

Chap 5.2

```
1 md"# Chap 5.2"
```

```
1 versioninfo()
```

```
Julia Version 1.11.0
Commit 501a4f25c2b (2024-10-07 11:40 UTC)
Build Info:
  Official https://julialang.org/ release
Platform Info:
  OS: Linux (x86_64-linux-gnu)
  CPU: 32 × Intel(R) Xeon(R) CPU E5-2630 v3 @ 2.40GHz
  WORD_SIZE: 64
  LLVM: libLLVM-16.0.6 (ORCJIT, haswell)
Threads: 16 default, 0 interactive, 8 GC (on 32 virtual cores)
Environment:
  JULIA_PKG_SERVER = https://mirrors.tuna.tsinghua.edu.cn/julia
  JULIA_REVISE_WORKER_ONLY = 1
```

```
1 html""
2 <style>
3     main {
4         margin: 0 auto;
5         max-width: max(1800px, 75%);
6         padding-left: max(5px, 1%);
7         padding-right: max(350px, 10%);
8     }
9 </style>
10 ""
```

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```
1 begin
2     using Pkg, DrWatson
3     using PlutoUI
4     TableOfContents()
5 end
```

```
1 begin
2   using Distributions
3   using Optim
4   using StatsPlots
5   using StatsBase
6   using LaTeXStrings
7   using CSV
8   using DataFrames
9   using LinearAlgebra
10  using Logging
11  using Random
12  using Turing
13  using Dagitty
14  using StatisticalRethinking
15  using StatisticalRethinkingPlots
16 end
```

Error message from Main

```
LoadError: UndefVarError: `ModeResult` not defined in
`StatisticalRethinking`

Suggestion: check for spelling errors or missing imports.

in expression starting at
/y/home/huangyu/.julia/packages/StatisticalRethinking/RYYWV/src/require
/turing/turing_optim_sample.jl:5

in expression starting at
/y/home/huangyu/.julia/packages/StatisticalRethinking/RYYWV/src/require
/turing/turing.jl:7
```

Stack trace

Here is what happened, the most recent locations are first:

- 1. from | *turing_optim_sample.jl:5*
- 2. `include(mod::Module, _path::String)`
from | `julia` → *Base.jl:557* | [docs](#)
- 3. `include(x::String)`
from | `StatisticalRethinking` → *StatisticalRethinking.jl:1* | [docs](#)
- 4. from | *turing.jl:7*
- 5. `include(mod::Module, _path::String)`
from | `julia` → *Base.jl:557* | [docs](#)
- 6. `include(x::String)`
from | `StatisticalRethinking` → *StatisticalRethinking.jl:1* | [docs](#)
- 7. from | *Requires.jl:40*
- 8. `eval`
from | *boot.jl:430*

Set defaults for plotting and logging.

```
1 begin
2   Plots.default(label=false)
3   #Logging.disable_logging(Logging.Warn);
4 end
```

5.2 Masked relationship.

```
1 md"## 5.2 Masked relationship."
```

Code 5.28

```
1 md"### Code 5.28"
```

	variable	mean	min	median	max	nmissi
1	:clade	nothing	"Ape"	nothing	"Strepsirrhine"	0
2	:species	nothing	"A palliata"	nothing	"Symphalangus syndactylus"	0
3	:kcal_per_g	0.641724	0.46	0.6	0.97	0
4	:perc_fat	33.9903	3.93	36.84	55.51	0
5	:perc_protein	16.4034	7.37	15.8	25.3	0
6	:perc_lactose	49.6062	27.09	48.64	71.91	0
7	:mass	14.7269	0.12	3.47	97.72	0
8	:neocortex_perc	67.5759	55.16	68.85	76.3	12

```
1 begin
2   d = CSV.read(sr_datadir("milk.csv"), missingstring="NA", DataFrame)
3
4   # get rid of dots in column names
5
6   rename!(n -> replace(n, "." => "_"), d)
7
8   describe(d)
9
10 end
```

Code 5.29

```
1 begin
2   d[:,K] = standardize(ZScoreTransform, d.kcal_per_g)
3   d[:,M] = standardize(ZScoreTransform, log.(d.mass))
4
5   # column contains missing values, need to propagate them on standartization
6
7   d[:,N] = d.neocortex_perc
8   non_miss = findall(!ismissing, d.N);
9   d[non_miss,:N] = standardize(ZScoreTransform, disallowmissing(d.N[non_miss]));
10 end;
```

Code 5.30

model_m5_5_draft (generic function with 2 methods)

```
1 @model function model_m5_5_draft(N, K)
2   a ~ Normal(0, 1)
3   bN ~ Normal(0, 1)
4   σ ~ Exponential(1)
5   μ = @. a + bN * N
6   K ~ MvNormal(μ, σ)
7 end
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```

Sampling 100%

```
MethodError: no method matching Distributions.MvNormal{::Vector{Union{Missi
ng, Float64}}, ::Float64}
The type `Distributions.MvNormal` exists, but no method is defined for this co
mbination of argument types when trying to construct it.

Closest candidates are:
  Distributions.MvNormal{!Matched{::Int64, ::Real}
    @ Distributions deprecated.jl:103
  Distributions.MvNormal{!Matched{::Tracker.TrackedVector{<:Real}, ::Real}
    @ DistributionsADTrackerExt ~/.julia/packages/DistributionsAD/tWlyT/ext/Dis
tributionsADTrackerExt.jl:472
  Distributions.MvNormal{!Matched{::AbstractVector{<:Real}, ::Real}
    @ Distributions deprecated.jl:103
  ...
```

Code 5.31

```
SentinelArrays.SentinelVector{Float64, Float64, Missing, Vector{Float64}}: [-2.0802, missing]
1 d.neocortex_perc
```

Code 5.32

```
1 dcc = d[completecases(d[:, :K, :N, :M]), :];
```

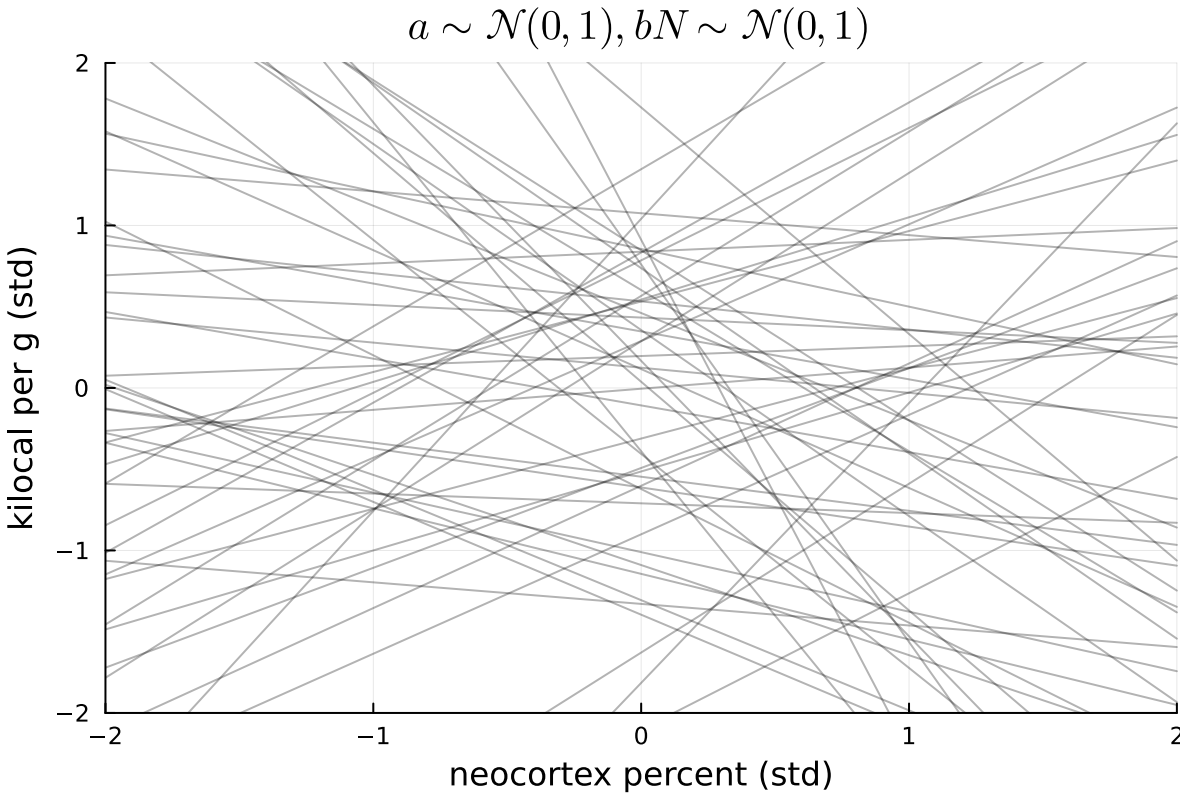
Code 5.33

```
1 m5_5_draft = sample(model_m5_5_draft(dcc.N, dcc.K), NUTS(), 1000);

Sampling 100%

Found initial step size
ϵ: 0.05
```

Code 5.34



```
1 let
2   prior = sample(model_m5_5_draft(dcc.N, dcc.K), Prior(), 1000)
3   prior_df = DataFrame(prior)
4   xseq = [-2, 2]
5   μ = StatisticalRethinking.link(prior_df, [:a, :bN], xseq)
6   μ = hcat(μ...);
7
8   p = plot(; xlim=xseq, ylim=xseq,
9             xlabel="neocortex percent (std)", ylabel="kilocal per g (std)",
10            title=L"a \sim \mathcal{N}(0,1), bN \sim \mathcal{N}(0,1)"
11          )
12   for y ∈ first(eachrow(μ), 50)
13     plot!(p, xseq, y; c=:black, alpha=0.3)
14   end
15   p
16 end
```

Sampling 100%

Code 5.35

```
model_m5_5 (generic function with 2 methods)

1 @model function model_m5_5(N, K)
2   a ~ Normal(0, 0.2)
3   bN ~ Normal(0, 0.5)
4   σ ~ Exponential(1)
5   μ = @. a + bN * N
6   K ~ MvNormal(μ, σ)
7 end
```

	variable	mean	min	median	max	nmissing	eltype
1	:a	0.0294851	-0.427188	0.0320271	0.54324	0	Float64
2	:bN	0.117184	-0.938296	0.116591	0.998277	0	Float64
3	:σ	1.11373	0.683783	1.09157	2.31612	0	Float64

```
1 begin
2     m5_5 = sample(model_m5_5(dcc.N, dcc.K), NUTS(), 1000)
3     m5_5_df = DataFrame(m5_5)
4     describe(m5_5_df)
5 end
```

Sampling

Found initial step size
ε: 0.8

```
1 let
2     prior = sample(model_m5_5(dcc.N, dcc.K), Prior(), 1000)
3     prior_df = DataFrame(prior)
4     xseq = [-2, 2]
5
6
7     μ = StatisticalRethinking.link(prior_df, [:a, :bN], xseq)
8     μ = hcat(μ...);
9
10    p2 = plot(; xlim=xseq, ylim=xseq,
11              xlab="neocortex percent (std)", ylab="kilocal per g (std)",
12              title=L"a \sim \mathcal{N}(0,0.2), bN \sim \mathcal{N}(0,0.5)"
13            )
14    for y ∈ first(eachrow(μ), 50)
15        plot!(p2, xseq, y; c=:black, alpha=0.3)
16    end
17 end
```

Sampling

Code 5.36

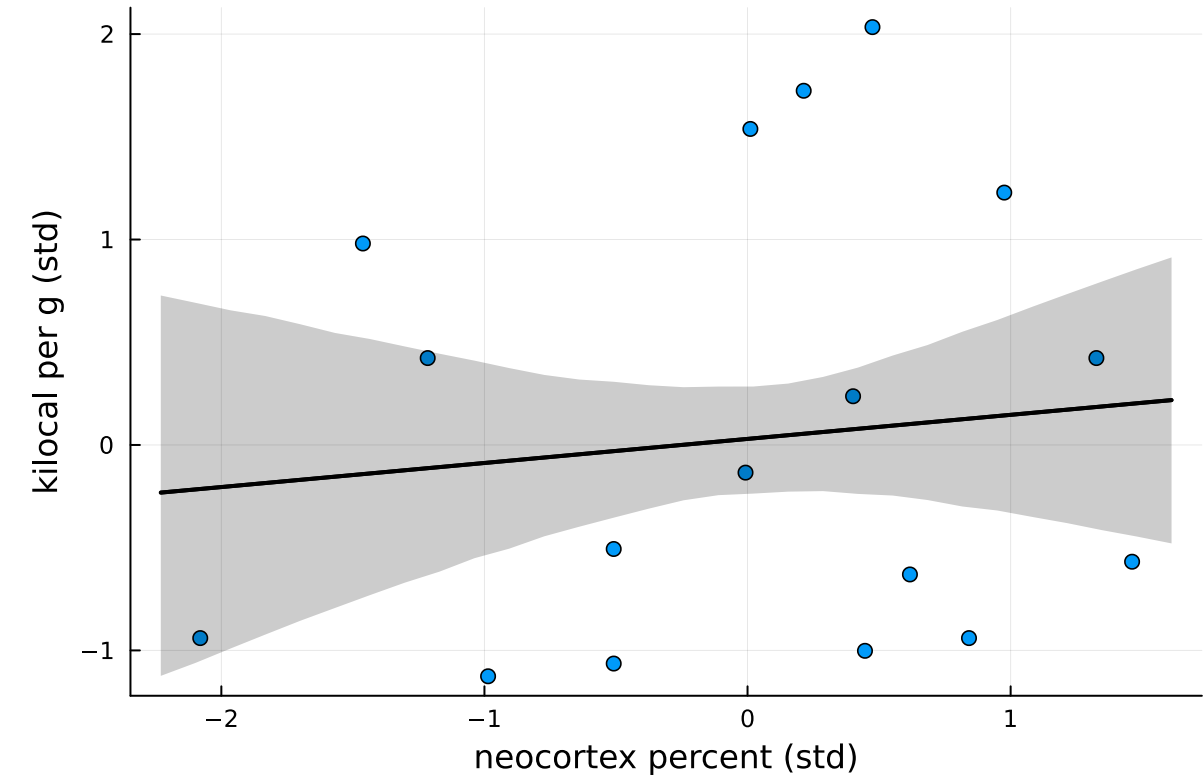
```
1 md"### Code 5.36"
```

	variable	mean	min	median	max	nmissing	eltype
1	:a	0.0294851	-0.427188	0.0320271	0.54324	0	Float64
2	:bN	0.117184	-0.938296	0.116591	0.998277	0	Float64
3	:σ	1.11373	0.683783	1.09157	2.31612	0	Float64

```
1 describe(m5_5_df)
```

Code 5.37

```
1 md"### Code 5.37"
```



```
1 let
2   xseq = range(minimum(dcc.N) - 0.15, maximum(dcc.N) + 0.15; length=30)
3   μ = StatisticalRethinking.link(m5_5_df, [:a, :bN], xseq);
4   μ = hcat(μ...)
5   μ_mean = mean.(eachcol(μ))
6   μ_PI = PI.(eachcol(μ))
7   μ_PI = vcat(μ_PI'...)
8
9   @df dcc scatter(:N, :K; xlab="neocortex percent (std)",
10    ylab="kilocal per g (std)")
11   plot!(xseq, [μ_mean, μ_mean]; lw=2, fillrange=μ_PI, fillalpha=0.2, color=:black)
12 end
```

Code 5.38

model_m5_6 (generic function with 2 methods)

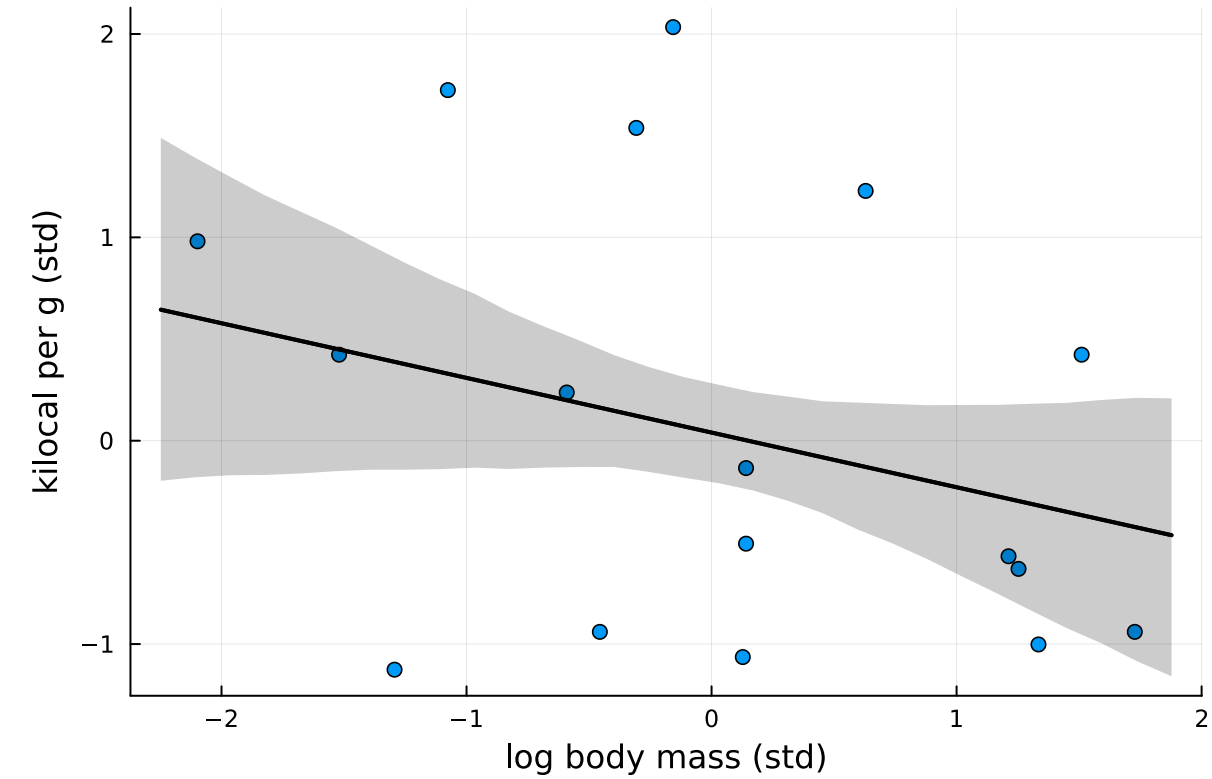
```
1 @model function model_m5_6(M, K)
2   a ~ Normal(0, 0.2)
3   bM ~ Normal(0, 0.5)
4   σ ~ Exponential(1)
5   μ = @. a + bM * M
6   K ~ MvNormal(μ, σ)
7 end
```

	variable	mean	min	median	max	nmissing	eltype
1	:a	0.0400568	-0.452114	0.0395988	0.61117	0	Float64
2	:bM	-0.268843	-1.05115	-0.264128	0.5195	0	Float64
3	:σ	1.07009	0.617333	1.03909	2.45566	0	Float64

```
1 begin
2   m5_6 = sample(model_m5_6(dcc.M, dcc.K), NUTS(), 1000)
3   m5_6_df = DataFrame(m5_6)
4   describe(m5_6_df)
5 end
```

Sampling

Found initial step size
ε: 0.2



```
1 let
2   xseq = range(minimum(dcc.M) - 0.15, maximum(dcc.M) + 0.15; length=30)
3   μ = StatisticalRethinking.link(m5_6_df, [:a, :bM], xseq);
4   μ = hcat(μ...)
5   μ_mean = mean.(eachcol(μ))
6   μ_PI = PI.(eachcol(μ))
7   μ_PI = vcat(μ_PI'...)
8
9   @df dcc scatter(:M, :K; xlab="log body mass (std)", ylab="kilocal per g (std)")
10  plot!(xseq, [μ_mean, μ_mean]; lw=2, fillrange=μ_PI, fillalpha=0.2, color=:black)
11 end
```

model_m5_7 (generic function with 2 methods)

```
1 @model function model_m5_7(N, M, K)
2   a ~ Normal(0, 0.2)
3   bN ~ Normal(0, 0.5)
4   bM ~ Normal(0, 0.5)
5   σ ~ Exponential(1)
6   μ = @. a + bN * N + bM * M
7   K ~ MvNormal(μ, σ)
8 end
```

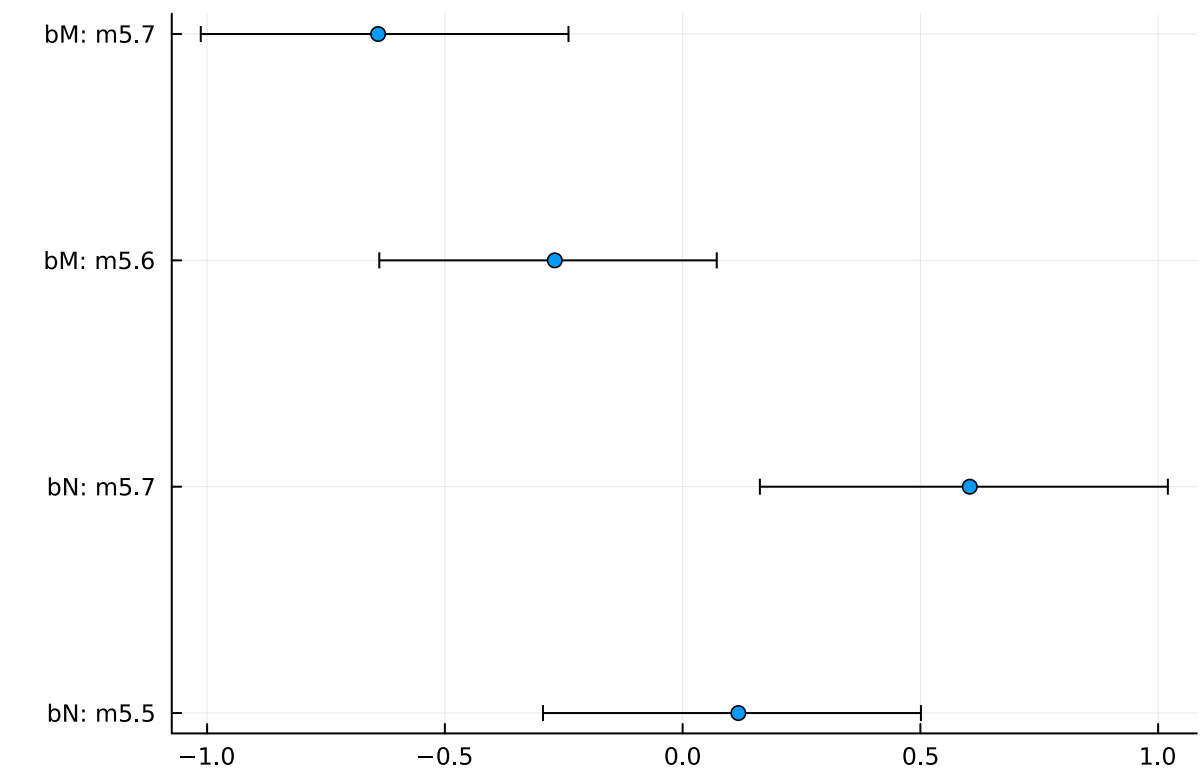
	variable	mean	min	median	max	nmissing	eltype
1	:a	0.0616477	-0.343501	0.0658871	0.501113	0	Float64
2	:bM	-0.640344	-1.27066	-0.637607	0.174693	0	Float64
3	:bN	0.603824	-0.332555	0.603862	1.49049	0	Float64
4	:σ	0.864988	0.521428	0.844152	1.87738	0	Float64

```
1 begin
2   m5_7 = sample(model_m5_7(dcc.N, dcc.M, dcc.K), NUTS(), 1000)
3   m5_7_df = DataFrame(m5_7)
4   describe(m5_7_df)
5 end
```

Sampling

Found initial step size
ε: 0.4

Code 5.40



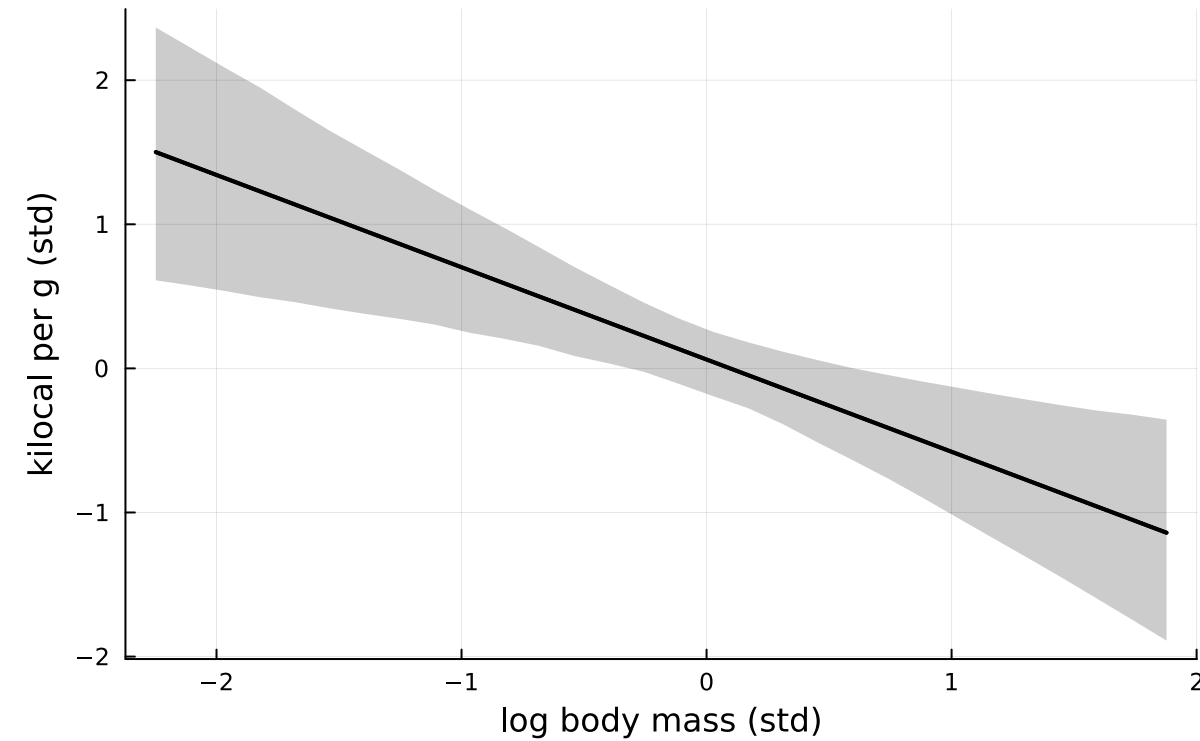
```
1 coefplot(m5_7_df, m5_6_df, m5_5_df; pars=(:bM, :bN),
2         names=("m5.7", "m5.6", "m5.5"))
```

Code 5.41

The code in the book corresponds to the bottom-right figure, which keeps N=0 (despite stated in the text).

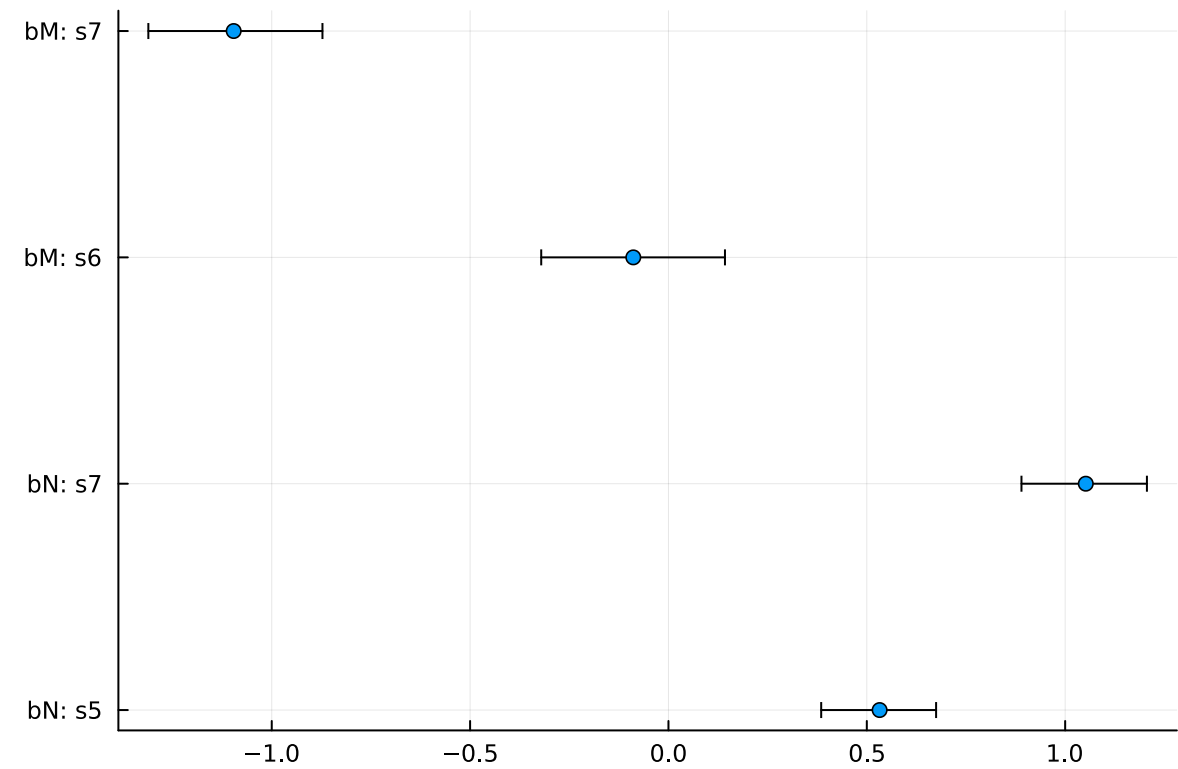
Below is the code to produce the bottom-left figure (M=0).

Counterfactual holding N=0



```
1 let
2   xseq = range(minimum(dcc.N) - 0.15, maximum(dcc.N) + 0.15; length=30)
3   μ = StatisticalRethinking.link(m5_7_df, [:a, :bN], xseq);
4   μ = hcat(μ...)
5   μ_mean = mean.(eachcol(μ))
6   μ_PI = PI.(eachcol(μ))
7   μ_PI = vcat(μ_PI'...)
8
9   plot(title="Counterfactual holding M=0",
10        xlab="neocortex percent (std)", ylab="kilocal per g (std)")
11   plot!(xseq, [μ_mean, μ_mean]; lw=2, fillrange=μ_PI, fillalpha=0.2, color=:black)
12
13   # +
14   xseq = range(minimum(dcc.M) - 0.15, maximum(dcc.M) + 0.15; length=30)
15   μ = StatisticalRethinking.link(m5_7_df, [:a, :bM], xseq);
16   μ = hcat(μ...)
17   μ_mean = mean.(eachcol(μ))
18   μ_PI = PI.(eachcol(μ))
19   μ_PI = vcat(μ_PI'...)
20
21   plot(title="Counterfactual holding N=0",
22        xlab="log body mass (std)", ylab="kilocal per g (std)")
23   plot!(xseq, [μ_mean, μ_mean]; lw=2, fillrange=μ_PI, fillalpha=0.2, color=:black)
24 end
```


Code 5.42



```
1 let
2   # M → K ← N
3   # M → N
4
5   n = 100
6   M = rand(Normal(), n)
7   N = [rand(Normal(μ)) for μ ∈ M]
8   K = [rand(Normal(μ)) for μ ∈ N .- M]
9   d_sim = DataFrame(:K => K, :N => N, :M => M);
10
11  s5 = sample(model_m5_5(d_sim.N, d_sim.K), NUTS(), 1000)
12  s6 = sample(model_m5_6(d_sim.M, d_sim.K), NUTS(), 1000)
13  s7 = sample(model_m5_7(d_sim.N, d_sim.M, d_sim.K), NUTS(), 1000)
14  s5_df = DataFrame(s5)
15  s6_df = DataFrame(s6)
16  s7_df = DataFrame(s7)
17  coeftab_plot(s7_df, s6_df, s5_df; pars=(:bM, :bN), names=("s7", "s6", "s5"))
18 end
```

Sampling

Found initial step size
ε: 0.0125

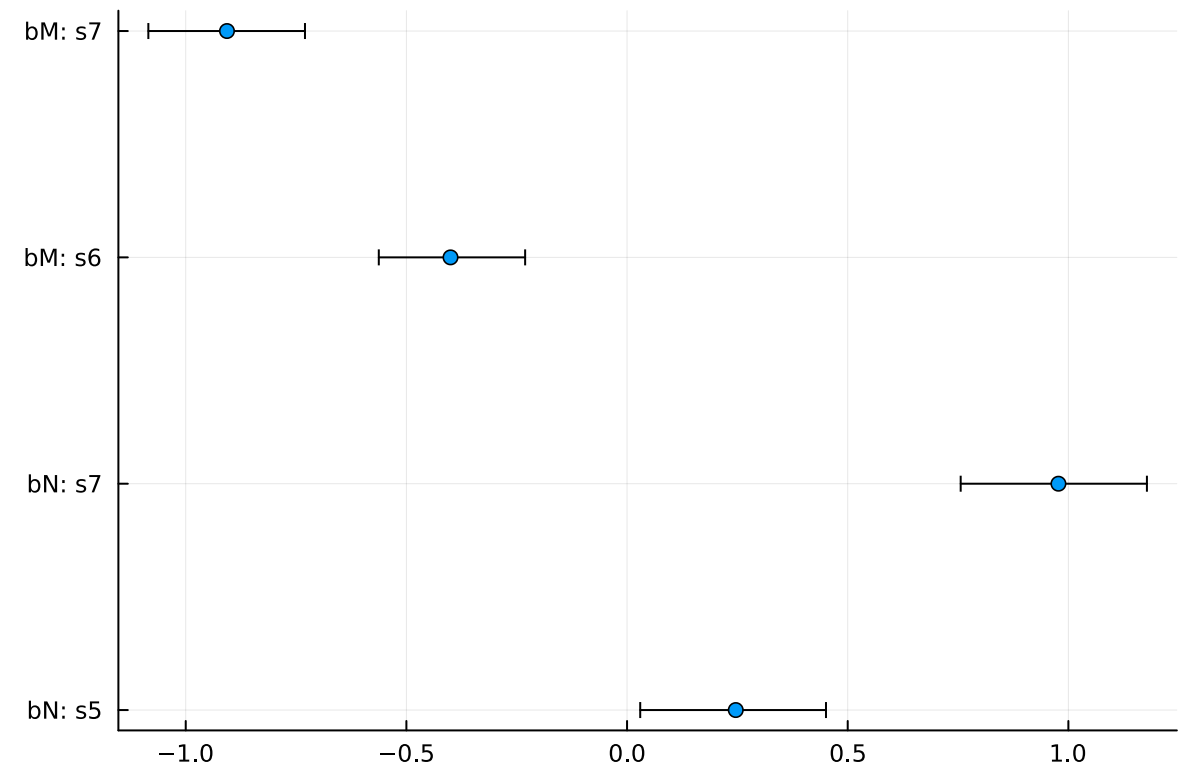
Sampling

Found initial step size
ε: 0.4

Sampling

Found initial step size
ε: 0.05

Code 5.43



```
1 let
2   # M → K ← N
3   # N → M
4   n = 100
5   N = rand(Normal(), n)
6   M = [rand(Normal(μ)) for μ ∈ N]
7   K = [rand(Normal(μ)) for μ ∈ N .- M]
8   d_sim2 = DataFrame(:K => K, :N => N, :M => M);
9
10  # M → K ← N
11  # M ← U → N
12  n = 100
13  U = rand(Normal(), n)
14  N = [rand(Normal(μ)) for μ ∈ U]
15  M = [rand(Normal(μ)) for μ ∈ U]
16  K = [rand(Normal(μ)) for μ ∈ N .- M]
17  global d_sim3 = DataFrame(:K => K, :N => N, :M => M);
18  # -
19
20  s5 = sample(model_m5_5(d_sim2.N, d_sim2.K), NUTS(), 1000)
21  s6 = sample(model_m5_6(d_sim2.M, d_sim2.K), NUTS(), 1000)
22  s7 = sample(model_m5_7(d_sim2.N, d_sim2.M, d_sim2.K), NUTS(), 1000)
23  s5_df = DataFrame(s5)
24  s6_df = DataFrame(s6)
25  s7_df = DataFrame(s7)
26  coeftab_plot(s7_df, s6_df, s5_df; pars=(:bM, :bN), names=("s7", "s6", "s5"))
27 end
```

Sampling

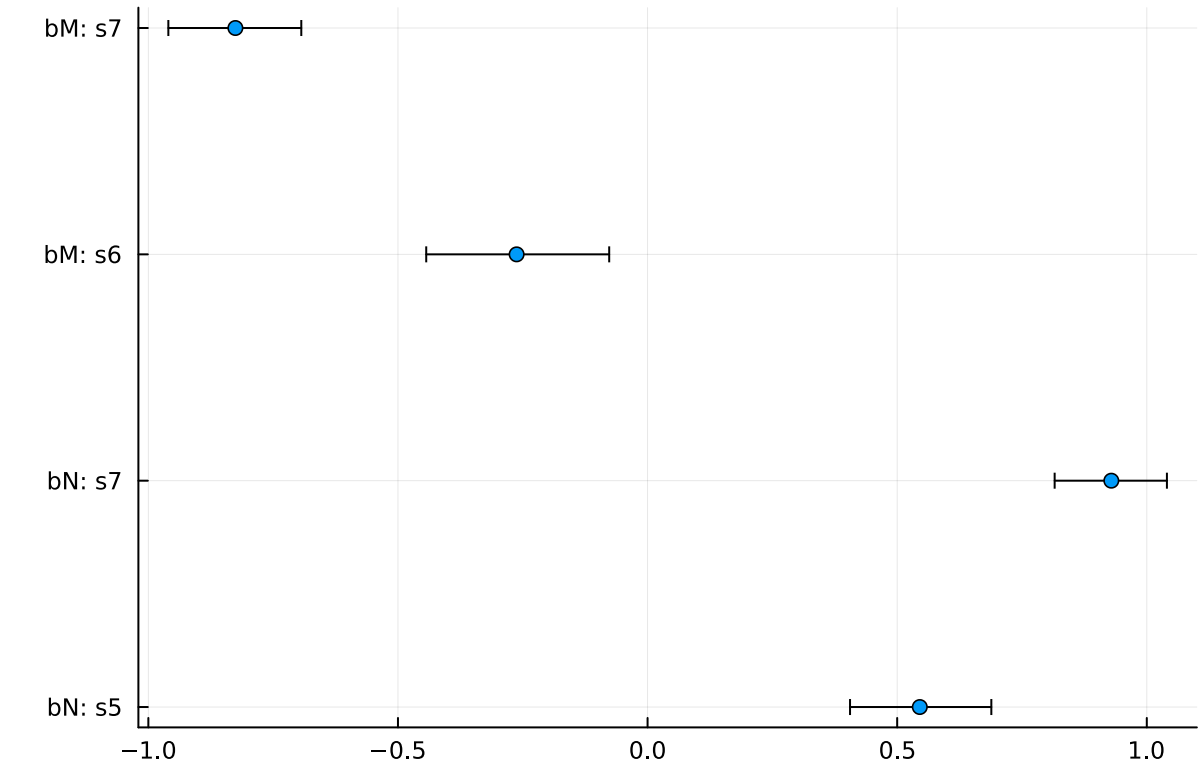
Found initial step size
ε: 0.2015625

Sampling

Found initial step size
ε: 0.2

Sampling

Found initial step size
ε: 0.05



```
1 let
2 s5 = sample(model_m5_5(d_sim3.N, d_sim3.K), NUTS(), 1000)
3 s6 = sample(model_m5_6(d_sim3.M, d_sim3.K), NUTS(), 1000)
4 s7 = sample(model_m5_7(d_sim3.N, d_sim3.M, d_sim3.K), NUTS(), 1000)
5 s5_df = DataFrame(s5)
6 s6_df = DataFrame(s6)
7 s7_df = DataFrame(s7)
8 coeftab_plot(s7_df, s6_df, s5_df; pars=(:bM, :bN), names=("s7", "s6", "s5"))
9 end
```

Sampling

Found initial step size
ϵ: 0.2

Sampling

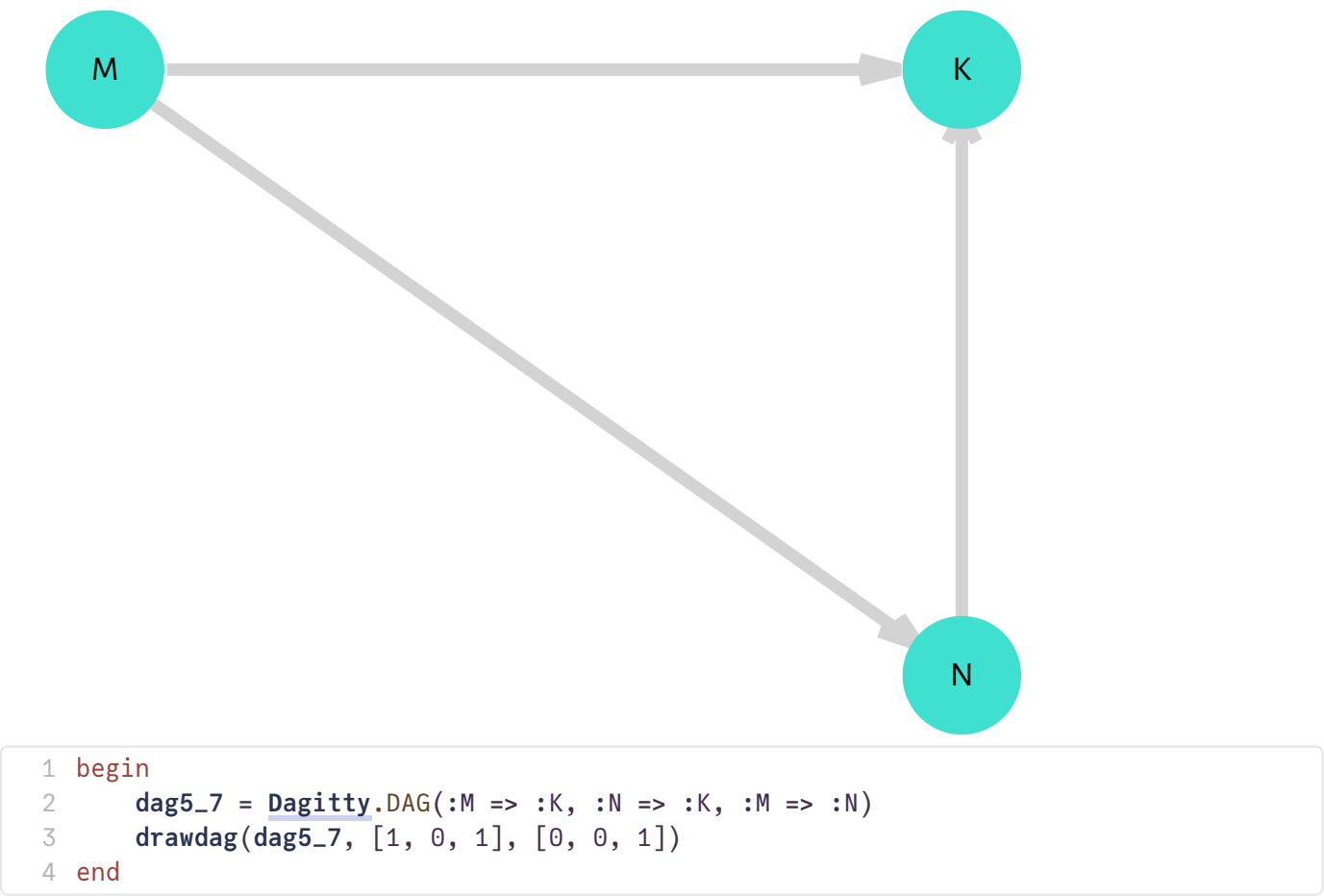
Found initial step size
ϵ: 0.025

Sampling

Found initial step size
ϵ: 0.4

Code 5.44

```
1 md"### Code 5.44"
```



```
1 begin
2 dag5_7 = Dagitty.DAG(:M => :K, :N => :K, :M => :N)
3 drawdag(dag5_7, [1, 0, 1], [0, 0, 1])
4 end
```

EquivalentDAGs is TODO in Dagitty.jl.

