

# Project 3: Concrete Strength Prediction

This manuscript ([permalink](#)) was automatically generated from [qinyuz2/project3@e9972f4](#) on December 5, 2020.

## Authors

---

- **Qinyu Zhang**

•  [qinyuz2](#)

Department of Civil & Environmental Engineering, University of Illinois at Urbana-Champaign

- **Jane Roe**

 [XXXX-XXXX-XXXX-XXXX](#) •  [janeroe](#)

Department of Something, University of Whatever; Department of Whatever, University of Something

# Introduction

---

This manuscript is a template (aka “rootstock”) for [Manubot](#), a tool for writing scholarly manuscripts. Use this template as a starting point for your manuscript.

The rest of this document is a full list of formatting elements/features supported by Manubot. Compare the input ( `.md` files in the `/content` directory) to the output you see below.

## Basic formatting

---

**Bold text**

**Semi-bold text**

Centered text

Right-aligned text

*Italic text*

Combined *italics* and **bold**

~~Strikethrough~~

1. Ordered list item
2. Ordered list item
  - a. Sub-item
  - b. Sub-item
    - i. Sub-sub-item
3. Ordered list item
  - a. Sub-item

- List item
- List item
- List item

subscript: H<sub>2</sub>O is a liquid

superscript: 2<sup>10</sup> is 1024.

[unicode superscripts](#)<sup>0123456789</sup>

[unicode subscripts](#)<sub>0123456789</sub>

A long paragraph of text. Lorem ipsum dolor sit amet, consectetur adipiscing elit, sed do eiusmod tempor incididunt ut labore et dolore magna aliqua. Ut enim ad minim veniam, quis nostrud exercitation ullamco laboris nisi ut aliquip ex ea commodo consequat. Duis aute irure dolor in reprehenderit in voluptate velit esse cillum dolore eu fugiat nulla pariatur. Excepteur sint occaecat cupidatat non proident, sunt in culpa qui officia deserunt mollit anim id est laborum.

Putting each sentence on its own line has numerous benefits with regard to [editing](#) and [version control](#).

Line break without starting a new paragraph by putting two spaces at end of line.

## Document organization

---

Document section headings:

# Heading 1

## Heading 2

---

### Heading 3

#### Heading 4

##### Heading 5

###### Heading 6

**A heading centered on its own printed page**

Horizontal rule:

---

Heading 1's are recommended to be reserved for the title of the manuscript.

Heading 2's are recommended for broad sections such as *Abstract*, *Methods*, *Conclusion*, etc.

Heading 3's and Heading 4's are recommended for sub-sections.

## Links

---

Bare URL link: <https://manubot.org>

[Long link with lots of words and stuff and junk and bleep and blah and stuff and other stuff and more stuff yeah](#)

[Link with text](#)

[Link with hover text](#)

[Link by reference](#)

## Citations

---

Citation by DOI [[1](#)].

Citation by PubMed Central ID [[2](#)].

Citation by PubMed ID [[3](#)].

Citation by Wikidata ID [[4](#)].

Citation by ISBN [[5](#)].

Citation by URL [[6](#)].

Citation by alias [[7](#)].

Multiple citations can be put inside the same set of brackets [[1](#),[5](#),[7](#)]. Manubot plugins provide easier, more convenient visualization of and navigation between citations [[2](#),[3](#),[7](#),[8](#)].

Citation tags (i.e. aliases) can be defined in their own paragraphs using Markdown's reference link syntax:

## Referencing figures, tables, equations

---

Figure [1](#)

Figure [2](#)

Figure [3](#)

Figure [4](#)

Table [1](#)

Equation [1](#)

Equation [2](#)

## Quotes and code

---

Quoted text

Quoted block of text

Two roads diverged in a wood, and I—  
I took the one less traveled by,  
And that has made all the difference.

Code `in the middle` of normal text, aka `inline code`.

Code block with Python syntax highlighting:

```
from manubot.cite.doi import expand_short_doi

def test_expand_short_doi():
    doi = expand_short_doi("10/c3bp")
    # a string too long to fit within page:
    assert doi == "10.25313/2524-2695-2018-3-vliyanie-enhansera-copia-i-
        insulyatora-gypsy-na-sintez-ernk-modifikatsii-hromatina-i-
        svyazyvanie-insulyatornyh-belkov-vtransfetsirovannyh-geneticheskikh-
        konstruktsiyah"
```

Code block with no syntax highlighting:

```
Exporting HTML manuscript
Exporting DOCX manuscript
Exporting PDF manuscript
```

## Figures

---



**Figure 1: A square image at actual size and with a bottom caption.** Loaded from the latest version of image on GitHub.



**Figure 2: An image too wide to fit within page at full size.** Loaded from a specific (hashed) version of the image on GitHub.



**Figure 3: A tall image with a specified height.** Loaded from a specific (hashed) version of the image on GitHub.



**Figure 4: A vector `.svg` image loaded from GitHub.** The parameter `sanitize=true` is necessary to properly load SVGs hosted via GitHub URLs. White background specified to serve as a backdrop for transparent sections of the image.

## Tables

**Table 1:** A table with a top caption and specified relative column widths.

<i>Bowling Scores</i>	Jane	John	Alice	Bob
Game 1	150	187	210	105
Game 2	98	202	197	102
Game 3	123	180	238	134

**Table 2:** A table too wide to fit within page.

	Digits 1-33	Digits 34-66	Digits 67-99	Ref.
pi	3.14159265358979323846264338327950	288419716939937510582097494459230	781640628620899862803482534211706	<a href="#">piday.org</a>
e	2.71828182845904523536028747135266	249775724709369995957496696762772	407663035354759457138217852516642	<a href="#">nasa.gov</a>

**Table 3:** A table with merged cells using the `attributes` plugin.



	Colors	
Size	Text Color	Background Color
big	blue	orange
small	black	white

## Equations

A LaTeX equation:

$$\int_0^\infty e^{-x^2} dx = \frac{\sqrt{\pi}}{2} \tag{1}$$

An equation too long to fit within page:

$$x = a + b + c + d + e + f + g + h + i + j + k + l + m + n + o + p + q + r + s + t + u + v + w + x + y + z + 1 + 2 + 3 + 4 + 5 + 6 + 7 + 8 + 9 \tag{2}$$

## Special

**⚠ WARNING** The following features are only supported and intended for `.html` and `.pdf` exports. Journals are not likely to support them, and they may not display correctly when converted to other formats such as `.docx`.

LINK STYLED AS A BUTTON

Adding arbitrary HTML attributes to an element using Pandoc's attribute syntax:

Manubot Manubot Manubot Manubot Manubot. Manubot Manubot Manubot Manubot. Manubot Manubot Manubot. Manubot Manubot. Manubot.

Adding arbitrary HTML attributes to an element with the Manubot `attributes` plugin (more flexible than Pandoc's method in terms of which elements you can add attributes to):

Manubot Manubot Manubot Manubot Manubot. Manubot Manubot Manubot Manubot. Manubot Manubot Manubot. Manubot Manubot. Manubot.

Available background colors for text, images, code, banners, etc:

white lightgrey grey darkgrey black lightred lightyellow lightgreen lightblue lightpurple red orange yellow green blue purple

Using the [Font Awesome](#) icon set:

✓ ? ★ 🔔 ✖ …

#### Light Grey Banner

useful for *general information* - [manubot.org](https://manubot.org)

#### Blue Banner

useful for *important information* - [manubot.org](https://manubot.org)

#### Light Red Banner

useful for *warnings* - [manubot.org](https://manubot.org)

## Method

---

### 3. Discussion

---

#### 3.1 Model Training and Evaluation

---

##### 3.1.1 Linear Regression

Linear Regression is the simplest but powerful model. In the previous studies, it was widely used in the prediction of concrete strength. This model assumes a linear relationship between independent and dependent variables.

##### Code for Linear Regression Model

```
from sklearn.linear_model import LinearRegression

lin_reg = LinearRegression()
lin_reg.fit(train_x, train_y)
y_pred_lin= lin_reg.predict(test_x)
```

Accuracy of Model is: 0.5177053629131334

Root Mean Squared Error of Model is: 11.420285520195613

##### 3.1.2 Lasso Method

The Lasso is a shrinkage and selection method for linear regression. It minimizes the usual sum of squared errors, with a bound on the sum of the absolute values of the coefficients.

##### Code for Lasso Model

```
from sklearn.linear_model import Lasso

las = Lasso(alpha=0.1)
model2 = las.fit(train_x, train_y)
predictions2 = las.predict(test_x)
```

Accuracy of Model is: 0.38967572787640603

Root Mean Squared Error of Model is: 11.988560504390488

### 3.1.3 K-nearest Neighbor

The k-nearest neighbor is a simple, supervised machine learning algorithm that can be used to solve both classification and regression problems.

#### Code for K-nearest Neighbor Model

```
from sklearn.neighbors import KNeighborsRegressor

knn = KNeighborsRegressor()
model3=knn.fit(train_x, train_y)
predictions3 = knn.predict(test_x)
```

Accuracy of Model is: 0.34345271643724284

Root Mean Squared Error of Model is: 12.434253663809674

### 3.1.4 Support Vector Machine

Support vector machine is a supervised machine learning algorithm used for classification, regression and outlier detection. We use a linear Support Vector Machine model.

#### Code for Support Vector Machine Model

```
from sklearn.svm import SVR

svm= SVR(kernel='linear')
model4=svm.fit(train_x, train_y)
predictions4 = svm.predict(test_x)
```

Accuracy of Model is: 0.34808748601553163

Root Mean Squared Error of Model is: 12.390287319386937

### 3.1.5 Neural Network

Neural Network is also used in previous studies to predict concrete strength. A neural network is a series of algorithms that endeavors to recognize underlying relationships in a set of data. A neural network consists of input layer, hidden layers and output layer. It's able to learn and model non-linear and complex relationships between independent and dependent variables.

### Code for Neural Network Model

```
import tensorflow as tf

layer_width = 128
l1 = 0.0
l2 = 0.05

model1_split = tf.keras.Sequential()

model1_split.add(tf.keras.layers.Dense(512, activation="relu",
    kernel_regularizer = tf.keras.regularizers.l1_l2(l1=l1, l2=l2)))
model1_split.add(tf.keras.layers.BatchNormalization())
model1_split.add(tf.keras.layers.Dense(256, activation="relu"))
model1_split.add(tf.keras.layers.BatchNormalization())
model1_split.add(tf.keras.layers.Dense(128, activation="relu"))
model1_split.add(tf.keras.layers.BatchNormalization())
model1_split.add(tf.keras.layers.Dense(128, activation="relu"))

model1_split.add(tf.keras.layers.Dense(32, activation="relu"))

model1_split.add(tf.keras.layers.Dense(1))

model1_split.compile(optimizer=tf.keras.optimizers.Adam(lr=0.0015),
    loss='mean_squared_error',
    metrics=[tf.keras.metrics.RootMeanSquaredError()]
)

history_split = model1_split.fit(train_x, train_y, batch_size=1000,
    epochs=500, shuffle=True)
epochs_split = history_split.epoch
hist_split = pd.DataFrame(history_split.history)
rmse_split = hist_split["root_mean_squared_error"]

model1_split.summary()

model1_split_prediction = model1_split.predict(test_x)
```

Accuracy of Model is: 0.34808748601553163

Root Mean Squared Error of Model is: 12.390287319386937

### 3.1.6 Decision Tree Regressor

Decision-tree algorithm is a kind of supervised learning algorithms. It can be used in classification and regression problems.

#### Code for Decision Tree Regressor

```
from sklearn.tree import DecisionTreeRegressor

dtregressor = DecisionTreeRegressor(random_state = 0, min_samples_split=5)
dtregressor.fit(train_x, train_y)
y_pred_dt= dtregressor.predict(test_x)
```

Accuracy of Model is: 0.8204795438030693

Root Mean Squared Error of Model is: 6.9675118677407

### 3.1.7 Random Forest Regression

Random Forest Regression is a type of supervised learning algorithms. It constructs multiple decision tree classifiers on various sub-samples of the dataset and uses averaging to improve the prediction accuracy and it controls over-fitting as well.

#### Code for Random Forest Model

```

from sklearn.model_selection import RandomizedSearchCV
from sklearn.ensemble import RandomForestRegressor

#Use the random grid to search for best hyperparameter
# Number of trees in random forest
n_estimators = [int(x) for x in np.linspace(start = 200, stop = 2000, num =
10)]

# Number of features to consider at every split
max_features = ['auto', 'sqrt']

# Maximum number of levels in tree
max_depth = [int(x) for x in np.linspace(10, 110, num = 11)]
max_depth.append(None)

# Minimum number of samples required to split a node
min_samples_split = [2, 5, 10]

# Minimum number of samples required at each leaf node
min_samples_leaf = [1, 2, 4]

# Method of selecting samples for training each tree
bootstrap = [True, False]

# Create the random grid
random_grid = {'n_estimators': n_estimators,
                'max_features': max_features,
                'max_depth': max_depth,
                'min_samples_split': min_samples_split,
                'min_samples_leaf': min_samples_leaf,
                'bootstrap': bootstrap}

# First create the base model to tune
rf_split = RandomForestRegressor()

# Random search of parameters, using 3 fold cross validation,
# search across 100 different combinations, and use all available cores
rf_random_split = RandomizedSearchCV(estimator = rf_split,
                                     param_distributions = random_grid, n_iter = 100, cv = 3, verbose=2,
                                     random_state=None, n_jobs = -1)

# Fit the random search model
rf_random_split.fit(train_x, train_y)

```

The best parameters for the model show below. {'n\_estimators': 1200, 'min\_samples\_split': 2, 'min\_samples\_leaf': 1, 'max\_features': 'auto', 'max\_depth': 100, 'bootstrap': True}

```
# create a model
model2_split = RandomForestRegressor(n_estimators =
    rf_random_split.best_params_['n_estimators'],
    min_samples_split =
    rf_random_split.best_params_['min_samples_split'],
    min_samples_leaf =
    rf_random_split.best_params_['min_samples_leaf'],
    max_features =
    rf_random_split.best_params_['max_features'],
    max_depth =
    rf_random_split.best_params_['max_depth'],
    bootstrap =
    rf_random_split.best_params_['bootstrap'])

model2_split.fit(train_x, train_y)

model2_split_prediction = model2_split.predict(test_x)
```

Accuracy of Model is: 0.9053846430868259

Root Mean Squared Error of Model is: 5.058264806966998

## 3.2 Comparison and Result

The accuracy and root mean squared error are two parameters to evaluate the model performance. The two parameters of all the seven models we used are shown in the following table.

**Table 4:** Summary of Model Performance

<i>Method</i>	<b>Accuracy</b>	<b>Root Mean Squared Error</b>
Linear Regression	0.5177053629131334	11.420285520195613
Lasso Method	0.38967572787640603	11.988560504390488
K-nearest Neighbor	0.34345271643724284	12.434253663809674
Support Vector Machine	0.34808748601553163	12.390287319386937
Neural Network	98	202
Decision Tree Regressor	0.8204795438030693	6.9675118677407
Random Forest Regression	0.9053846430868259	5.058264806966998

## Conclusion

# References

---

## 1. Sci-Hub provides access to nearly all scholarly literature

Daniel S Himmelstein, Ariel Rodriguez Romero, Jacob G Levernier, Thomas Anthony Munro, Stephen Reid McLaughlin, Bastian Greshake Tzovaras, Casey S Greene

*eLife* (2018-03-01) <https://doi.org/ckcj>

DOI: [10.7554/elife.32822](https://doi.org/10.7554/elife.32822) · PMID: [29424689](https://pubmed.ncbi.nlm.nih.gov/29424689/) · PMCID: [PMC5832410](https://pubmed.ncbi.nlm.nih.gov/PMC5832410/)

## 2. Reproducibility of computational workflows is automated using continuous analysis

Brett K Beaulieu-Jones, Casey S Greene

*Nature biotechnology* (2017-04) <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6103790/>

DOI: [10.1038/nbt.3780](https://doi.org/10.1038/nbt.3780) · PMID: [28288103](https://pubmed.ncbi.nlm.nih.gov/28288103/) · PMCID: [PMC6103790](https://pubmed.ncbi.nlm.nih.gov/PMC6103790/)

## 3. Bitcoin for the biological literature.

Douglas Heaven

*Nature* (2019-02) <https://www.ncbi.nlm.nih.gov/pubmed/30718888>

DOI: [10.1038/d41586-019-00447-9](https://doi.org/10.1038/d41586-019-00447-9) · PMID: [30718888](https://pubmed.ncbi.nlm.nih.gov/30718888/)

## 4. Plan S: Accelerating the transition to full and immediate Open Access to scientific publications

cOAlition S

(2018-09-04) <https://www.wikidata.org/wiki/Q56458321>

## 5. Open access

Peter Suber

*MIT Press* (2012)

ISBN: [9780262517638](https://www.isbn-international.org/view/title/9780262517638)

## 6. Open collaborative writing with Manubot

Daniel S. Himmelstein, Vincent Rubinetti, David R. Slochower, Dongbo Hu, Venkat S. Malladi, Casey S. Greene, Anthony Gitter

*Manubot* (2020-05-25) <https://greenelab.github.io/meta-review/>

## 7. Opportunities and obstacles for deep learning in biology and medicine

Travers Ching, Daniel S. Himmelstein, Brett K. Beaulieu-Jones, Alexandr A. Kalinin, Brian T. Do, Gregory P. Way, Enrico Ferrero, Paul-Michael Agapow, Michael Zietz, Michael M. Hoffman, ... Casey S. Greene

*Journal of The Royal Society Interface* (2018-04-04) <https://doi.org/gddkhn>

DOI: [10.1098/rsif.2017.0387](https://doi.org/10.1098/rsif.2017.0387) · PMID: [29618526](https://pubmed.ncbi.nlm.nih.gov/29618526/) · PMCID: [PMC5938574](https://pubmed.ncbi.nlm.nih.gov/PMC5938574/)

## 8. Open collaborative writing with Manubot

Daniel S. Himmelstein, Vincent Rubinetti, David R. Slochower, Dongbo Hu, Venkat S. Malladi, Casey S. Greene, Anthony Gitter

*PLOS Computational Biology* (2019-06-24) <https://doi.org/c7np>

DOI: [10.1371/journal.pcbi.1007128](https://doi.org/10.1371/journal.pcbi.1007128) · PMID: [31233491](https://pubmed.ncbi.nlm.nih.gov/31233491/) · PMCID: [PMC6611653](https://pubmed.ncbi.nlm.nih.gov/PMC6611653/)