Laplace approximation to fit random effects models in Julia

Sean L. Wu

2025-06-19

Table of contents

In this notebook we'll see how to use DifferentiationInterface.jl with Julia's other facilities for optimization to estimate a statistical model of realistic complexity. The example chosen from Simon Wood's book Core Statistics, available for free on his website (click the link and scroll down), described on pp 99-111. The original implementation was in R, the Julia implementation in some cases is similar but differs in other cases, most obviously by using automatic differentiation to replace the mixture of symbolic differentiation (via the somewhat awkward `expr` interface) and finite differencing from the R code. This method of maximum likelihood estimation (MLE) via a Laplace approximation is generic across a wide variety of models, and hopefully should be easy to follow for R users who wish to adopt Julia.

Urchin model

The model is one of sea urchin growth. There is a mechanistic model to relate volume V to age a by the differential equation:

$$\frac{dV}{da} = \begin{cases} g_i V, & V < p_i/g_i \\ p_i & \text{otherwise} \end{cases}$$

This is an "individual-based" model, because the growth parameters p and g are indexed by the individual urchin. In the statistical model sitting "on top" of the mechanistic model, these

are *random effects*. Each urchin has an initial condition for the ODE (initial volume) which is ω, a fixed effect common to all urchins. The differential equation changes when the animal hits reproductive age, which is:

$$a_{mi} = \frac{1}{g_i} \log\left(\frac{p_i}{g_i \omega}\right)$$

The ODE has the analytical solution:

$$V(a) = \begin{cases} \omega \exp(g_i a_i), & a_i < a_{mi} \\ p_i/g_i + p_i(a_i - a_{mi}) & \text{otherwise} \end{cases}$$

The measured urchin volumes are v, and the likelihood model is:

$$\sqrt{v}_i \sim N(\sqrt{V(a_i)}, \sigma^2)$$

And we assume the random effects follow:

$$\log g_i \sim N(\mu_g, \sigma_g^2)$$
$$\log p_i \sim N(\mu_p, \sigma_p^2)$$

The model parameters ("fixed effects") are $\omega, \mu_g, \sigma_g, \mu_p, \sigma_p, \sigma$, and the random effects are g, p.

Laplace Approximation for MLE with Random Effects

When we fit statistical models with fixed and random effects, we need to optimize the marginal density of the data with respect to the fixed effects θ, integrating out the random effects b. Letting the joint density be $f_\theta(y, b)$ of the data y, random effects b, the marginal likelihood is:

$$L(\theta) = f_\theta(y) = \int f_\theta(y, b) db$$

A first order Laplce approximation will approximate the integral with another expression. For details of the derivation, see the book chapter. The important point is that the approximate marginal likelihood is much easier to calculate. Let $\hat{b}_y$ be the value of b maximizing $f_\theta(y, b)$, and n_b be the dimension of b. Let $H = -\nabla_b^2 \log f_\theta(y, \hat{b}_y)$. Then the approximation of the likelihood is:

$$f_\theta(y,b) \approx f_\theta(y,\hat{b}_y)\frac{(2\pi)^{n_b/2}}{|H|^{1/2}}$$

We will work with the negative log likelihood in practice. It is this approximation that we will implement and optimize for approximate maximum likelihood estimation of θ in this notebook.

Loading Data

We are going to load the data from Simon Wood's website.

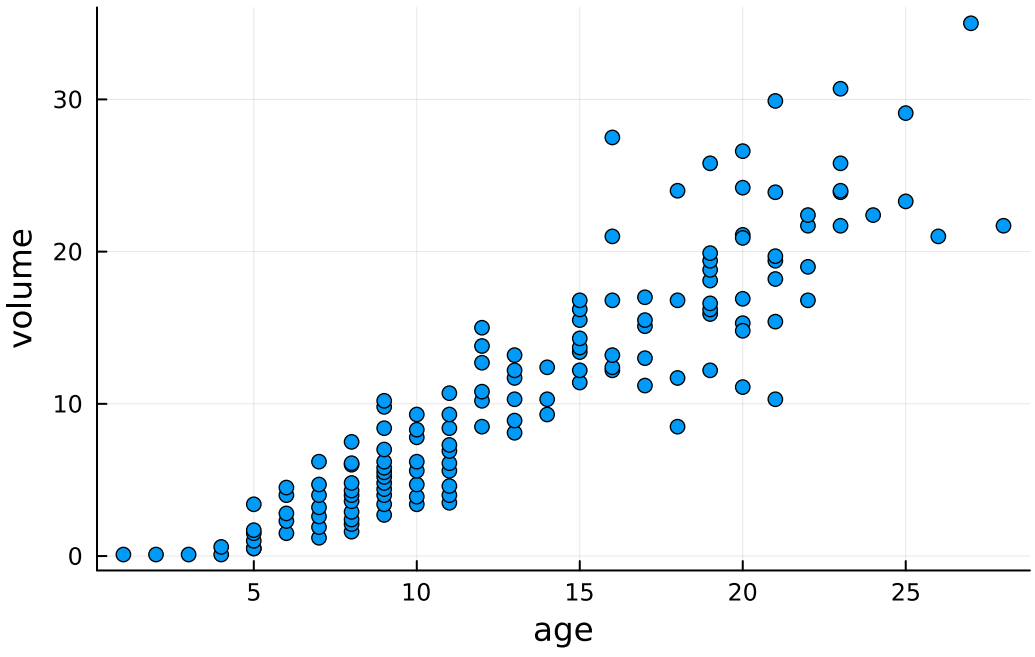
```
using CSV, HTTP, DataFrames

http_response = HTTP.request("GET", "https://www.maths.ed.ac.uk/~swood34/data/urchin-vol.txt
urchins = CSV.read(IOBuffer(http_response.body), DataFrame, header=["row", "age", "vol"], ski
select!(urchins, Not(:row))
```

We can take a look at it:

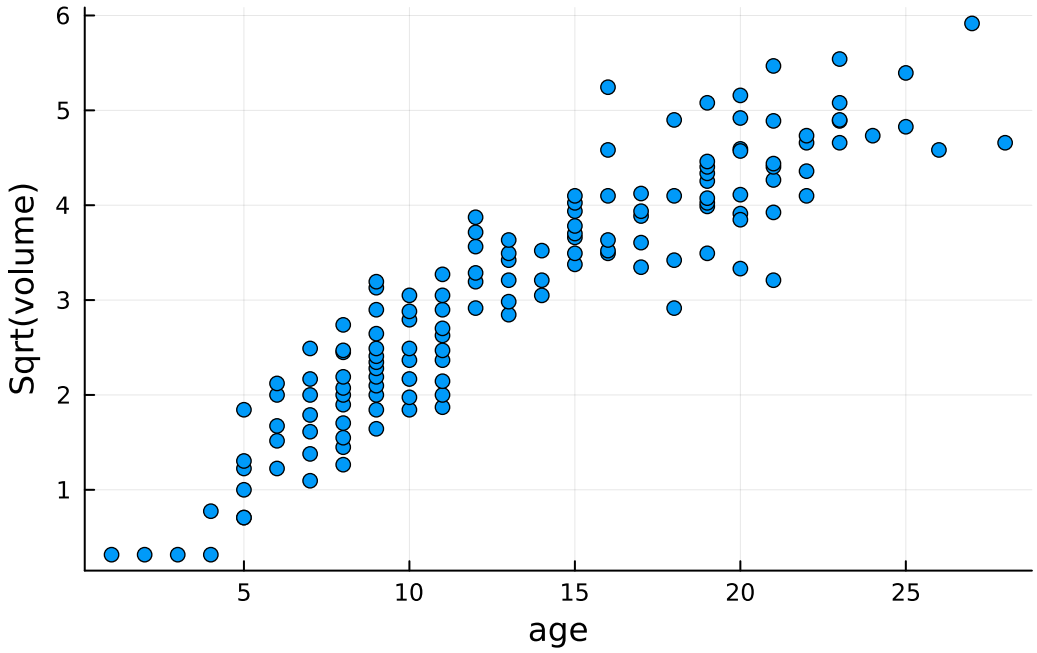
```
using Plots

scatter(urchins.age,urchins.vol,label=false,xlabel="age",ylabel="volume")
```



If we square root transform the input data we can see that the likelihood model's assumption of constant variance is probably not too bad, although we'd want to fix it for "real" modeling.

```
scatter(urchins.age,sqrt.(urchins.vol),label=false,xlabel="age",ylabel="Sqrt(volume)")
```



Julia Implementation

We will use DifferentiationInterface.jl to handle the hard work of calculating the gradients and Hessians we will need to compute the Laplace approximation of the likelihood and fit the resulting approximate model for inference. We'll load the packages we need below. For automatic differentiation (AD) we'll use the slow but reliable method of forward automatic differentiation, although DifferentiationInterface.jl makes it nearly trivial to change AD backends.

```
using LinearAlgebra, Distributions
using Optim, LineSearches
using DifferentiationInterface
import ForwardDiff

# for sparse AD
using SparseMatrixColorings
import Symbolics
using SparseArrays
```

```
const ad_sys = AutoForwardDiff()
```

Model and Likelihood

We need to pass the fixed and random effects as single vectors, so it's useful to define helper variables to index into them. It will be helpful to have, so we also define reasonable starting values for θ and b.

```
# index into a single vector for b (random effects)
const log_g_ix = 1:nrow(urchins)
const log_p_ix = range(start=nrow(urchins)+1, length=nrow(urchins))

# index into a single vector for   (fixed effects)
const log_ _ix = 1
const  _g_ix = 2
const log_ _g_ix = 3
const  _p_ix = 4
const log_ _p_ix = 5
const log_ _ix = 6

# initial starting values for θ
th_init = [
    -4.0,
    -0.2,
    log(0.1),
    0.2,
    log(0.1),
    log(0.5)
]

# initial starting values for b
b_init = [
    fill(th_init[ _g_ix], nrow(urchins)); fill(th_init[ _p_ix], nrow(urchins))
]
```

Now let's define the biological model, and the negative log likelihood of y and b, $-\log f_\theta(y, b)$. We will need both the gradient and the Hessian of the negative log likelihood to find $\widehat{b}_y$ for a given value of θ, and the Hessian for the Laplace approximation of the marginal likelihood of θ for optimization, so we also prepare the data objects which will be reused for multiple evaluations of the gradient/Hessian to improve performance.

Note that we take advantage of sparsity in the Hessian by using DifferentiationInterface.jl's support for sparse Hessian computations. In particular, we don't need to input a sparsity pattern, we can just let other packages figure it out!

```
function model_urchin_vol( , g, p, a)
    a  = log(p / (g* ))/g
    return ifelse(a < a ,  *exp(g*a), p/g + p*(a-a ))
end

function nll_urchin(b,  , urchin)
    # extract fixed effects
      = exp( [log_ _ix])
     _g = exp( [log_ _g_ix])
     _p = exp( [log_ _p_ix])
      = exp( [log_ _ix])
    # extract random effects
    log_g = b[log_g_ix]
    log_p = b[log_p_ix]
    # calculate the loglikelihood of y and b
     logll = 0.0
     for i in axes(urchin,1)
          v = model_urchin_vol( , exp(log_g[i]), exp(log_p[i]), urchin[i, :age])
          logll += logpdf(Normal(sqrt(v),  ), sqrt(urchin[i, :vol]))
          logll += logpdf(Normal( [ _g_ix],  _g), log_g[i])
          logll += logpdf(Normal( [ _p_ix],  _p), log_p[i])
     end
     return -logll
end

const prep_g_nll = prepare_gradient(nll_urchin, ad_sys, zero(b_init), Constant(th_init), Cons

const sp_ad_sys = AutoSparse(
    ad_sys;
    sparsity_detector=Symbolics.SymbolicsSparsityDetector(),
    coloring_algorithm=GreedyColoringAlgorithm(),
)
const prep_sp_h_nll = prepare_hessian(nll_urchin, sp_ad_sys, rand(length(b_init)), Constant(t
```

Perturbing the Hessian

In the R code written by Simon Wood, a function `pdR` was provided which perturbs the returned Hessian (in R evaluated via finite differencing) if it is not positive definite such that the returned

matrix is positive definite, which is needed to fulfill assumptions in the approximation. We replicate this in Julia, although due to some complexities with how Cholesky factorizations are computed when the input is a sparse matrix, we write a specific method for sparse input.

```
function cholesky_check(m)
     try
          sparse(cholesky(m))
     catch
         nothing
     end
end

function cholesky_check(m::T) where {T<:SparseMatrixCSC}
     try
          # thanks to https://discourse.julialang.org/t/how-to-get-upper-triangular-cholesky-
          C = cholesky(m)
          perm = C.p
          invperm_vec = invperm(perm)
          L = sparse(C.L)[invperm_vec, invperm_vec]
          L'
     catch
         nothing
     end
end

function pdR(H, k_mult=20, tol=eps()^.8)
     k=1
     tol = tol * opnorm(H, 1)
     n = size(H, 2)
     R = cholesky_check(H + (k-1)*tol*I(n))
     while isnothing(R)
         k *= k_mult
         R = cholesky_check(H + (k-1)*tol*I(n))
     end
     return R
end
```

Marginal Log Likelihood

Now we're ready to write our Laplace approximation of $L(\theta)$. First, we make an object `b_cache` which will store the values of $\hat{b}_y$ from iteration to iteration, which speeds up optimization

slightly by letting the solver start from a good location in parameter space, and also because occasionally the estimates of b are of interest to the modeler.

Note that within the approximation of $L(\theta)$ we first find $\hat{b}_y$ via Newton's method. We then get $-\log f_\theta(y, \hat{b}_y)$. Taking the Hessian at $\hat{b}_y$ allows us to compute the remaining log determinant term needed for the Laplace approximation.

```
const b_cache = deepcopy(b_init)

function marginal_nll( )
     # the `llu` function from Wood's R code
     nb = length(b_cache)

     g_nll!(G, b) = gradient!(nll_urchin, G, prep_g_nll, ad_sys, b, Constant( ), Constant(urc
     H_nll!(H, b) = hessian!(nll_urchin, H, prep_sp_h_nll, sp_ad_sys, b, Constant( ), Constan

     nlfyb_optim = optimize(
          b -> nll_urchin(b,  , urchins),
          g_nll!,
          H_nll!,
          b_cache,
          Newton(;alphaguess=InitialStatic(scaled=true), linesearch=BackTracking())
     )
     b_hat = Optim.minimizer(nlfyb_optim)
     nll_hat = Optim.minimum(nlfyb_optim)

     b_cache .= b_hat # updated cached value for next iteration

     H = hessian(nll_urchin, prep_sp_h_nll, sp_ad_sys, b_hat, Constant( ), Constant(urchins))
     R = pdR(H)

     return nll_hat + logdet(R) - log(2 )*(nb/2)
end
```

Optimization

Now we're ready to optimize $L(\theta)$ with respect to θ to find the MLE estimates of the fixed effect parameters. For the outer optimziation of $L(\theta)$, we will use finite differentiation to get a search gradient, because most AD packages have difficulty differentiating through nested optimization calls. We compute the AIC of the fitted model, which is roughly equivalent to the R implementation, and return the $\hat{\theta}$ vector.

```
const fd_sys = AutoFiniteDiff()
marginal_nll_prep = prepare_gradient(marginal_nll, fd_sys, rand(length(th_init)))
g_marginal_nll!(G,  ) = gradient!(marginal_nll, G, marginal_nll_prep, fd_sys,  )

marginal_mle = optimize(
     marginal_nll,
     g_marginal_nll!,
     th_init,
     LBFGS(;alphaguess=InitialStatic(scaled=true), linesearch=BackTracking())
)

# model AIC
aic = 2*Optim.minimum(marginal_mle) + 2*length(th_init)
```

```
196.7140311382177
```

```
theta_hat = Optim.minimizer(marginal_mle)
```

```
6-element Vector{Float64}:
 -4.067579796476801
 -0.1894617900847541
 -1.812674022342363
  0.16382191570405602
 -1.6234136412201186
 -1.2129519442864463
```

Simulating from Sampling Distribution

To get some notion of what the sampling distribution of reasonable trajectories from the fited distributions of random effects look like, we draw 5,000 samples from g and p and hold the rest of the fixed effects parameters at their MLE estimates, and plot the resulting trajectories. This is not intended as a rigorous statistical investigation into the sampling distribution of these parameters.

```
ages = 1:0.1:28
vols = [
    let
          = exp(theta_hat[log_ _ix])
        g = exp(theta_hat[ _g_ix])
        p = exp(theta_hat[ _p_ix])
```

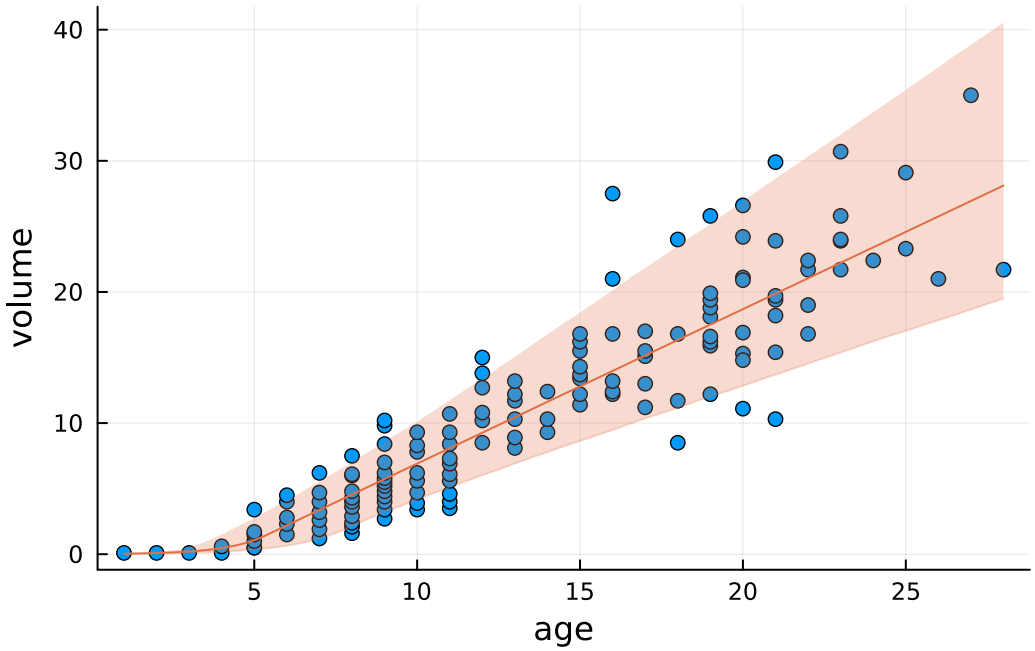
```
        model_urchin_vol( , g, p, a)
    end
    for a in ages
]

samples = 5_000
sampled_urchins = zeros(length(ages), samples)

for i in 1:samples
    log_g_i = rand(Normal(theta_hat[ _g_ix], exp(theta_hat[log_ _g_ix])))
    log_p_i = rand(Normal(theta_hat[ _p_ix], exp(theta_hat[log_ _p_ix])))
      = exp(theta_hat[log_ _ix])
    g = exp(log_g_i)
    p = exp(log_p_i)
    for a in eachindex(ages)
        sampled_urchins[a,i] = model_urchin_vol( , g, p, ages[a])
    end
end

quant_lo = quantile.(eachrow(sampled_urchins), 0.025)
quant_hi = quantile.(eachrow(sampled_urchins), 0.975)

scatter(urchins.age,urchins.vol,xlabel="age",ylabel="volume",legend=false)
plot!(ages,vols,seriescolor=2)
plot!(ages,quant_lo; fillrange = quant_hi,alpha=0.25,seriescolor=2)
```


volume
age
0
10
20
30
40
5
10
15
20
25