_utils  
pip install git+https://github.com/KarrLab/obj_tables.git#egg=obj_tables  
pip install git+https://github.com/KarrLab/wc_lang.git#egg=wc_lang
```





## 1.2 Overview of *wc\_lang*

### 1.2.1 Units

Quantity	Attributes	Dimensions	Units	Units class
Time	wc_lang. core.Model. time_units	time	s	wc_lang.core. TimeUnit
Compartment density	wc_lang.core. Compartment. density wc_lang.core. Compartment. density_units	mass / volume	g l <sup>-1</sup>	wc_lang.core. DensityUnit
Compartment volume	wc_lang.core. Compartment. volume wc_lang.core. Compartment. volume_units	volume	l <sup>-1</sup>	wc_lang.core. VolumeUnit
Distribution of initial concentration of a species at the beginning of the cell cycle	wc_lang.core. Concentration. distribution wc_lang.core. Concentration. mean wc_lang.core. Concentration. std wc_lang.core. Concentration. units	molecule, molecule volume <sup>-1</sup>	molecule, M	wc_lang.core. ConcentrationUnit
Species count	wc_lang.core. Species.units	molecule	molecule	wc_lang.core. MoleculeCountUnit
Observable count	wc_lang.core. ObservableExpression. expression wc_lang.core. Observable. units	molecule	molecule	wc_lang.core. MoleculeCountUnit
Observable coefficient	wc_lang.core. ObservableExpression. expression	<i>dimensionless</i>	<i>none</i>	wc_lang.core. ObservableCoefficientUnit
Reaction participant	wc_lang.core. SpeciesCoefficient. coefficient	<i>dimensionless</i>	<i>none</i>	wc_lang.core. ReactionParticipantUnit
Reaction rate		time <sup>-1</sup>	s <sup>-1</sup> ,	wc_lang.core.

## 1.3 Tutorial

## 1.4 About

### 1.4.1 License

The software is released under the MIT license

```
The MIT License (MIT)
```

```
Copyright (c) 2016 Karr Lab
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### 1.4.2 Development team

This package was developed by the [Karr Lab](#) at the Icahn School of Medicine at Mount Sinai in New York, USA.

### 1.4.3 Acknowledgements

This work was supported by a National Science Foundation INSPIRE award [grant number 1649014].

### 1.4.4 Questions and comments

Please contact the [Karr Lab](#) with any questions or comments.

## 1.5 References