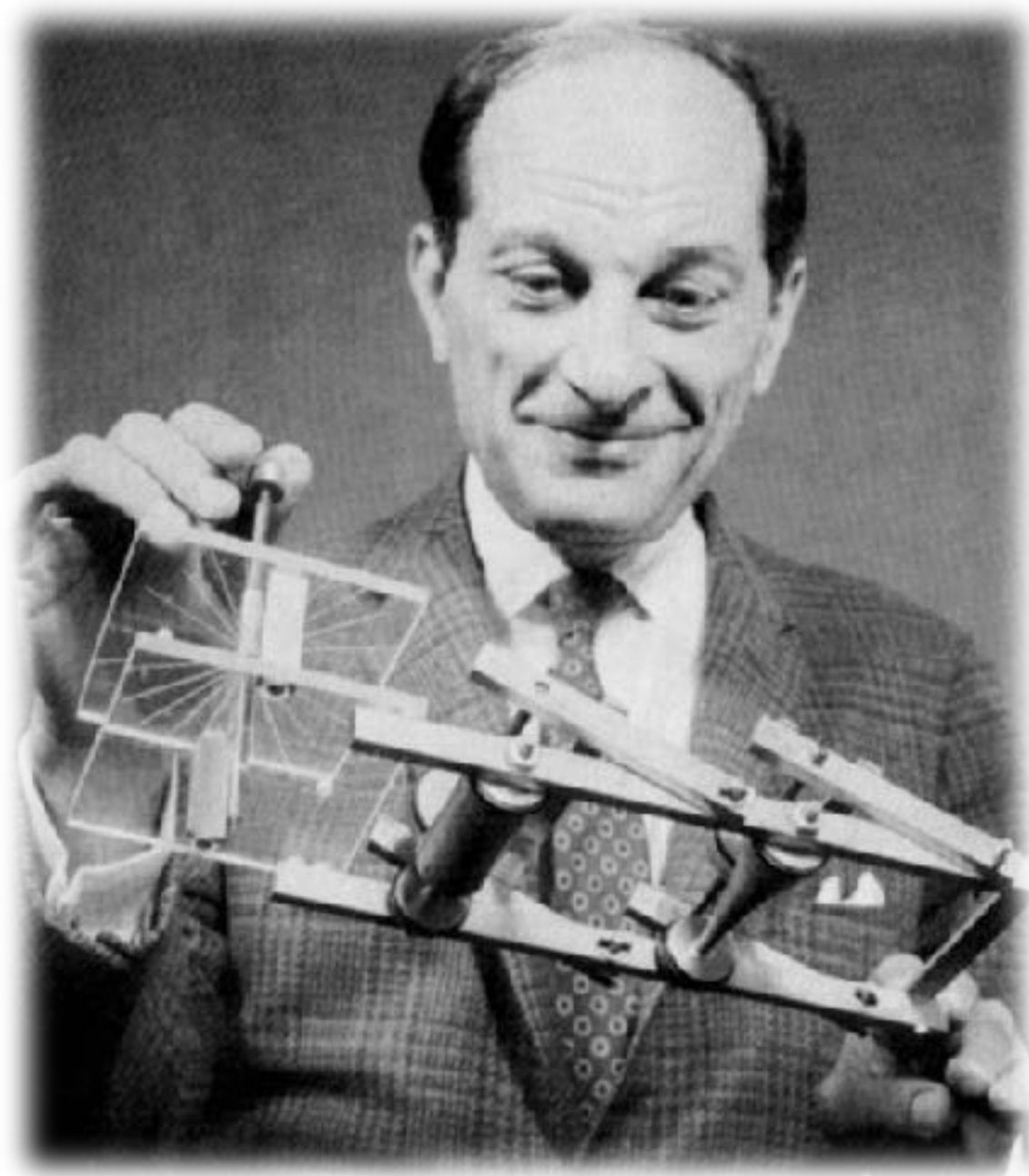
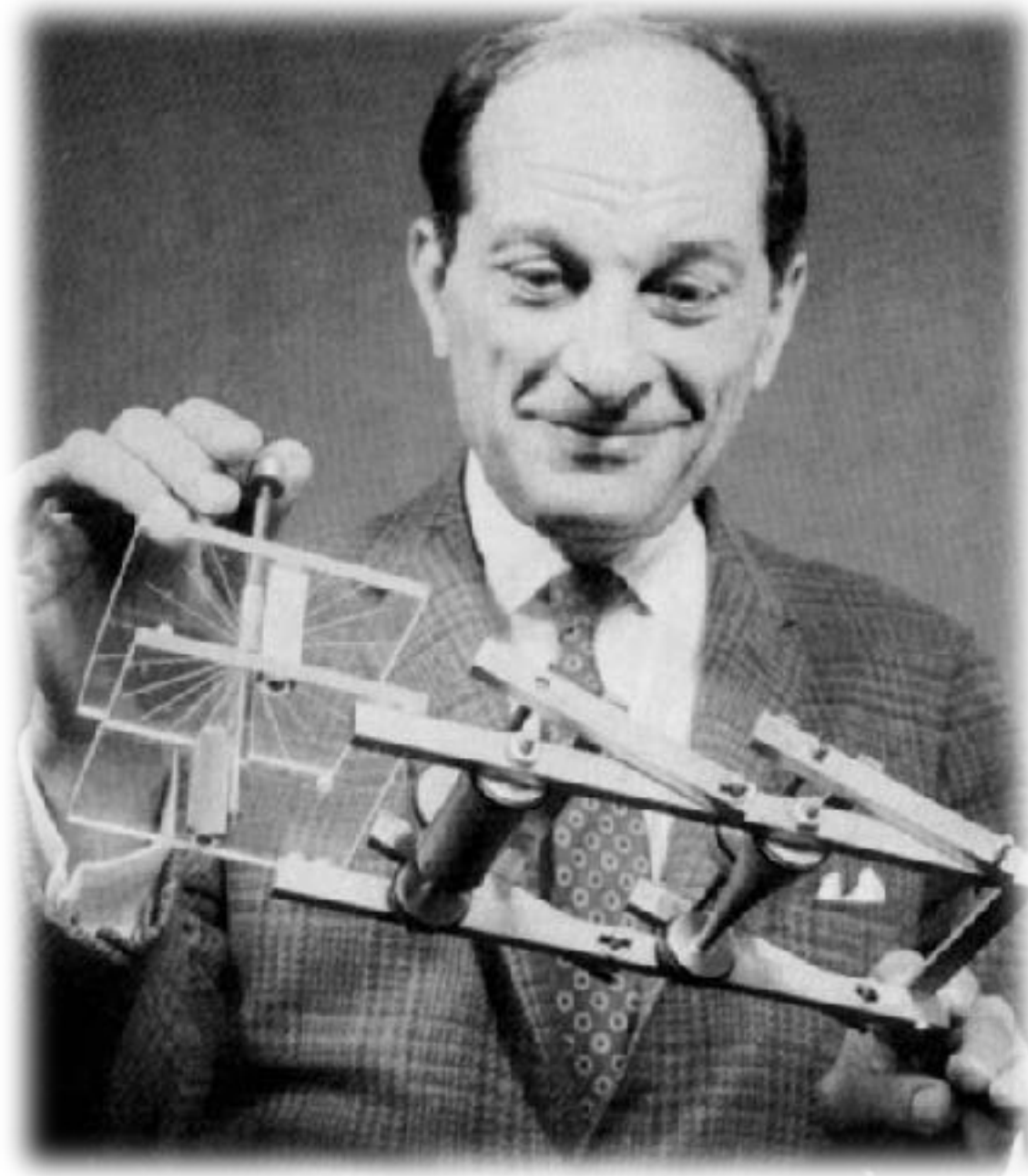




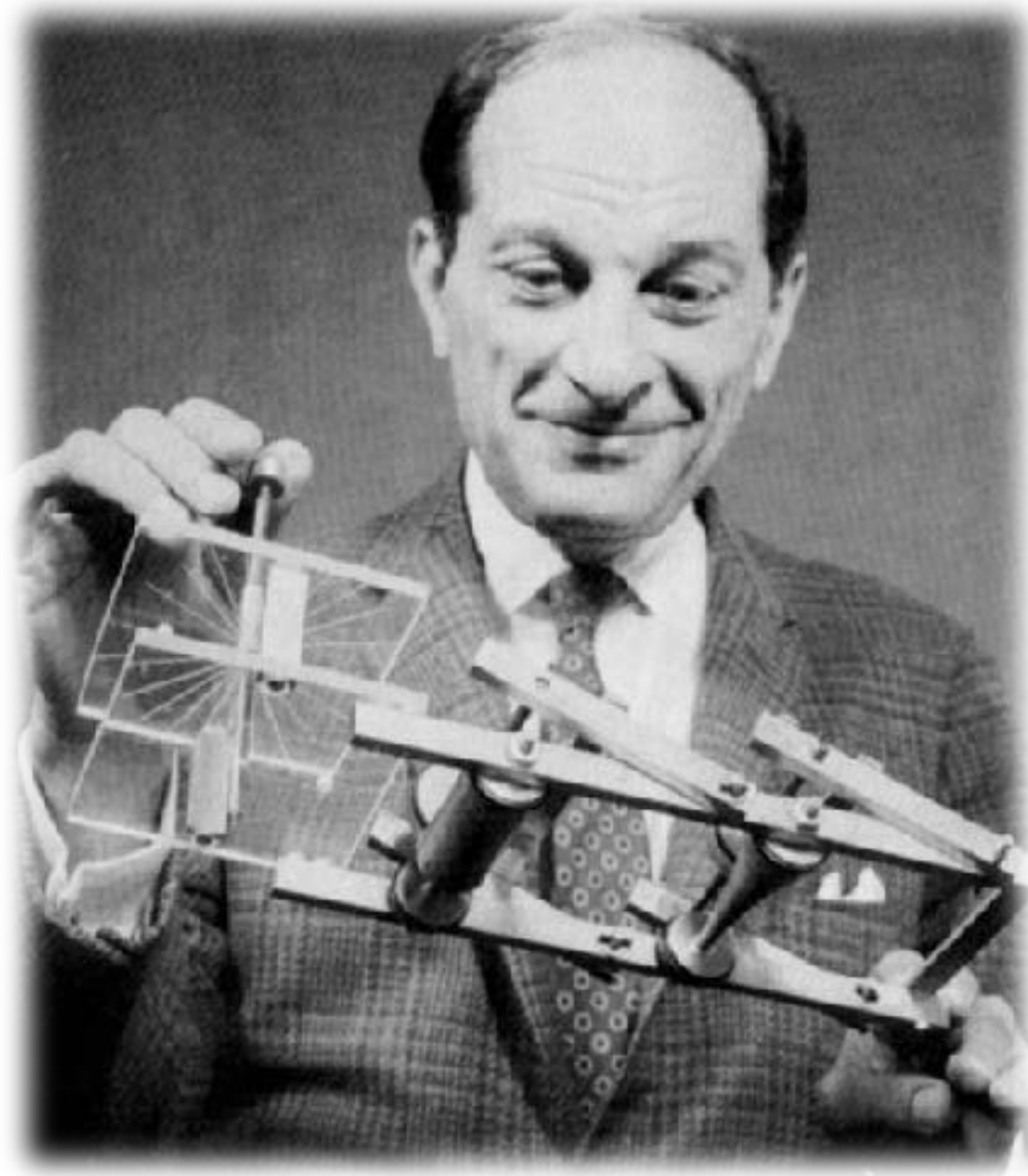
Stan

Software Ecosystem for Modern Bayesian Inference



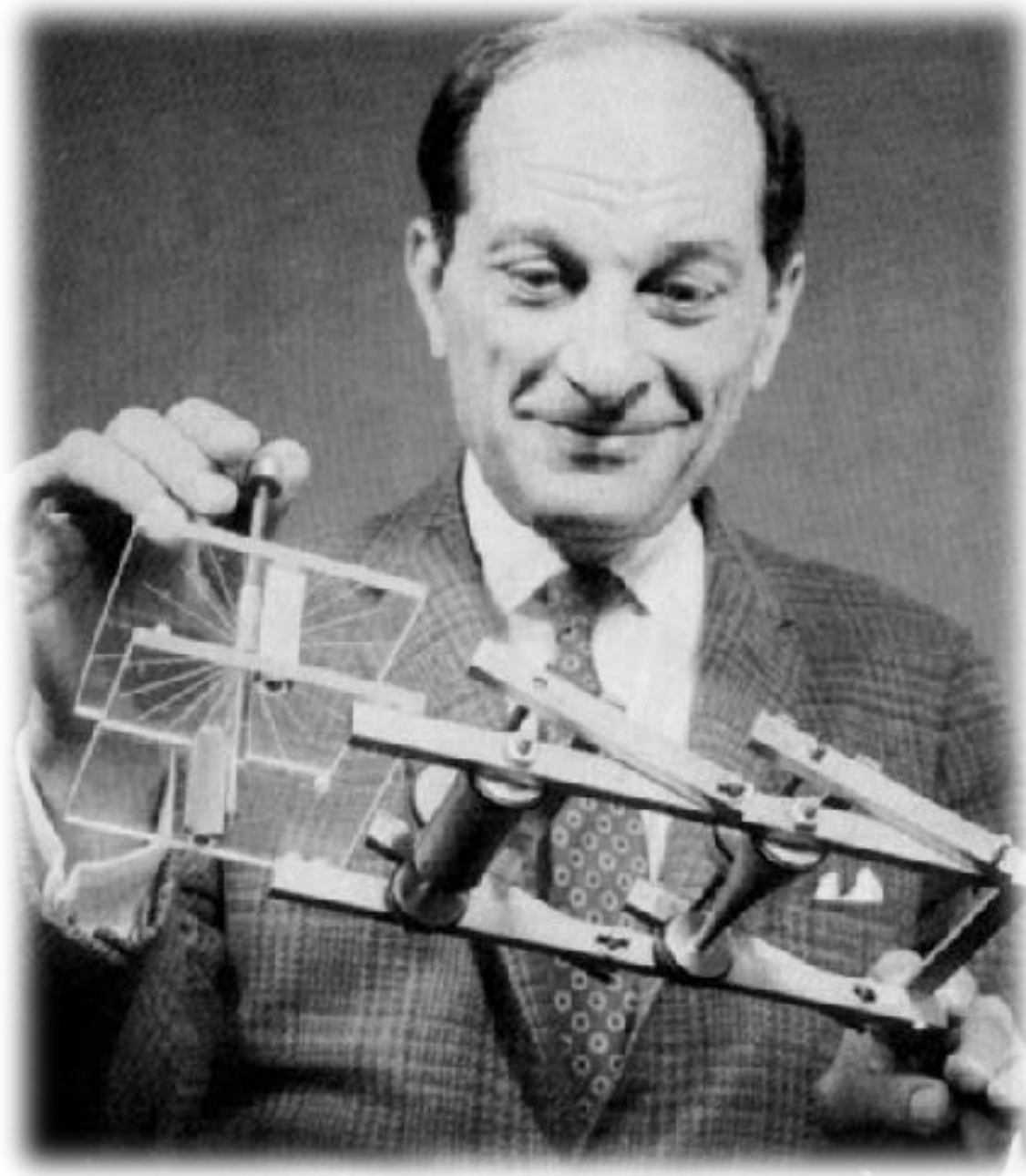


Stanislaw Ulam
(1909–1984)



Stanislaw Ulam
(1909–1984)

Monte Carlo
Method



**Stanislaw Ulam
(1909–1984)**

H-Bomb

**Monte Carlo
Method**

What is Stan?

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- Probabilistic **programming language** and **inference algorithms**

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 - declares data and (constrained) parameter variables
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 - VB for approximate Bayes
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 - MCMC for full Bayes
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- Stan **ecosystem**
 - lang, math library (C++)
 - interfaces and tools (**R**, Python, Julia, many more)
 - documentation (example model repo, user guide & reference manual, case studies, R package vignettes)
 - online community (Stan Forums on discourse)

Users

statistical analysis with Stan

Interfaces and Installation

In order to facilitate inference, Stan provides both a modeling language for specifying complex statistical models and a library of statistical algorithms for computing inferences with those models. These components are exposed through interfaces in environments such as R, Python, and the command line.

To get started with Stan head over to our interfaces page where you will find documentation and installation instructions about each of our interfaces:

- [Stan Interfaces](#)

Documentation, Tutorials, and Case Studies

Already playing with Stan in your favorite computing environment? Then it's time to put Stan to use and fit some models! For information on the Stan modeling language as well as tutorials, case studies, and examples, head over to our documentation page,

- [Stan Documentation](#)

Why Stan?

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 - HMC + NUTS
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- Fit rich Bayesian statistical models
- Efficiency
 - HMC + NUTS
 - Compiled to C++
- Flexible domain specific language
- “Freedom-respecting, open-source”
 - BSD (code)
 - CC-BY (doc & written materials)

Who is using Stan?

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Biological & physical sciences

Who is using Stan?

Biological & physical sciences

- clinical trials
- epidemiology
- genomics
- population ecology
- entomology
- ophthalmology
- neurology
- agriculture
- fisheries
- cancer biology
- astrophysics & cosmology
- molecular biology
- oceanography
- climatology

Who is using Stan?

Social Sciences

Who is using Stan?

Social Sciences

- population dynamics
- psycholinguistics
- social networks
- political science
- human development
- economics

Who is using Stan?

Many more...

Who is using Stan?

Many more...

- sports analytics
- public health
- publishing
- finance
- pharma
- actuarial
- recommender systems
- educational testing
- materials engineering

Who is using Stan?

mc-stan.org/users/citations

github.com/stan-dev/stancon_talks

Stan is many things

Stan is many things

Math

Stan is many things

Math ← Language

Stan is many things

Math ← Language ← Algorithms

Stan is many things

Math ← Language ← Algorithms ← Services

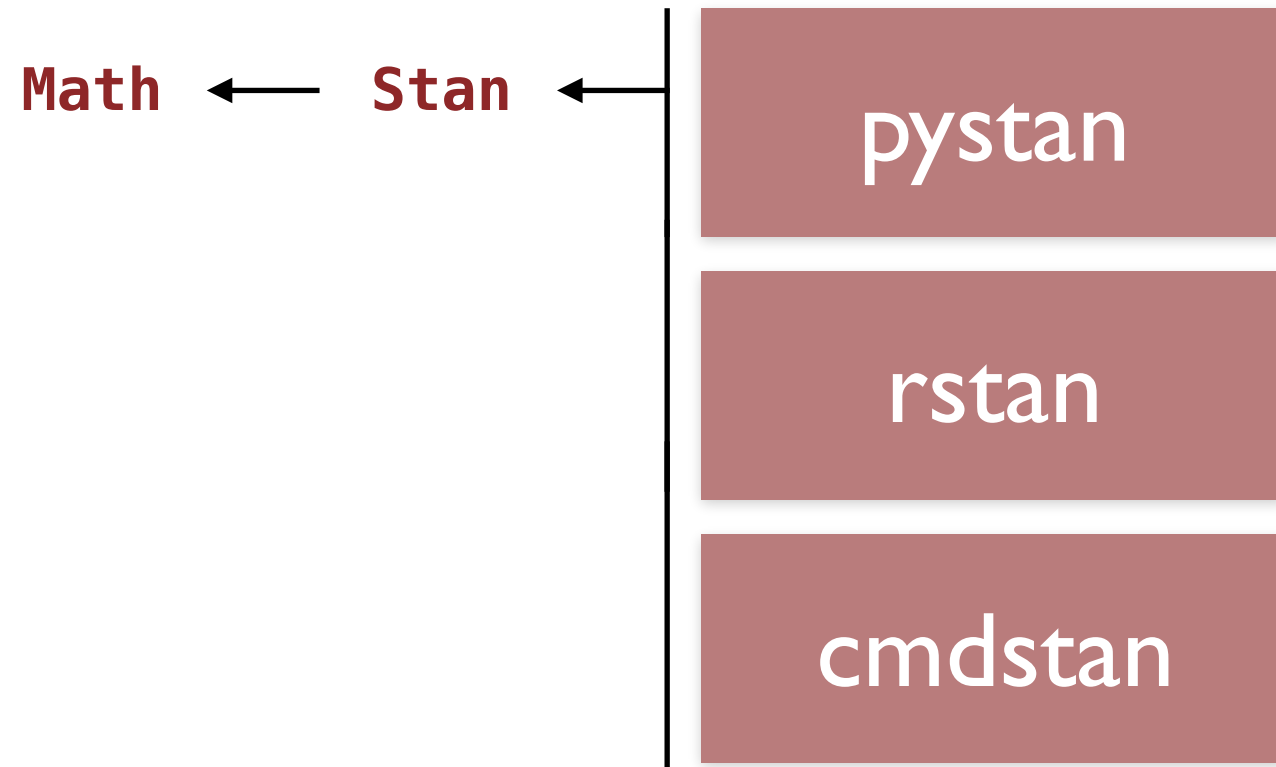
Stan is many things

Math ← **Stan**

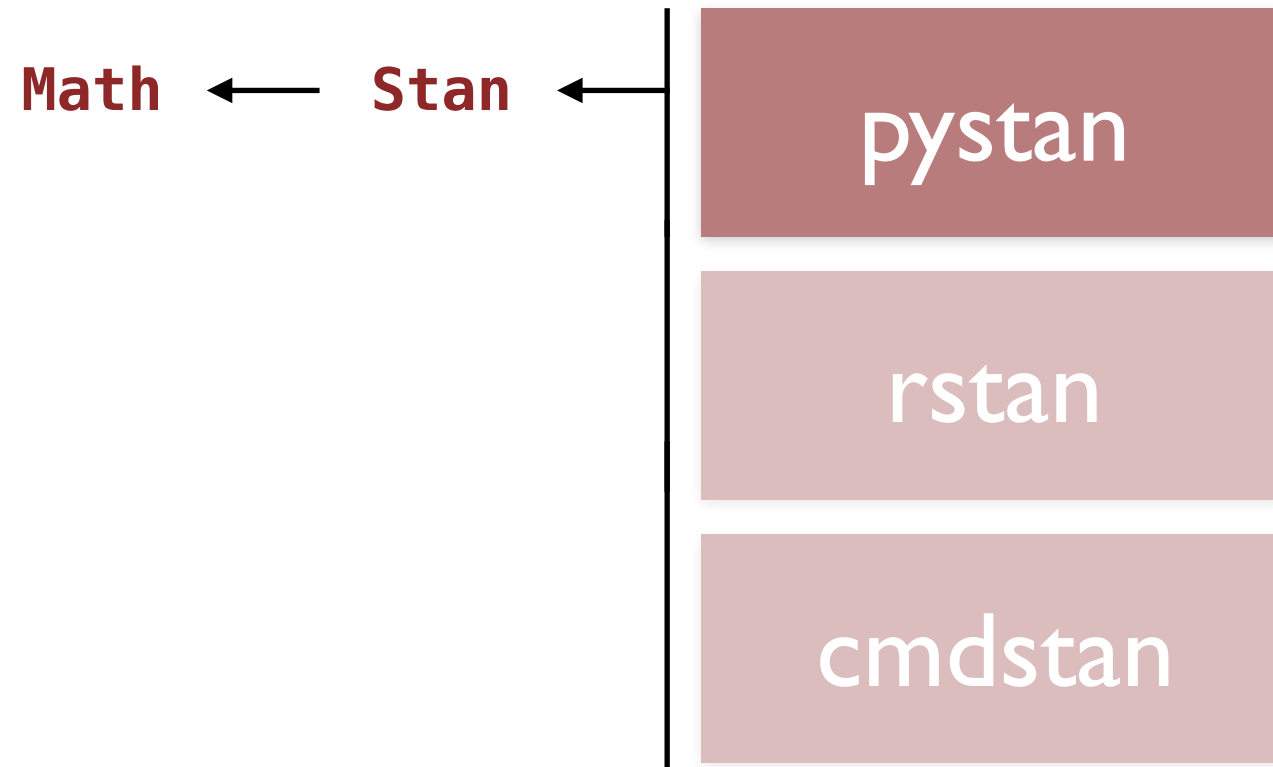
Interfaces

Math ← **Stan**

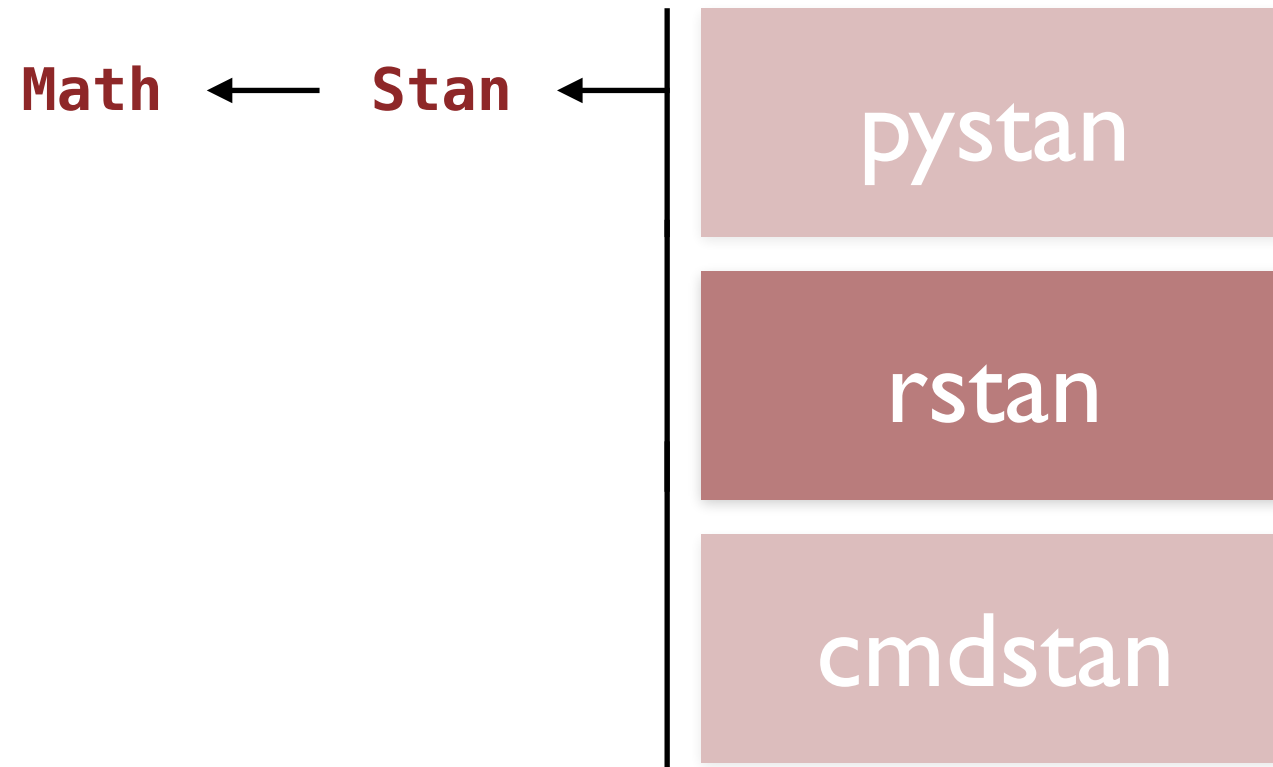
Interfaces



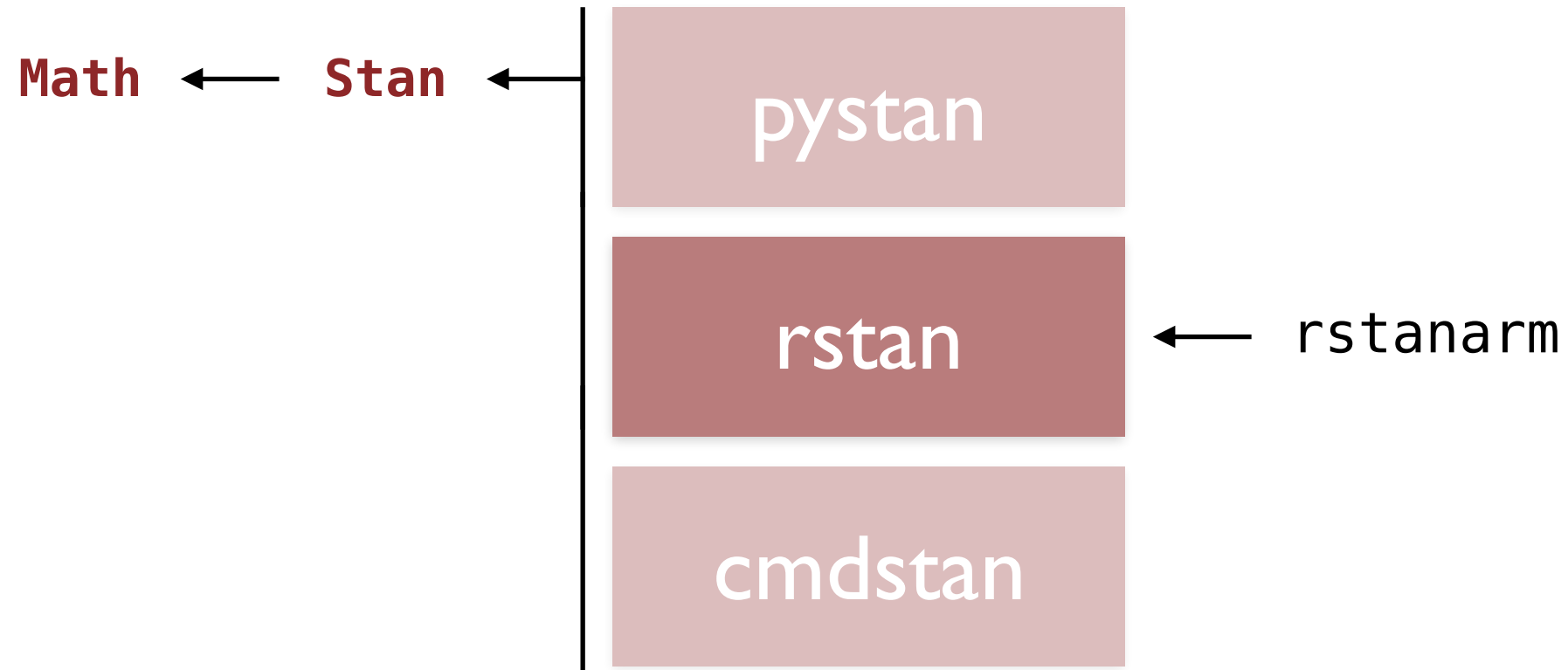
Interfaces



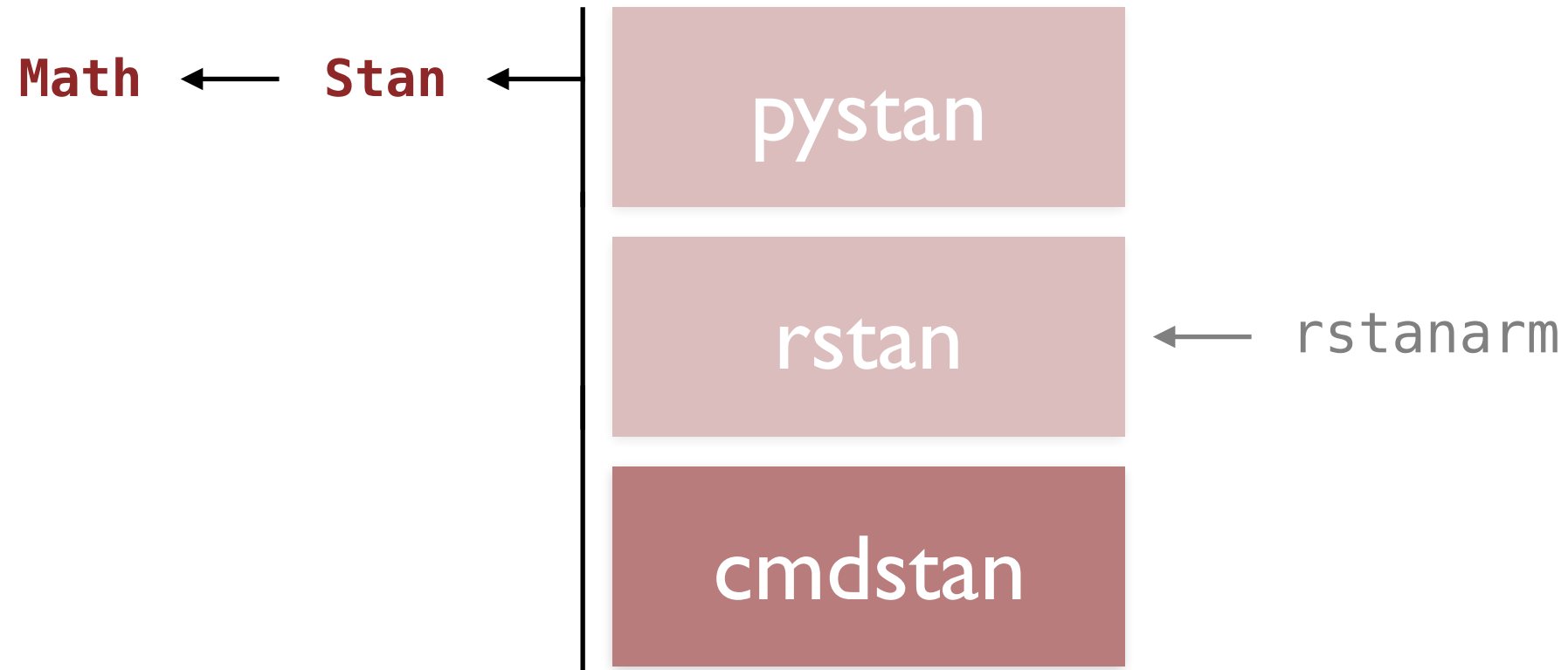
Interfaces



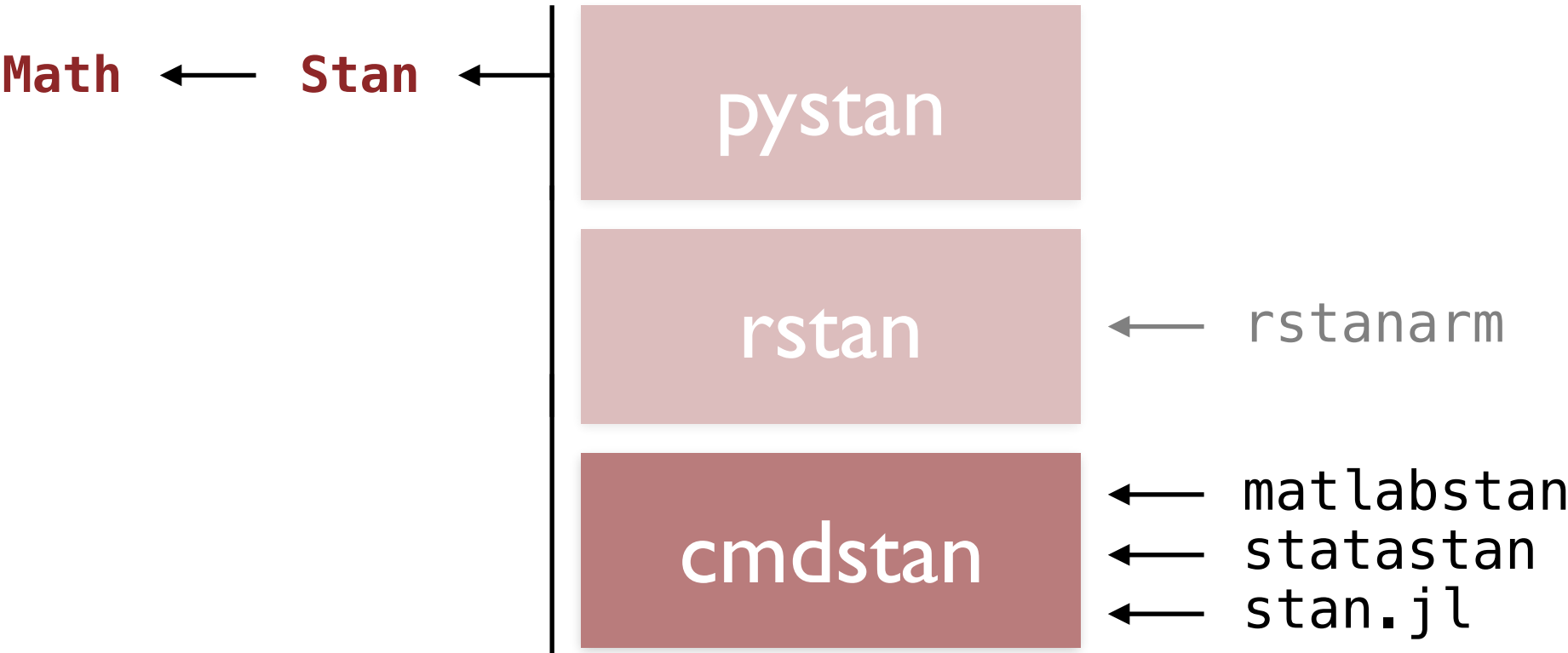
Interfaces



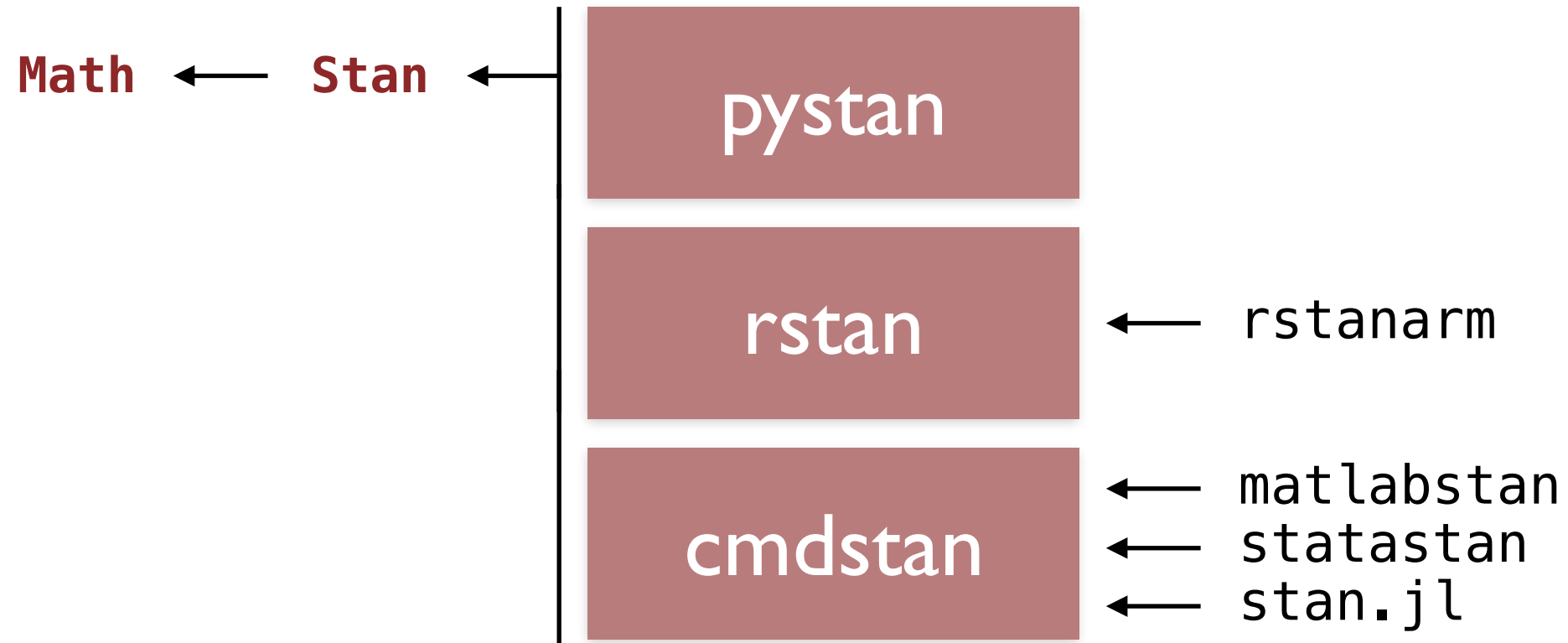
Interfaces



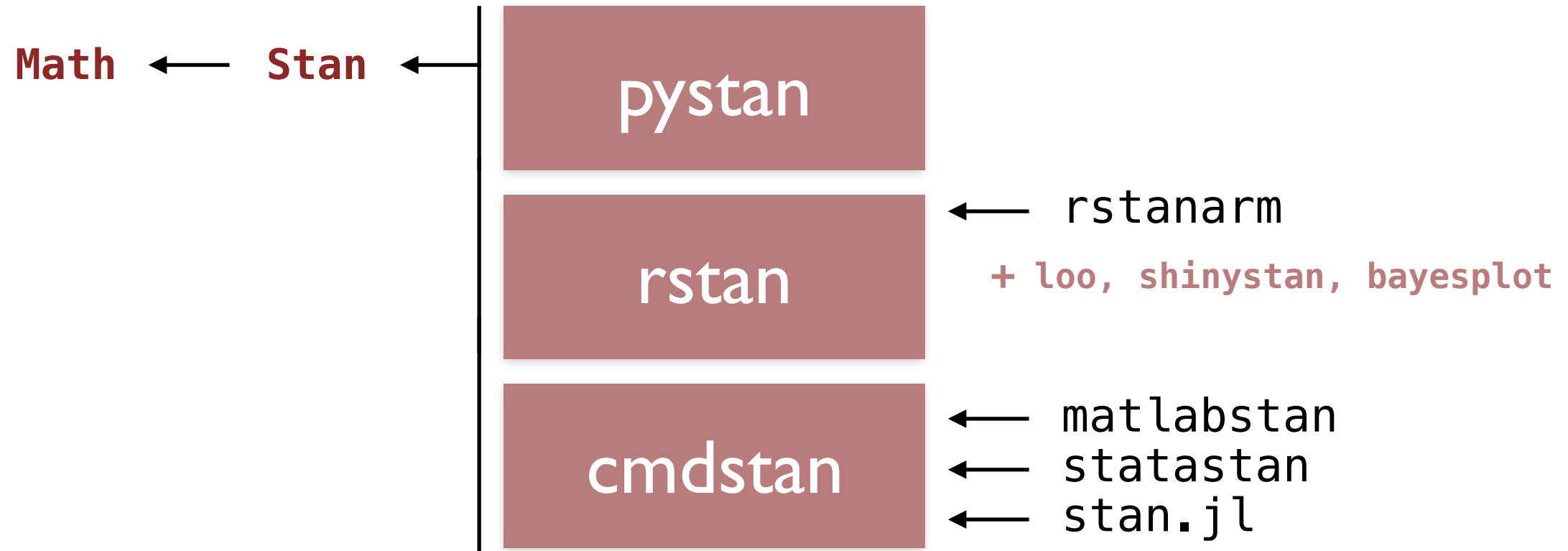
Interfaces



Interfaces



Interfaces + Tools



We're now going to write a
Stan program together

We're now going to write a
Stan program together

- Open a new empty file in RStudio

We're now going to write a Stan program together

- Open a new empty file in RStudio
- Save it as **linear-regression.stan**

Generative model of a system of interest

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Expressed as joint probability distribution of
observed and **unobserved** variables

$$\pi(\mathcal{D}, \theta)$$

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Decomposition (convenient but not required)

$$\pi(\mathcal{D} \mid \theta) \pi(\theta)$$

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Decomposition (convenient but not required)

$$\pi(\mathcal{D} \mid \theta) \pi(\theta)$$

Posterior is proportional to this joint distribution

$$\pi(\theta \mid \mathcal{D}) \propto \pi(\mathcal{D} \mid \theta) \pi(\theta)$$

All computations are actually done on *log* scale

$$\begin{aligned}\log \pi(\theta|\mathcal{D}) &= \log \pi(\mathcal{D}|\theta) \\ &\quad + \log \pi(\theta) \\ &\quad + \text{constant}\end{aligned}$$

All computations are actually done on *log* scale

$$\begin{aligned}\log \pi(\theta|\mathcal{D}) &= \log \pi(\mathcal{D}|\theta) \\ &\quad + \log \pi(\theta) \\ &\quad + \text{constant}\end{aligned}$$

Products become sums of logs

$$\pi(\mathcal{D}|\theta) = \prod_{n=1}^N \pi(\mathcal{D}_n|\theta) \longrightarrow \log \pi(\mathcal{D}|\theta) = \sum_{n=1}^N \log \pi(\mathcal{D}_n|\theta)$$

Stan programs are organized into *blocks*

Stan programs are organized into *blocks*

```
block name {  
    contents ...  
}
```

data block

data block

- Declare data types, sizes, and constraints

data block

- Declare data types, sizes, and constraints
- Read from data source and constraints validated

data block

- Declare data types, sizes, and constraints
- Read from data source and constraints validated
- Evaluated:
 - once

```
data {
```

```
// Dimensions
```

```
// Variables
```

```
}
```

data {

// Dimensions

int<lower=1> N;

// Variables

}

data {

// Dimensions

int<lower=1> N;

int<lower=1> K;

// Variables

}

data {

// Dimensions

int<lower=1> N;

int<lower=1> K;

// Variables

matrix[N, K] X;

}

data {

// Dimensions

int<lower=1> N;

int<lower=1> K;

// Variables

matrix[N, K] X;

vector[N] y;

}

data {

// Dimensions

int<lower=1> N;

int<lower=1> K;

// Variables

matrix[N, K] X;

vector[N] y;

}

// single line comment

data {

// Dimensions

int<lower=1> N;

int<lower=1> K;

// Variables

matrix[N, K] X;

vector[N] y;

}

// single line comment

/* multiple lines of
comments */

parameters block

parameters block

- Declare parameter types, sizes, and constraints

parameters block

- Declare parameter types, sizes, and constraints
- Transformations (under the hood) for constrained parameters

parameters block

- Declare parameter types, sizes, and constraints
- Transformations (under the hood) for constrained parameters
- Evaluated:
 - every log prob evaluation

parameters {

}

parameters {

real alpha;

}

parameters {

real alpha;

vector[K] beta;

}

```
parameters {  
    real alpha;  
    vector[K] beta;  
    real<lower=0> sigma;  
}
```

constraints *required* in
parameters block

model block

model block

- Statements defining the posterior density
 - log scale

model block

- Statements defining the posterior density
 - log scale
- Evaluated:
 - every log prob evaluation


```
model {
```

```
}
```

```
model {
```

```
  sigma ~ exponential(1);
```

```
}
```

```
model {
```

```
  sigma ~ exponential(1);
```

```
  alpha ~ normal(0, 10);
```

```
}
```

```
model {
```

```
  sigma ~ exponential(1);
```

```
  alpha ~ normal(0, 10);
```

```
  for (k in 1:K) beta[k] ~ normal(0, 5);
```

```
}
```

model {

// priors (flat, uniform, if omitted)

sigma ~ **exponential**(1);

alpha ~ **normal**(0, 10);

for (k in 1:K) beta[k] ~ **normal**(0, 5);

}

```
model {  
  // priors (flat, uniform, if omitted)  
  sigma ~ exponential(1);  
  alpha ~ normal(0, 10);  
  for (k in 1:K) beta[k] ~ normal(0, 5);  
  
}
```

Why is the default automatically uniform?

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model {  
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  sigma ~ exponential(1);  
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```

Why is the default automatically uniform?

- $p(\theta) \propto 1$ (0 on log scale)

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}
```

Why is the default automatically uniform?

- $p(\theta) \propto 1$ (0 on log scale)
- Nothing added to log prob


```
model {  
  // priors (flat, uniform, if omitted)  
  sigma ~ exponential(1);  
  alpha ~ normal(0, 10);  
  for (k in 1:K) beta[k] ~ normal(0, 5);  
  
  for (n in 1:N) {  
    y[n] ~ normal(X[n, ] * beta + alpha, sigma);  
  }  
}
```

Why is the default automatically uniform?

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- Nothing added to log prob

generated quantities block

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- Declare and define derived variables
 - (P)RNGs, predictions, event probabilities, decision making

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 - (P)RNGs, predictions, event probabilities, decision making
- Constraints validated

generated quantities block

- Declare and define derived variables
 - (P)RNGs, predictions, event probabilities, decision making
- Constraints validated
- Evaluated:
 - once per draw

generated quantities {

}

generated quantities {

vector[N] y_rep;

}

generated quantities {

vector[N] y_rep;

for (n in 1:N) {

}

}

generated quantities {

vector[N] y_rep;

for (n in 1:N) {

real y_hat = X[n,] * beta + alpha; // local/temp

}

}

generated quantities {

vector[N] y_rep;

for (n in 1:N) {

real y_hat = X[n,] * beta + alpha; // local/temp

y_rep[n] =

}

}

generated quantities {

vector[N] y_rep;

for (n in 1:N) {

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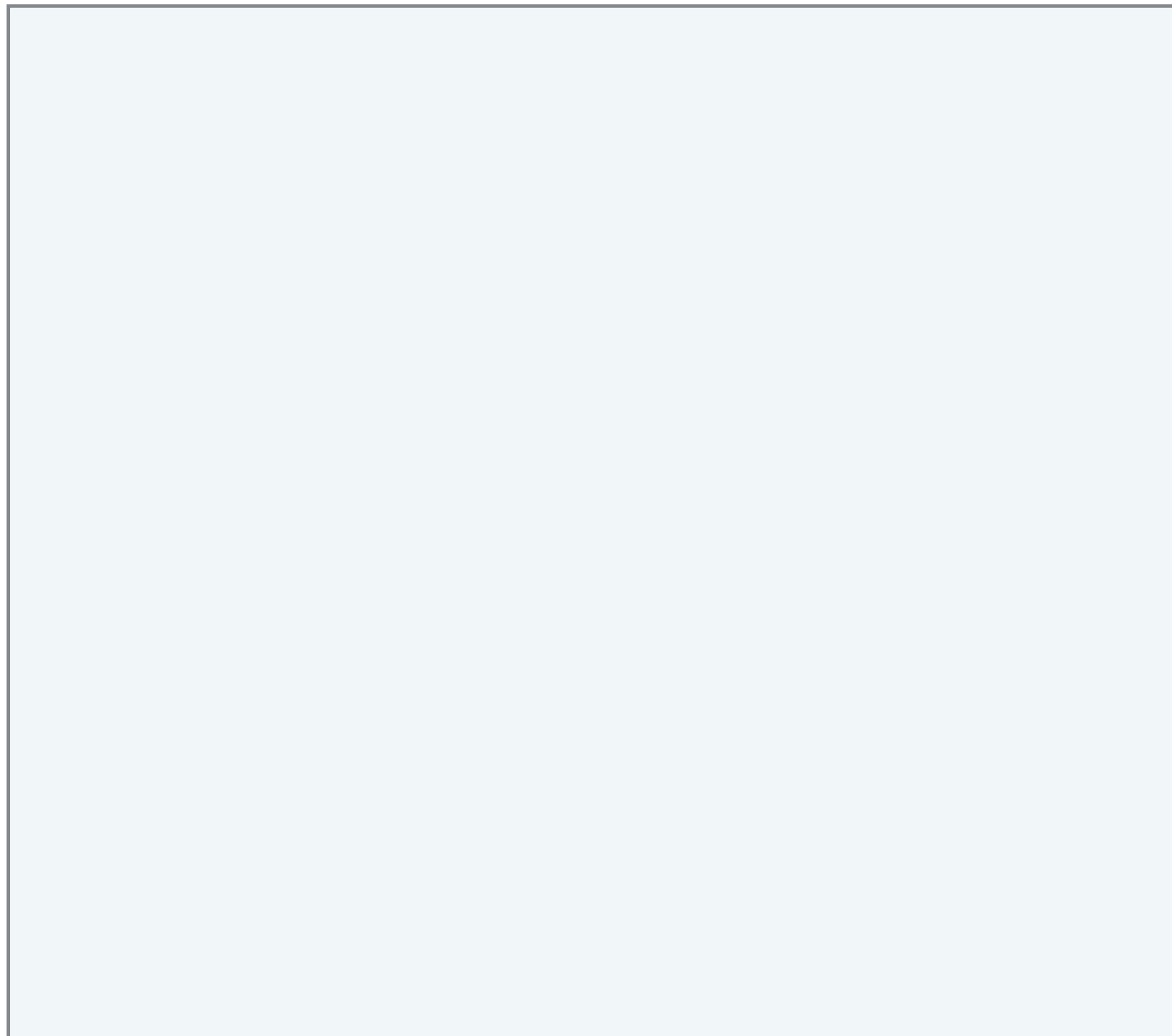
y_rep[n] = **normal_rng**(y_hat, sigma;)

}

}

The complete Stan program

The complete Stan program



Observed
variables

Unobserved
variables

$$\log \pi(\theta) \\ + \\ \log \pi(\mathcal{D}|\theta)$$

Simulate from
generative model

The complete Stan program

```
data {  
  int<lower=1> N;  
  int<lower=1> K;  
  matrix[N, K] X;  
  vector[N] y;  
}
```

Observed
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}  
model {  
  sigma ~ exponential(1);  
  alpha ~ normal(0, 10);  
  for (k in 1:K) beta[k] ~ normal(0, 5);  
  
  for (n in 1:N)  
    y[n] ~ normal(alpha + X[n, ] * beta, sigma);  
}
```

Observed
variables

Unobserved
variables

$\log \pi(\theta)$
+
 $\log \pi(\mathcal{D}|\theta)$

Simulate from
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parameters {  
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  vector[K] beta;  
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  for (n in 1:N)  
    y[n] ~ normal(alpha + X[n, ] * beta, sigma);  
}  
generated quantities {  
  vector[N] y_rep;  
  for (n in 1:N)  
    y_rep[n] = normal_rng(alpha + X[n, ] * beta, sigma);  
}
```

Observed
variables

Unobserved
variables

$\log \pi(\theta)$
+
 $\log \pi(\mathcal{D}|\theta)$

Simulate from
generative model

Best Practices



- 1a. Maintain reproducibility by saving the model, data, and inits in files and the R commands in scripts.

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3. Fit your model to simulated data to ensure that Stan can recover the true values.

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2. Start simple! Build your model in stages, ensuring good fits at each stage.
3. Fit your model to simulated data to ensure that Stan can recover the true values.
4. Keep an eye on the diagnostics!

http://mc-stan.org/workshops/learn_bayes/



Exercise: same model using
target +=



Under the hood, sampling statements just add to the total log probability

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$z \sim \text{normal}(0, 1);$

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z ~ normal(0, 1);
```



```
target += normal_lpdf(z | 0, 1);
```

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```
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```



Evaluate log-pdf of normal (with mean 0, sd 1) at the value z

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z ~ normal(0, 1);
```



```
target += normal_lpdf(z | 0, 1);
```



Evaluate log-pdf of normal (with mean 0, sd 1) at the value z

```
log( 1/sqrt(2 * pi) * exp(-z^2 / 2) )
```

Under the hood, sampling statements just add to the total log probability

```
z ~ normal(0, 1);
```



```
target += normal_lpdf(z | 0, 1);
```



Evaluate log-pdf of normal (with mean 0, sd 1) at the value z

$$\log\left(\frac{1}{\sqrt{2 * \pi}} * \exp(-z^2 / 2)\right)$$

Then add this value to the total log-probability