Activity of zebrafish and melatonin

CASE STUDIES IN STATISTICAL THINKING

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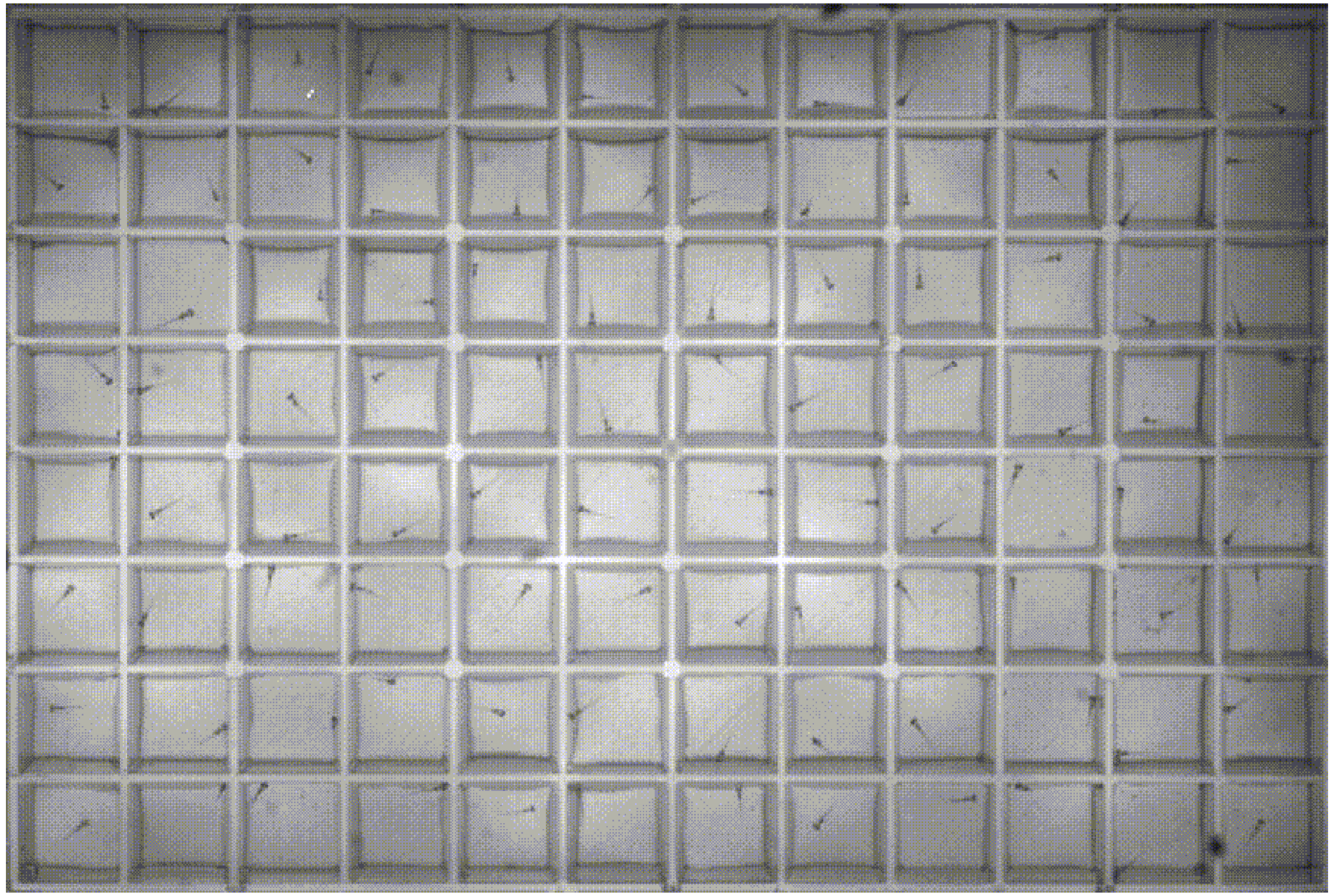
datacamp

Caltech

Case studies in statistical thinking

- Hone and extend your statistical thinking skills
- Work with real data sets
- Review of Statistical Thinking I and II

Warming up with zebrafish

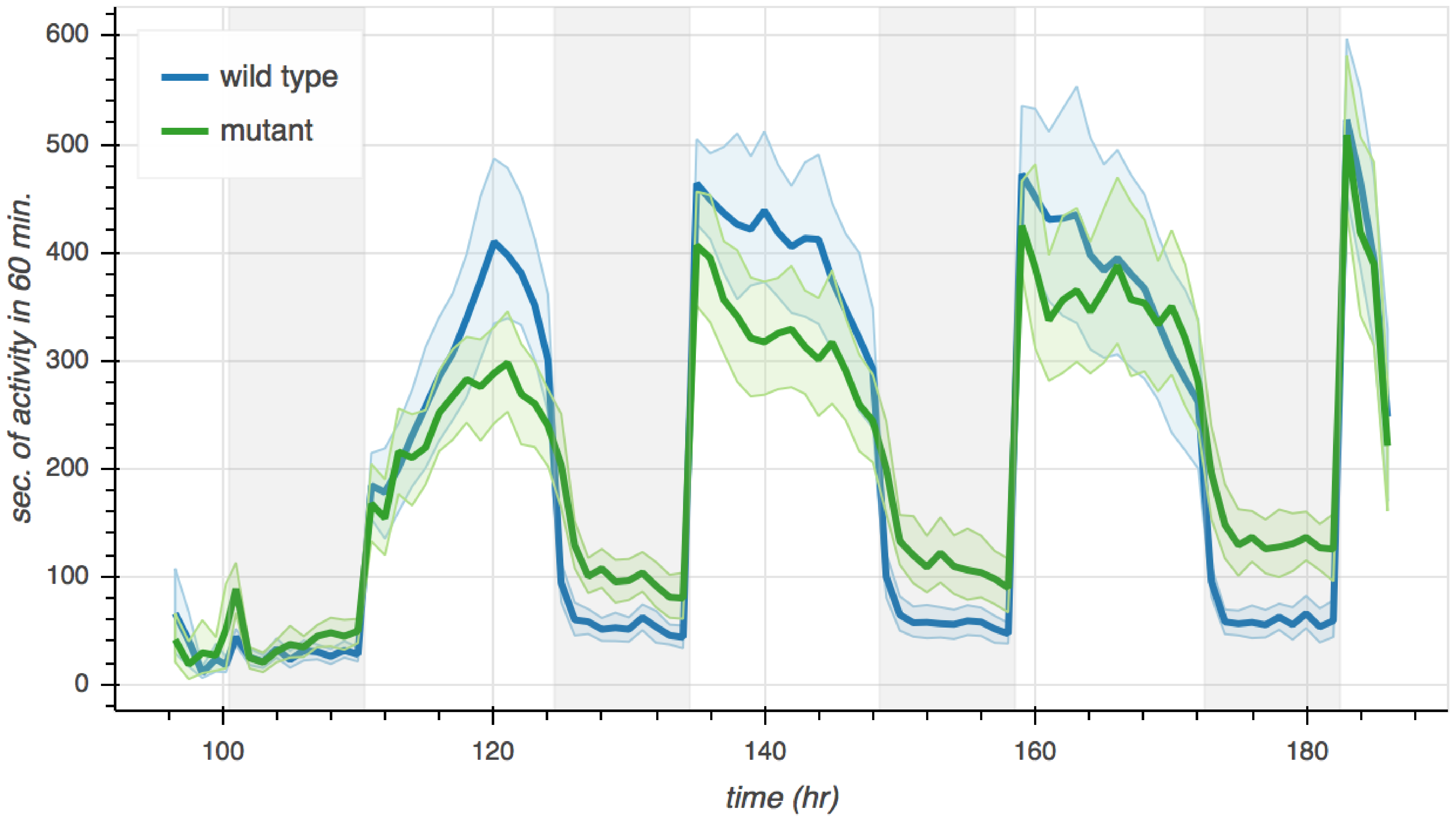


[1] Movie courtesy of David Prober, Caltech

Nomenclature

- **Mutant:** Has the mutation on both chromosomes
- **Wild type:** Does not have the mutation

Activity of fish, day and night



[1] Data courtesy of Avni Gandhi, Grigorios Oikonomou, and David Prober, Caltech

Active bouts: a metric for wakefulness

- **Active bout:** A period of time where a fish is consistently active
- **Active bout length:** Number of consecutive minutes with activity

Probability distributions and stories

- **Probability distribution**: A mathematical description of outcomes
- A probability distribution has a **story**

Distributions from Statistical Thinking I

- Uniform
- Binomial
- Poisson
- Normal
- Exponential

The Exponential distribution

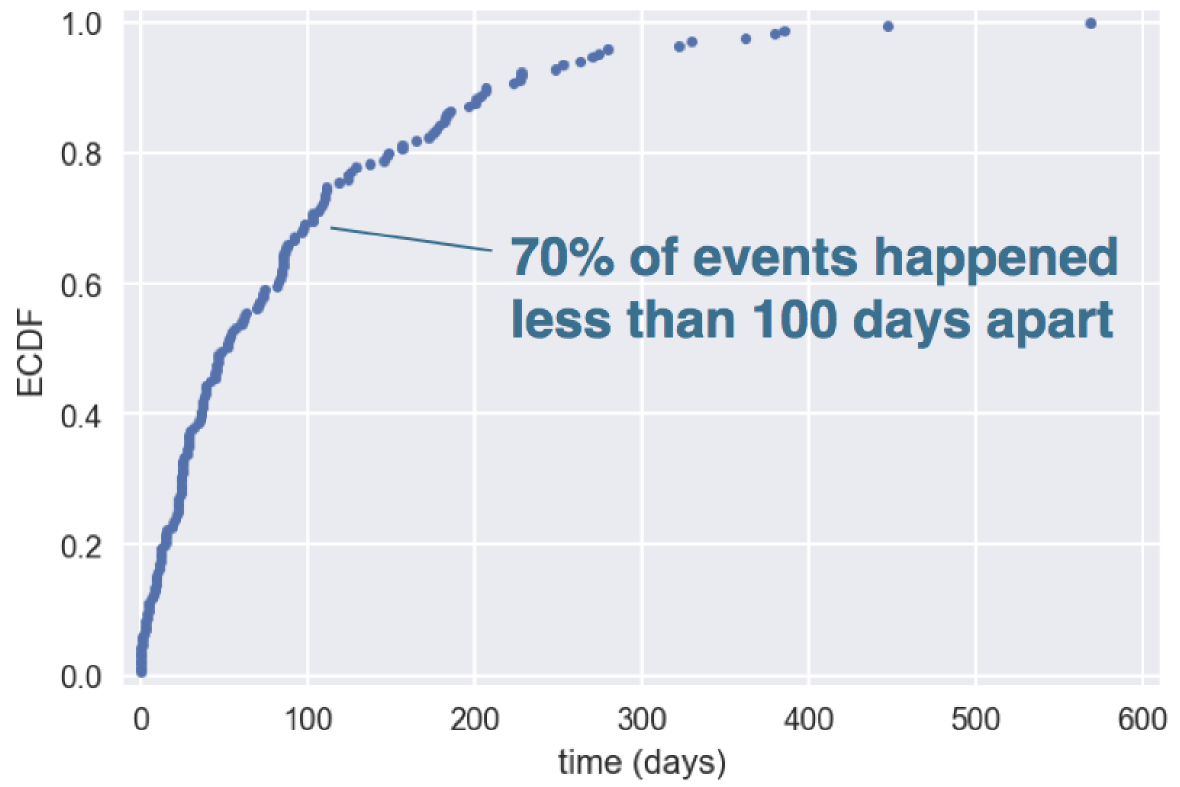
- **Poisson process:** The timing of the next event is completely independent of when the previous event happened

- **Story of the Exponential distribution:** The waiting time between arrivals of a Poisson process is Exponentially distributed

The Exponential CDF

```
x, y = ecdf(nuclear_incident_times)

_ = plt.plot(x, y, marker='.', linestyle='none')
```



[1] Data source: Wheatley, Sovacool, and Sornette, Nuclear Events Database

The Exponential CDF

```
x, y = ecdf(nuclear_incident_times)

_ = plt.plot(x, y, marker='.', linestyle='none')
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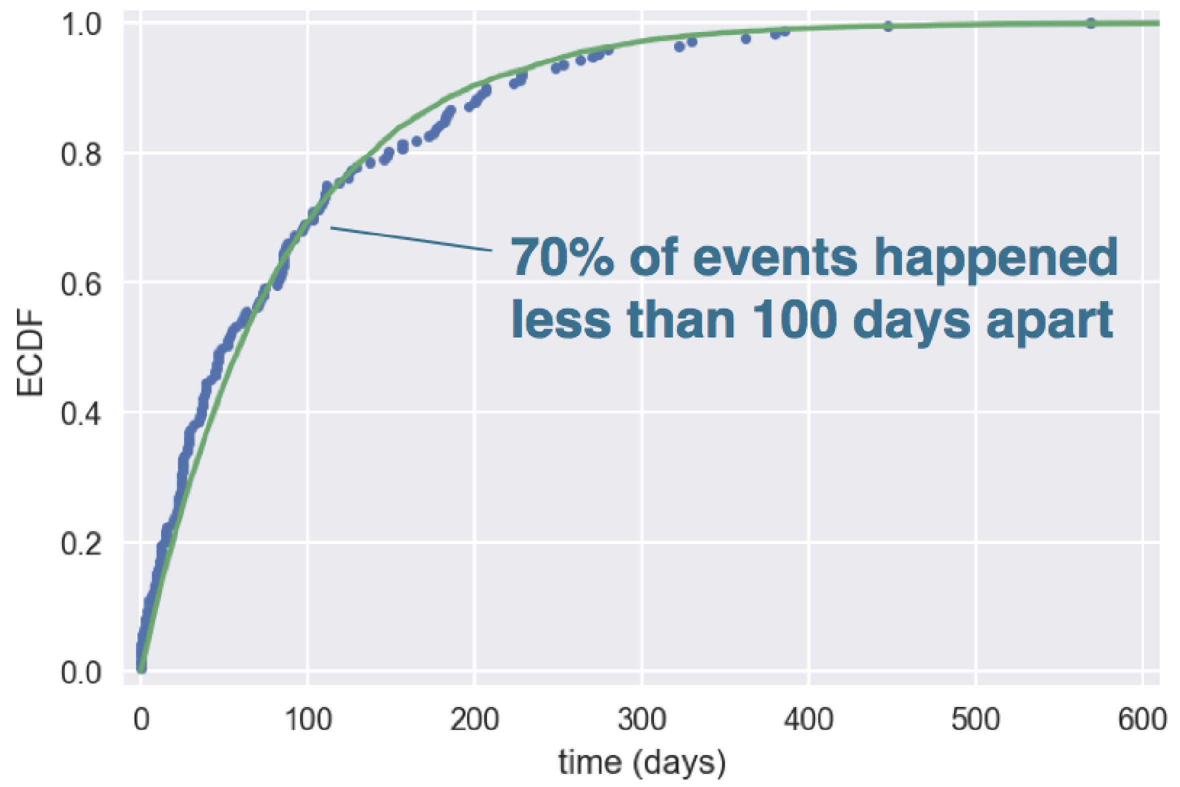

[1] Data source: Wheatley, Sovacool, and Sornette, Nuclear Events Database

```python
import dc_stat_think as dcst
dcst.pearson_r?
```

```
Signature: dcst.pearson_r(data_1, data_2)
Docstring: Compute the Pearson correlation coefficient between two
samples.
Parameters
----------
data_1 : array_like
    One-dimensional array of data.
data_2 : array_like
    One-dimensional array of  data.
Returns
-------
output : float
    The Pearson correlation coefficient between `data_1`
    and `data_2`.
File:      usr/local/lib/python3.5/site-packages/
           dc_stat_think-0.1.4-py3.6.egg/dc_stat_think/dc_stat_think.py
Type:      function
```

Using the dc_stat_think module

```
x, y = dcst.ecdf(nuclear_incident_times)
```

```
% pip install dc_stat_think
```

Let's practice!

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Bootstrap confidence intervals

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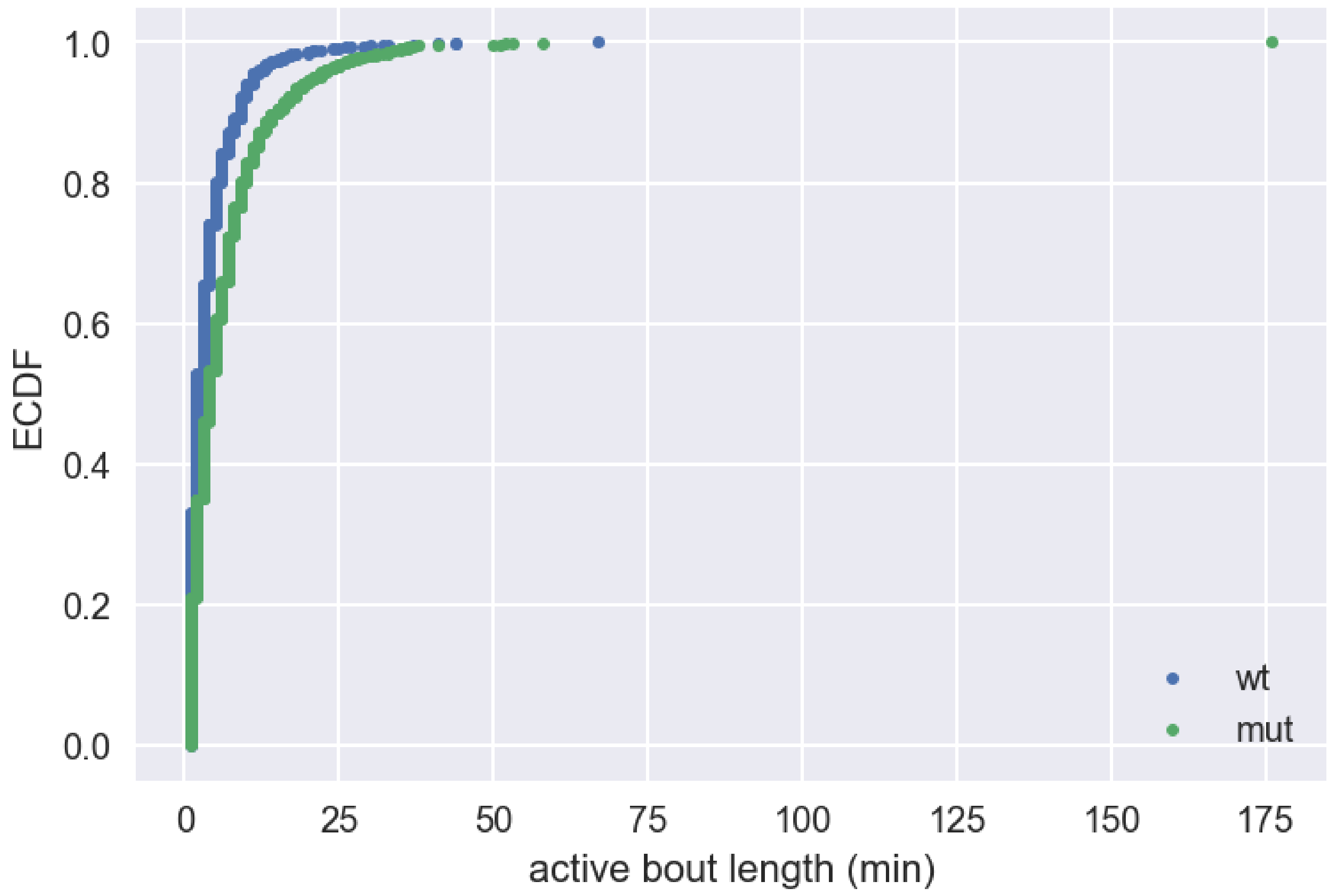
EDA is the first step

"Exploratory data analysis can never be the whole story, but nothing else can serve as a foundation stone, as the first step."

--John Tukey

Active bout length ECDFs



[1] Data courtesy of Avni Gandhi, Grigorios Oikonomou, and David Prober, Caltech

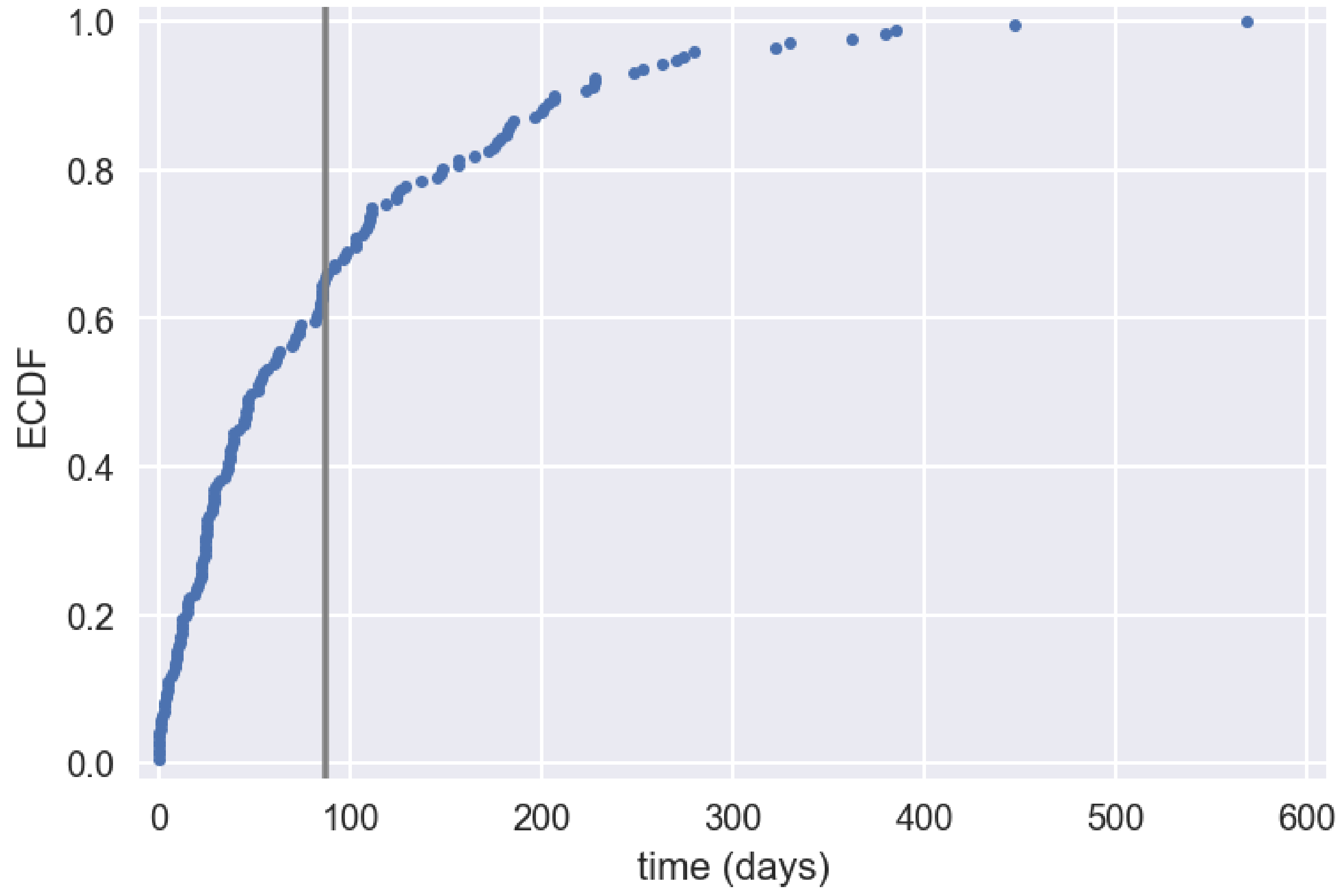
Optimal parameter value

- **Optimal parameter value:** The value of the parameter of a probability distribution that best describes the data

- **Optimal parameter for the Exponential distribution:** Computed from the mean of the data

```
np.mean(nuclear_incident_times)
```

```
87.14035087719298 6
```



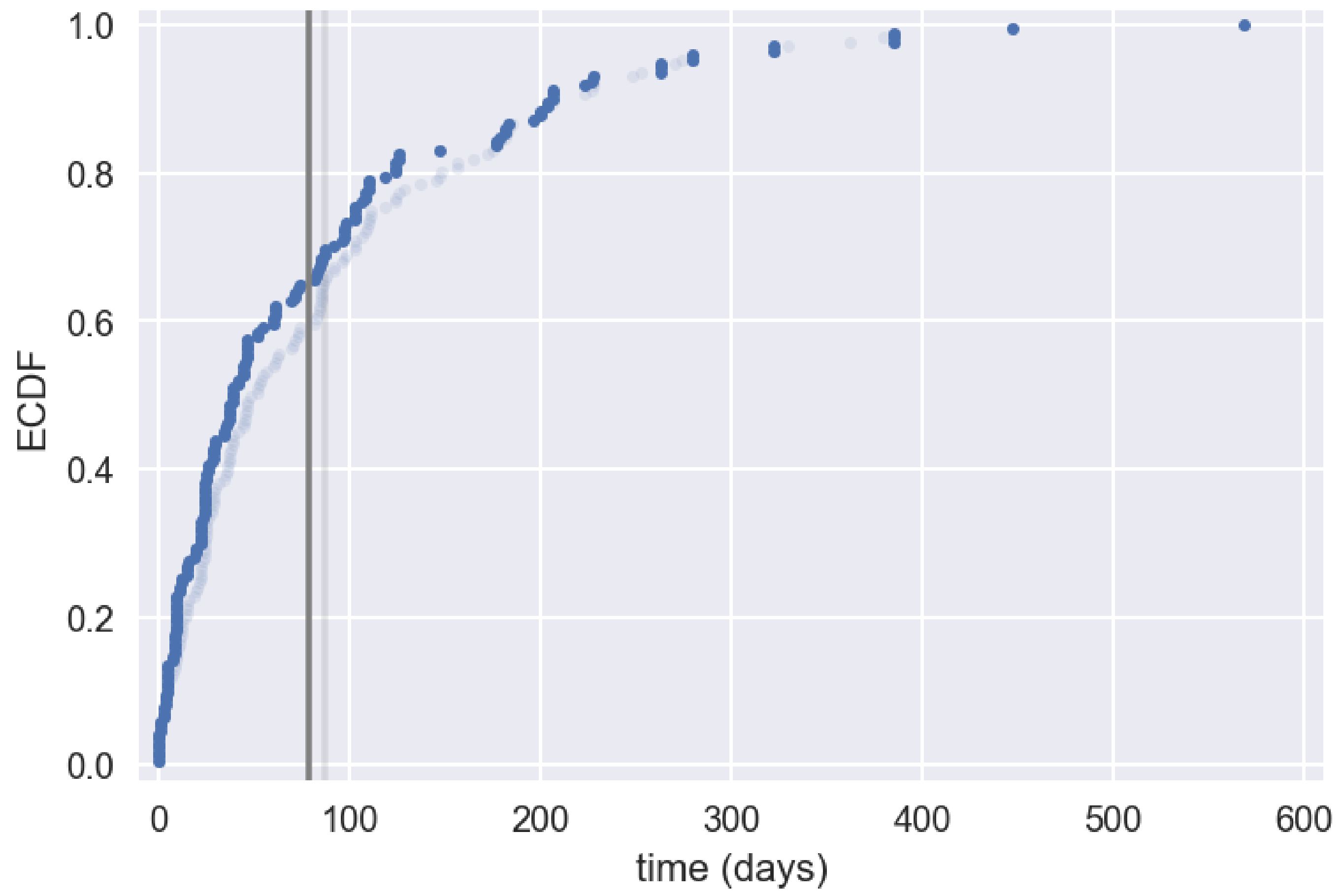
[1] Data source: Wheatley, Sovacool, and Sornette, Nuclear Events Database

Bootstrap sample

A resampled array of the data

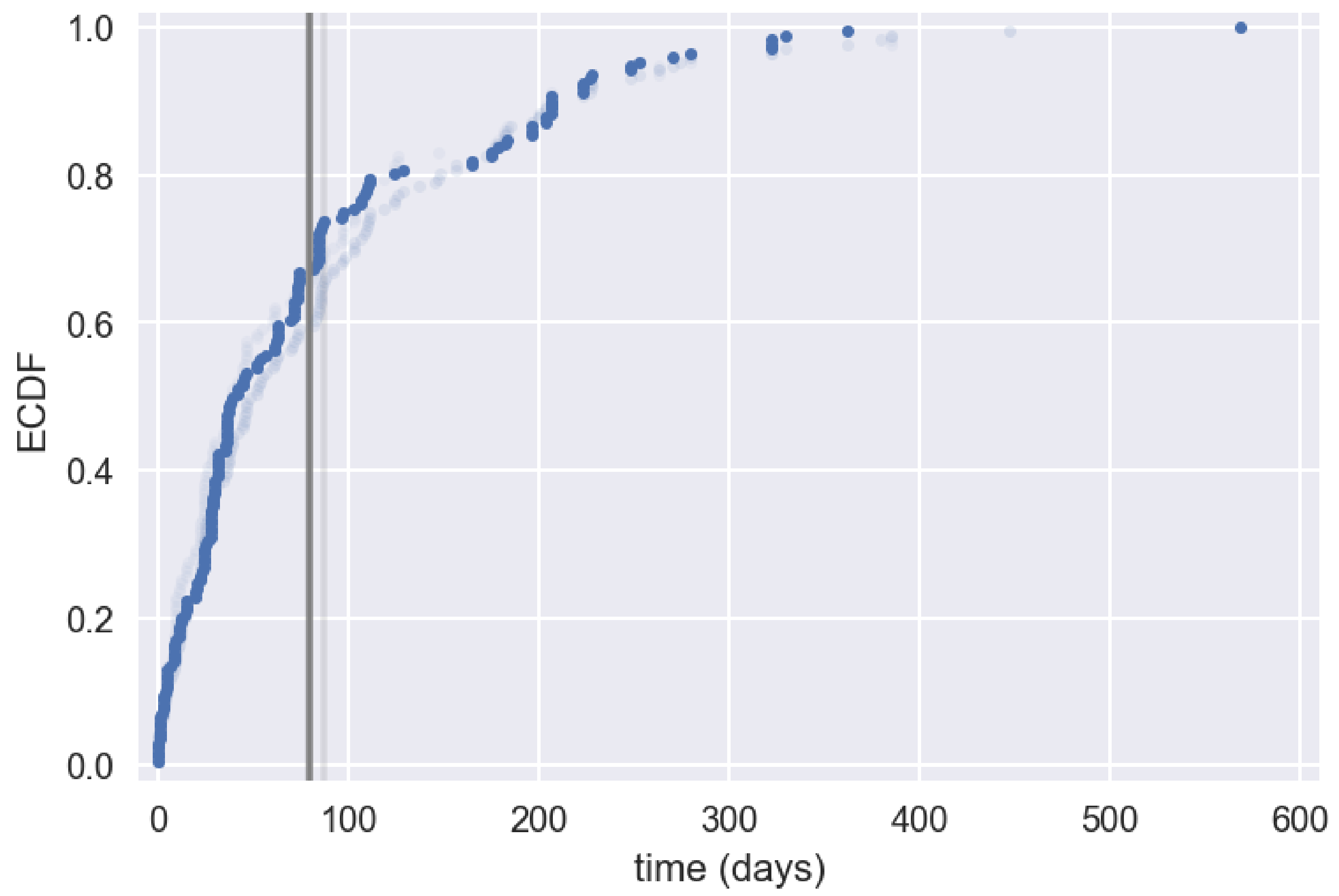
```python
# Resample nuclear_incident_times with replacement
bs_sample = np.random.choice(
  nuclear_incident_times,
  replace=True,
  size=len(inter_times)
)
```

Bootstrap replicates



[1] Data source: Wheatley, Sovacool, and Sornette, Nuclear Events Database

Bootstrap replicates



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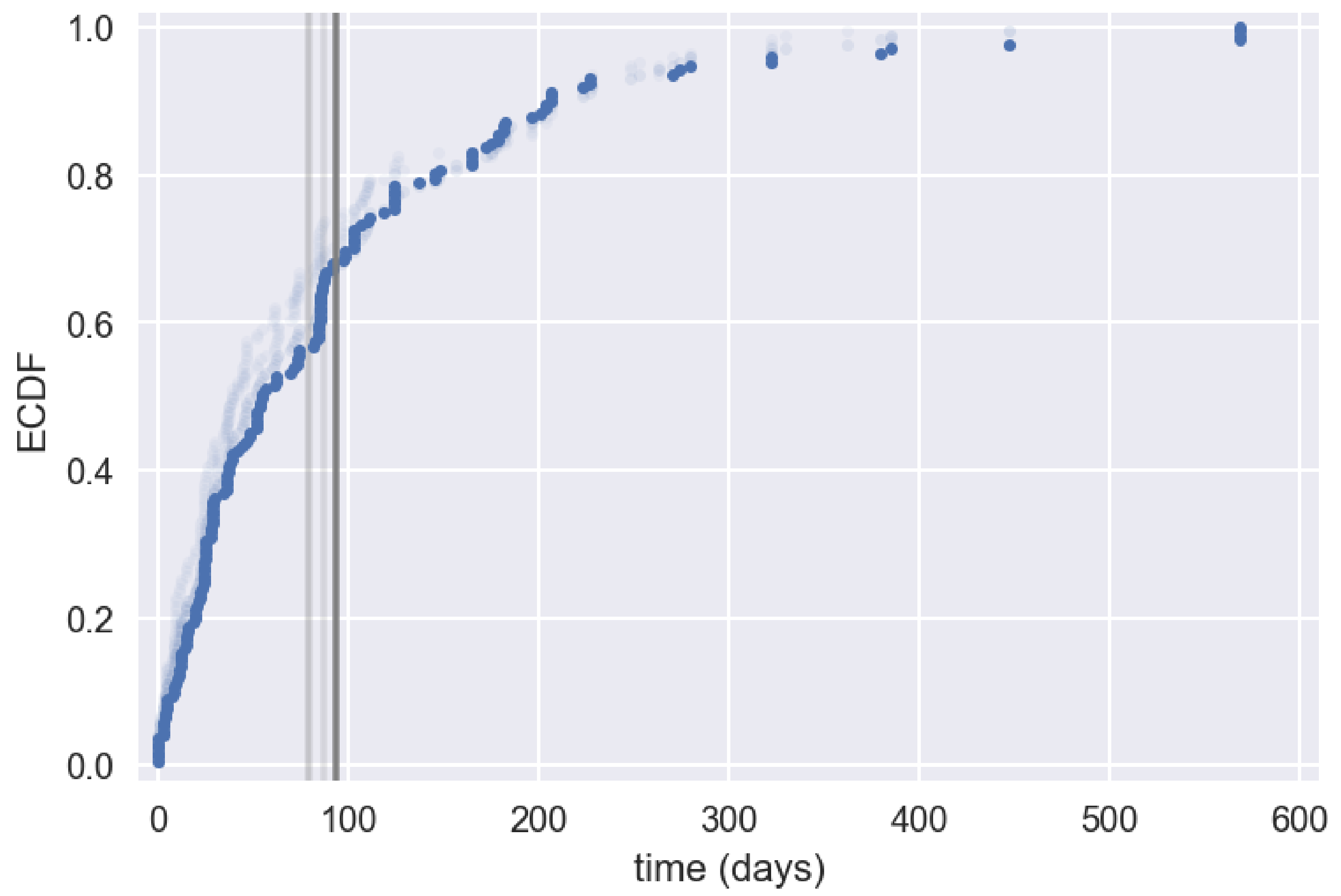
Bootstrap replicates



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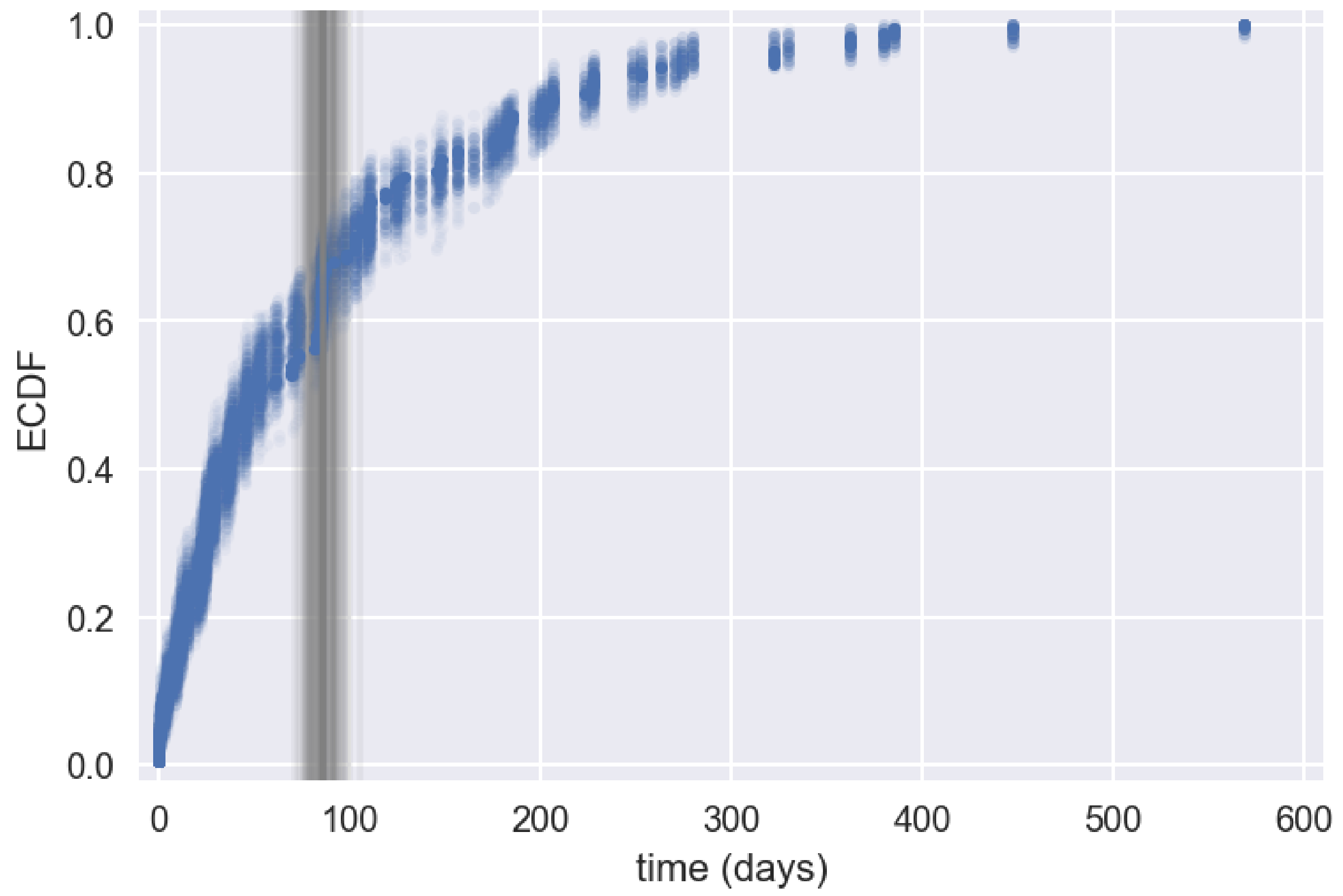
Bootstrap replicates



[1] Data source: Wheatley, Sovacool, and Sornette, Nuclear Events Database

Bootstrap replicates

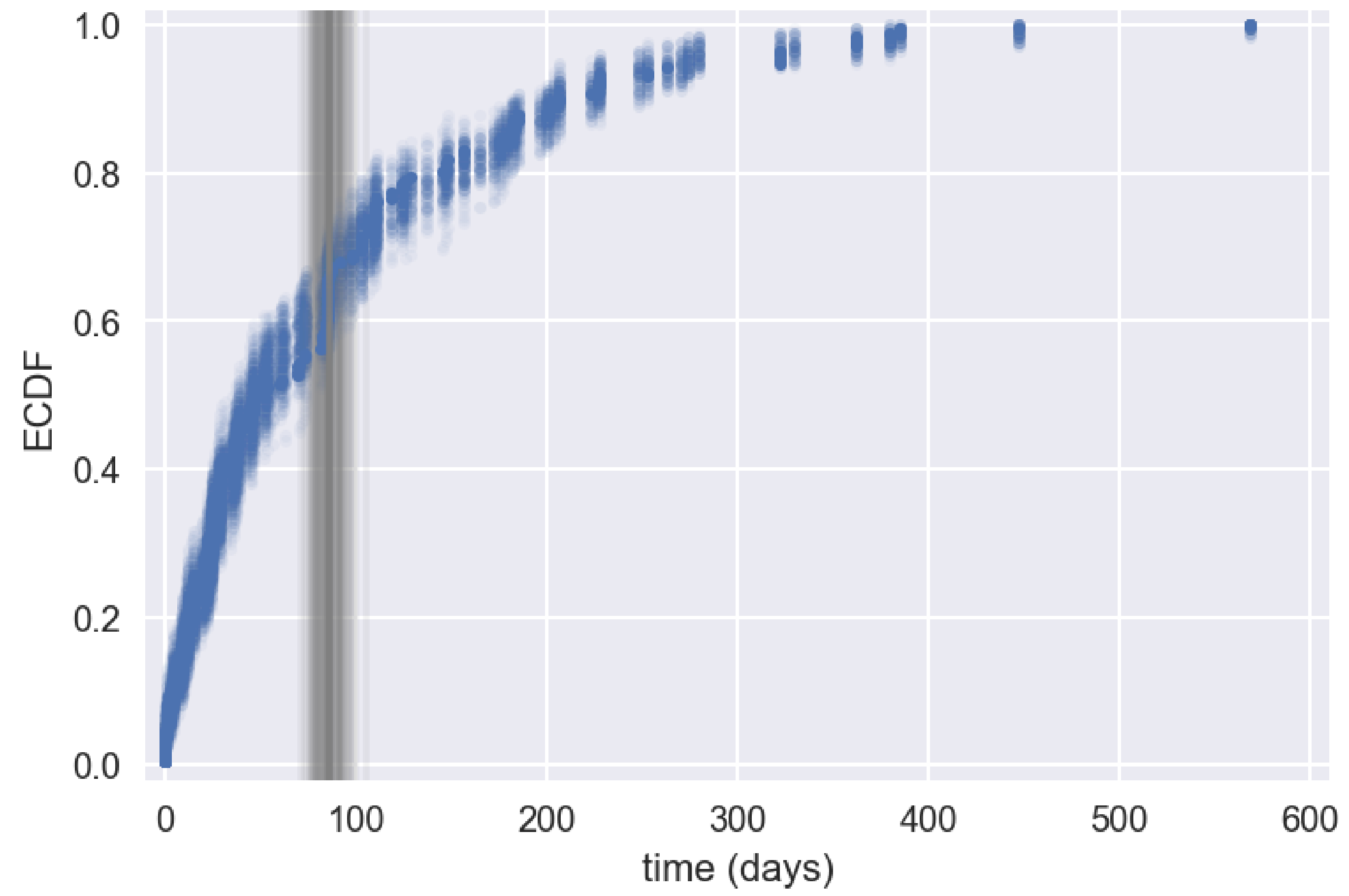
Bootstrap replicate: A statistic computed from a bootstrap sample

dcst.draw_bs_reps()

Function to draw bootstrap replicates from a data set

```python
# Draw 10000 replicates of the mean from
# nuclear_incident_times
bs_reps = dcst.draw_bs_reps(
  nuclear_incident_times, np.mean, size=10000
)
```

The bootstrap confidence interval



[1] Data source: Wheatley, Sovacool, and Sornette, Nuclear Events Database

The bootstrap confidence interval

If we repeated measurements over and over again, *p*% of the observed values would lie within the *p*% confidence interval

The bootstrap confidence interval

```
np.percentile(bs_reps, [2.5, 97.5])
```

```
array([  73.31505848,  102.39181287])
```

Let's practice!

Hypothesis tests

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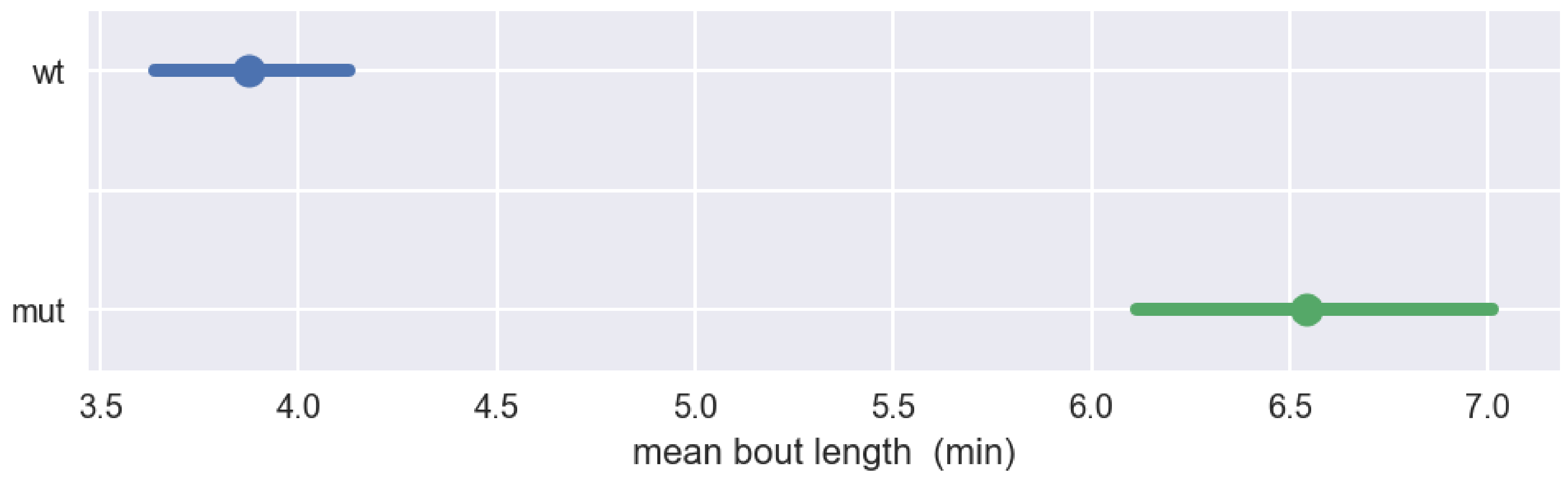
Effects of mutation on activity

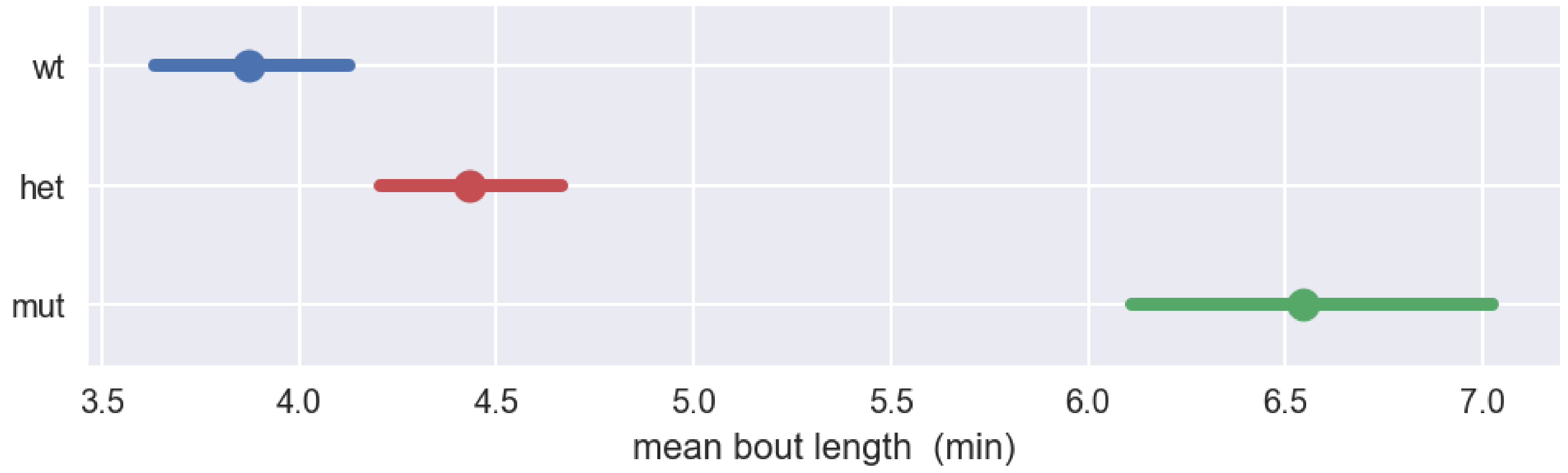


[1] Data courtesy of Avni Gandhi, Grigogios Oikonomou, and David Prober, Caltech

Genotype definitions

- **Wild type**: No mutations
- **Heterozygote:** Mutation on one of two chromosomes
- **Mutant:** Mutation on both chromosomes

Effects of mutation on activity



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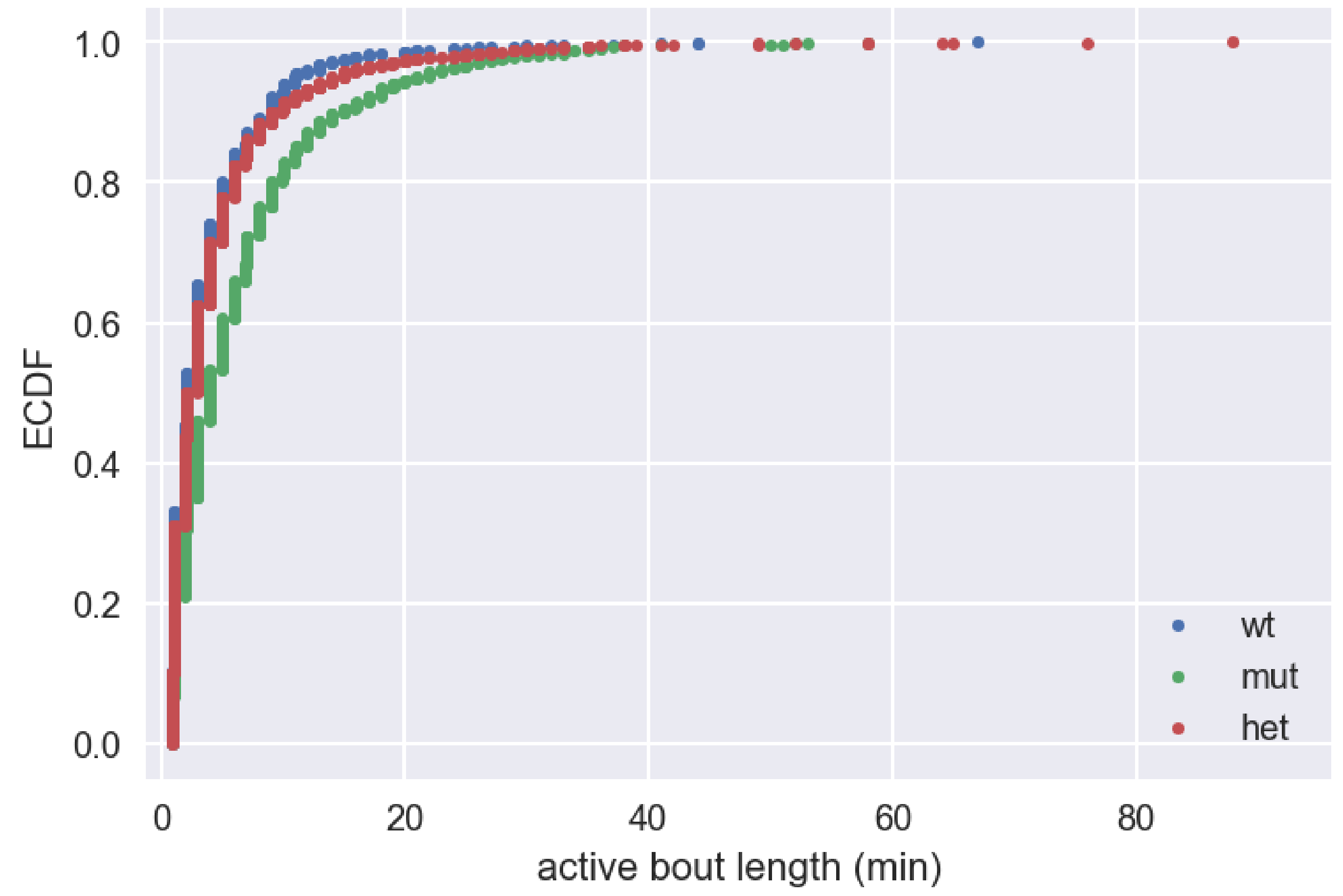
Effects of mutation on activity



[1] Data courtesy of Avni Gandhi, Grigogios Oikonomou, and David Prober, Caltech

Hypothesis test

Assessment of how reasonable the observed data are assuming a hypothesis is true

p-value

The probability of obtaining a value of your **test statistic** that is **at least as extreme as** what was observed, under the assumption the **null hypothesis** is true

Test statistic

- A single number that can be computed from observed data and from data you simulate under the null hypothesis
- Serves as a basis of comparison

p-value

The probability of obtaining a value of your **test statistic** that is **at least as extreme as** what was observed, under the assumption the **null hypothesis** is true

Requires clear specification of:

- **Null hypothesis** that can be simulated
- **Test statistic** that can be calculated from observed and simulated data
- Definition of **at least as extreme as**

Pipeline for hypothesis testing

- Clearly state the null hypothesis
- Define your test statistic
- Generate many sets of simulated data assuming the null hypothesis is true
- Compute the test statistic for each simulated data set
- The p-value is the fraction of your simulated data sets for which the test statistic is at least as extreme as for the real data

Specifying the test

Null hypothesis: the active bout lengths of wild type and heterozygotic fish are identically distributed

Test statistic: Difference in mean active bout length between heterozygotes and wild type

At least as extreme as: Test statistic is greater than or equal to what was observed

Permutation test

For each replicate:

- Scramble labels of data points
- Compute test statistic

```
perm_reps = dcst.draw_perm_reps(
    data_a, data_b, dcst.diff_of_means, size=10000
)
```

p-value is the fraction of replicates at least as extreme as what was observed

```
p_val = np.sum(perm_reps >= diff_means_obs) / len(perm_reps)
```

Let's practice!

CASE STUDIES IN STATISTICAL THINKING

Linear regressions and pairs bootstrap

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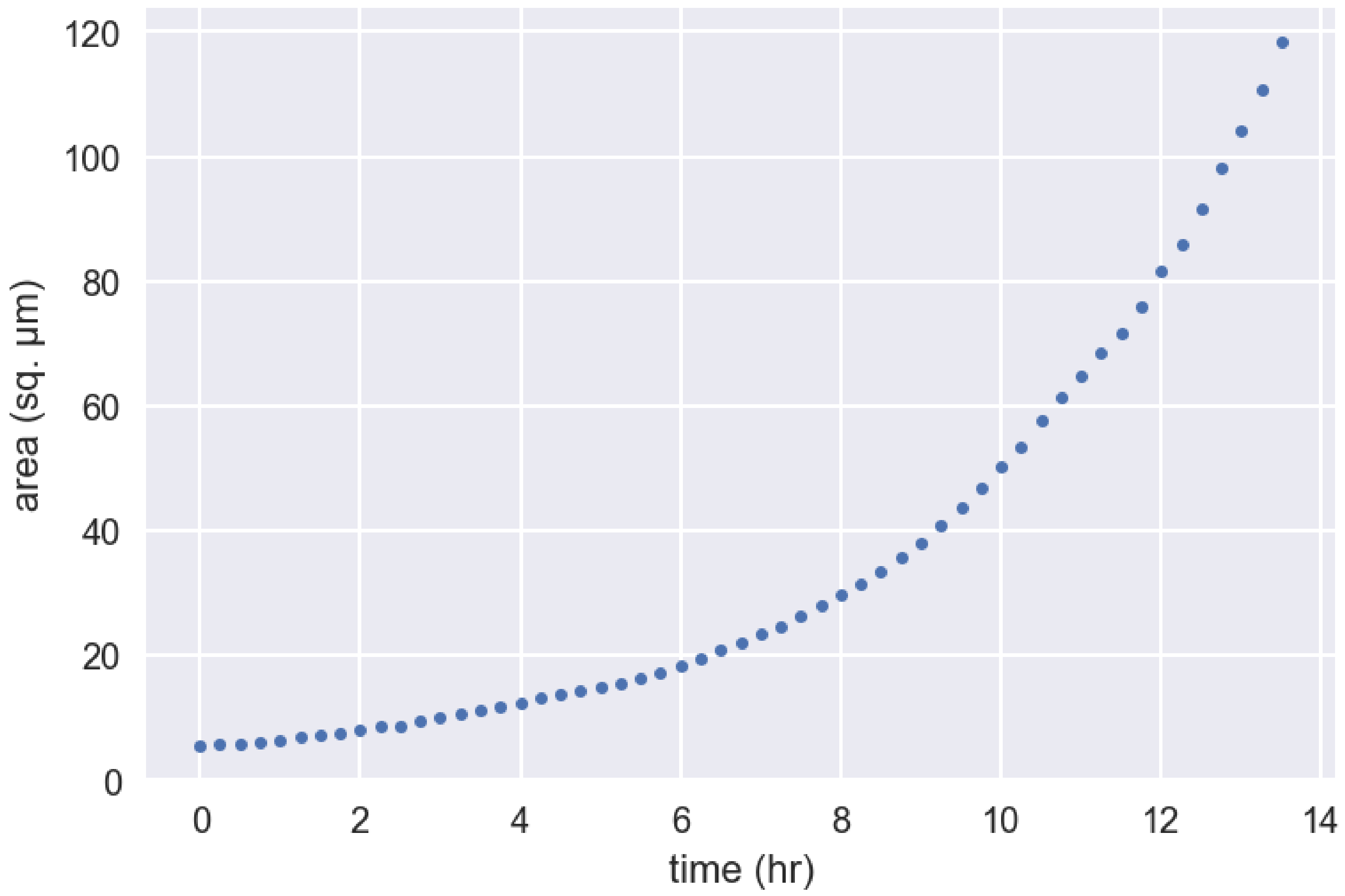
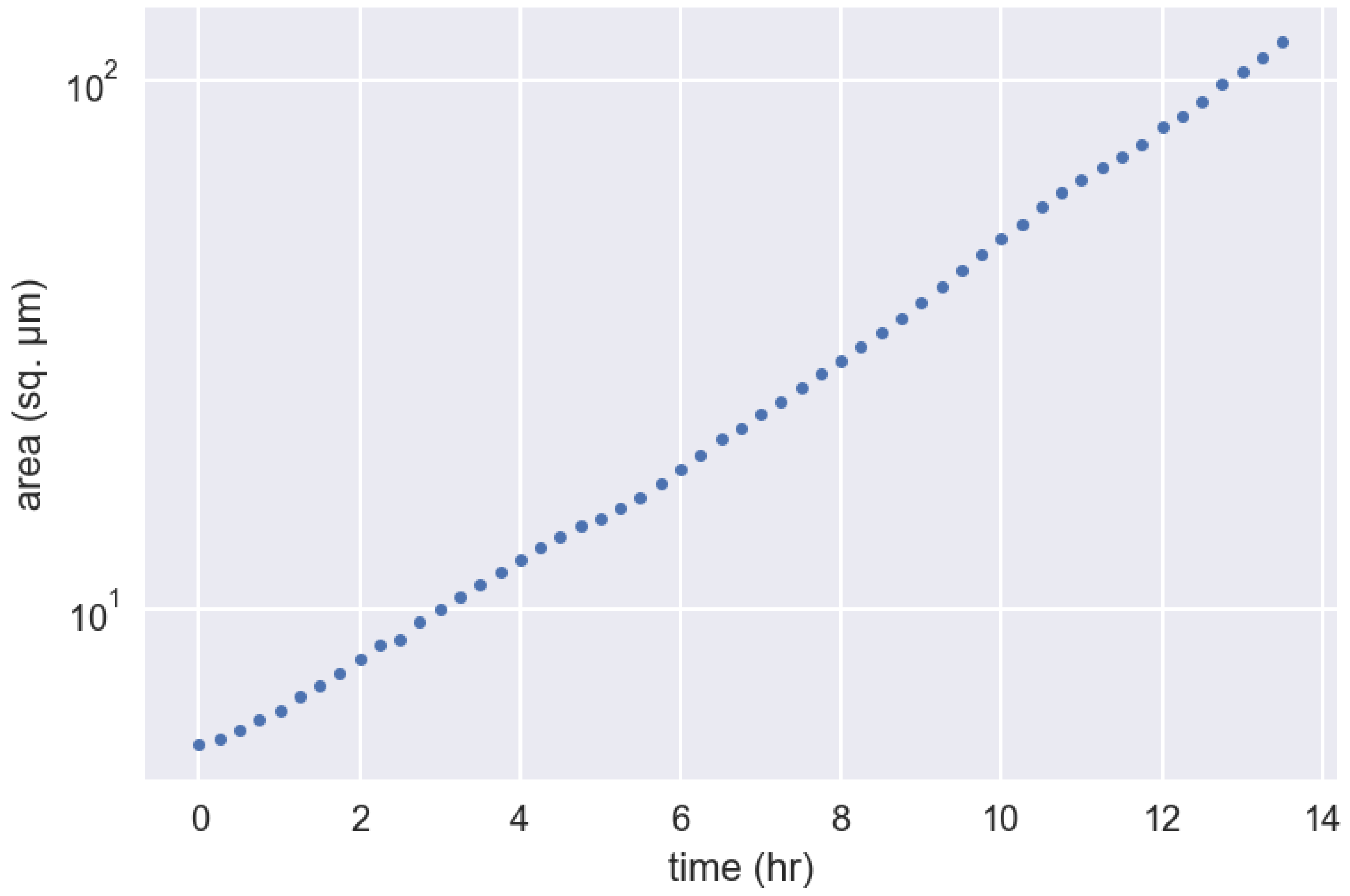
Bacterial growth

[1] Images courtesy of Jin Park and Michael Elowitz, Caltech

Bacterial growth



```
_ = plt.semilogy(t, bac_area, marker='.', linestyle='none')
_ = plt.xlabel('time (hr)')
_ = plt.ylabel('area (sq. µm)')
plt.show()
```



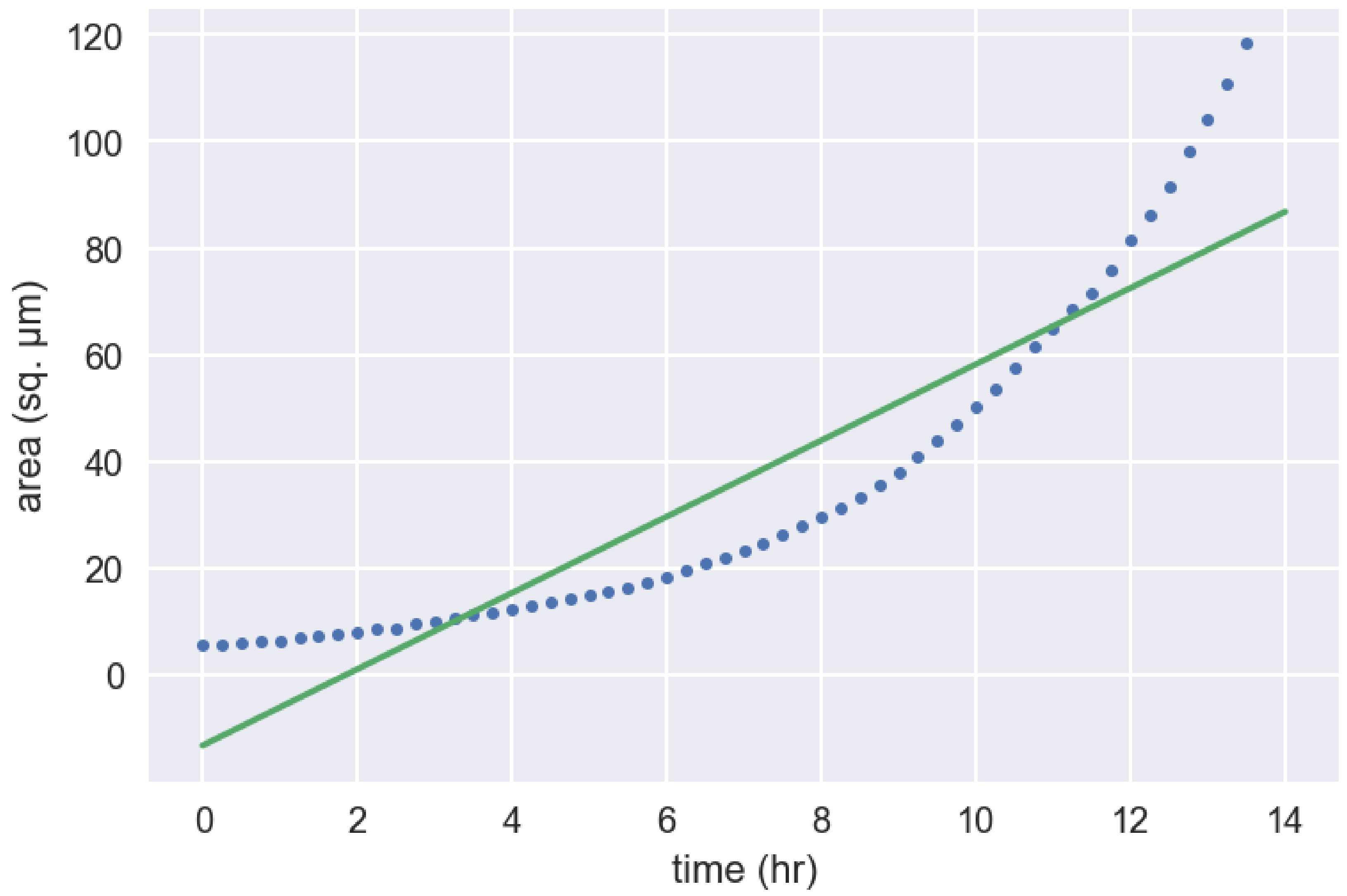
Linear regression with np.polyfit()

```
slope, intercept = np.polyfit(t, bac_area, 1)
```

```
t_theor = np.array([0, 14])
bac_area_theor = slope * t_theor + intercept
```

```
_ = plt.plot(t, bac_area, marker='.', linestyle='none')
_ = plt.plot(t_theor, bac_area_theor)
_ = plt.xlabel('time (hr)')
_ = plt.ylabel('area (sq. µm)')
plt.show()
```

Regression of bacterial growth



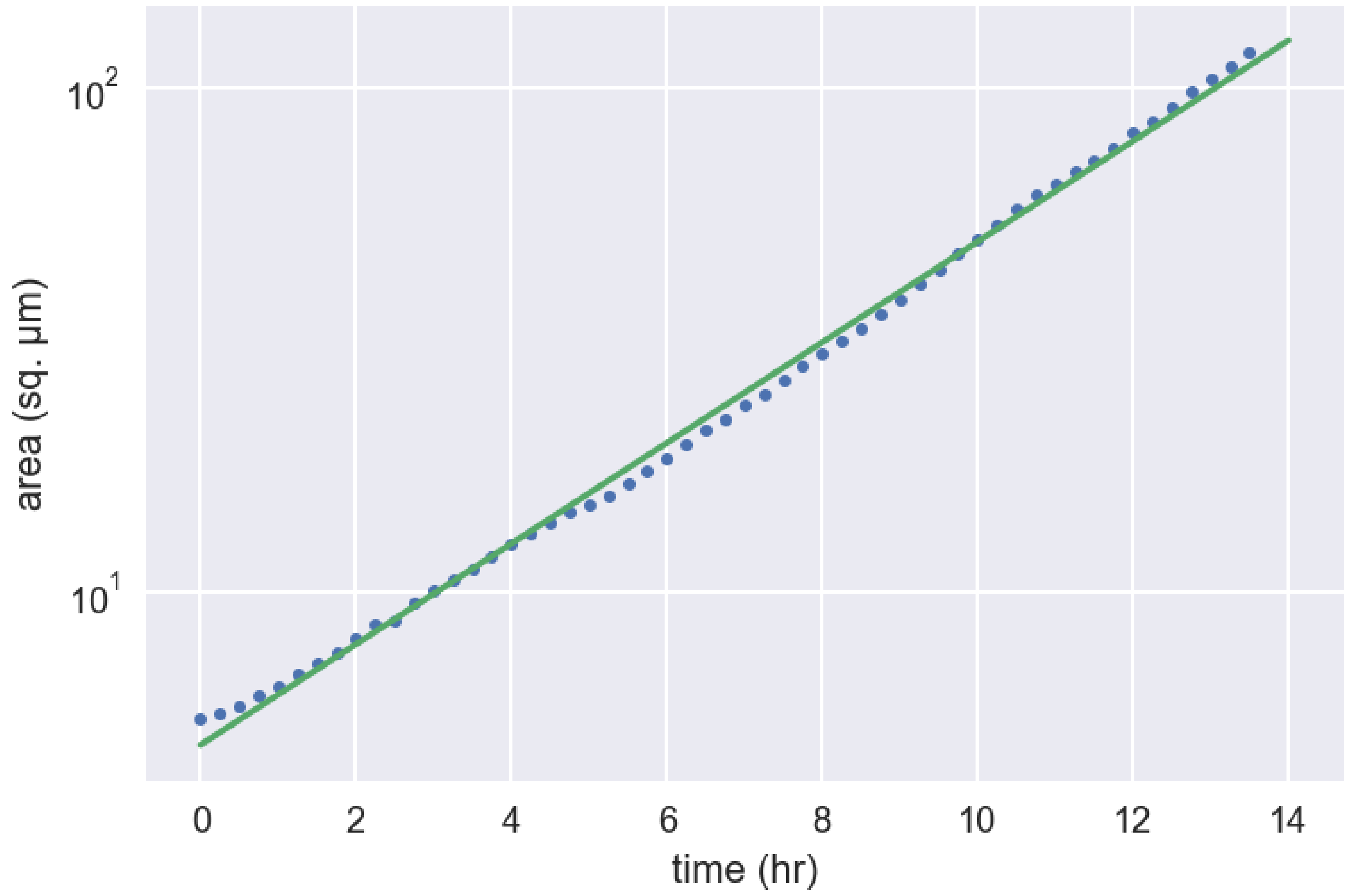
Semilog-linear regression with np.polyfit()

```
slope, intercept = np.polyfit(t, np.log(bac_area), 1)
```

```
t_theor = np.array([0, 14])
bac_area_theor = np.exp(slope * t_theor + intercept)
```

```
_ = plt.semilogy(t, bac_area, marker='.', linestyle='none')
_ = plt.semilogy(t_theor, bac_area_theor)
_ = plt.xlabel('time (hr)')
_ = plt.ylabel('area (sq. µm)')
plt.show()
```

Regression of bacterial growth



Pairs bootstrap

- Resample data in pairs
- Compute slope and intercept from resampled data
- Each slope and intercept is a bootstrap replicate
- Compute confidence intervals from percentiles of bootstrap replicates

Pairs bootstrap

```
# Draw 10000 pairs bootstrap reps
slope_reps, int_reps = dcst.draw_bs_pairs_linreg(
  x_data, y_data, size=10000
)

# Compute 95% confidence interval of slope
slope_conf_int = np.percentile(slope_reps, [2.5, 97.5])
```

Let's practice!

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