

STATS 477/577 – Data Analysis 1

Diasorin Case Study

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15 February 2018

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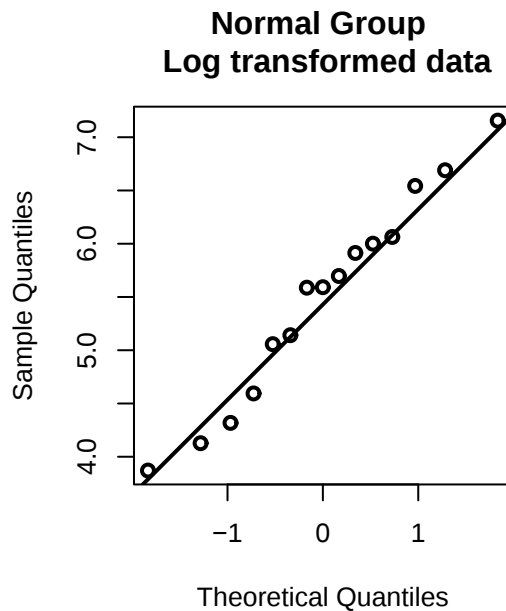
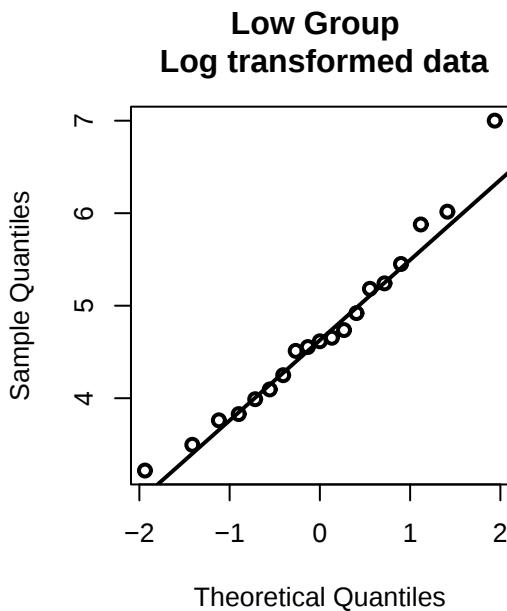
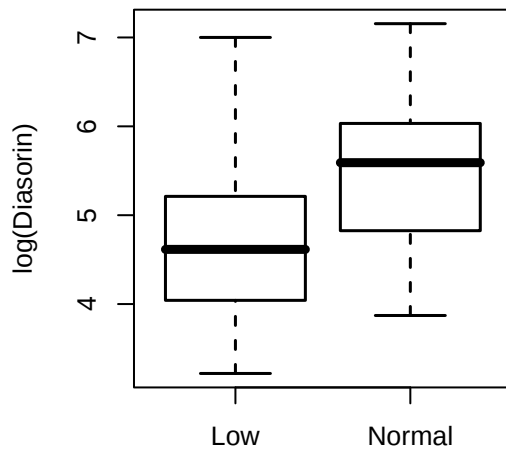
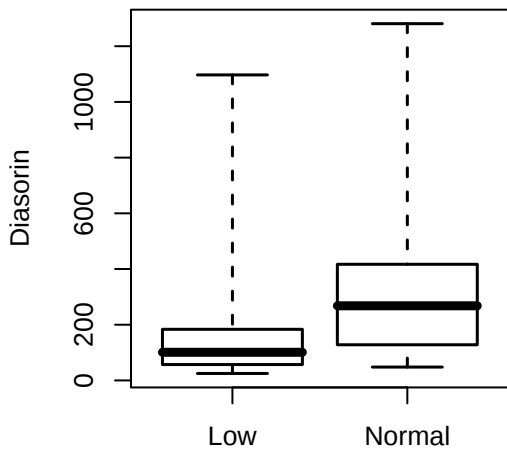
- Diasorin is a commercial assay (test) which, its manufacturers claim, can differentiate between individuals with low and normal bone turnover.
- Bone turnover refers to the continual process where old bone cells in the body are replaced with new bone cells.
- When kidneys fail to maintain proper levels of phosphorous and calcium in the blood, knowing a patient's rate of bone turnover is important for managing their health.

The Study

- 34 kidney patients from the bone registry at the University of Kentucky were identified as low or normal turnover by other means.
- These patients were then given the commercial assay to determine whether it could correctly identify them.

A Data Concern

- From boxplots a normal sampling model appears untenable due to marked skewness but boxplots and quantile plots of the log transformed data seem reasonably normal.



Data Structure

- In general we assume the sampling model

$$y_{11}, \dots, y_{1n_1} | \mu_1, \tau_1 \stackrel{\text{iid}}{\sim} N(\mu_1, 1/\tau_1) \quad \perp\!\!\!\perp$$

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- We can use any of the one-sample techniques: reference priors, conjugate priors, or independence priors, to determine the prior distributions.

Eliciting Priors on μ

- We need to elicit priors on both parameters of the log-normal distribution: μ and τ .
- We will elicit different priors for both our groups.
- We will also consider a reference prior for sensitivity analysis.

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- The median is unchanged by the transformation, however, so we'll elicit prior information on it.
- We specify a best guess, $\tilde{m}$, for the median, and a percentile, $\tilde{u}$, for which we are, say, 95% sure that the median is below (or above).

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- For the normal bone turnover group, he believes the median will be 220, with 95% certainty that it is below 240.

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- Why? The median of a Normal distribution is equal to the mean, so if we log-transform our expert's guesses at the median, we'll receive information on the mean of the Normal distribution for the log-transformed data.
- Then we obtain $\mu_L \equiv \mu_1 \sim N(4.87, 0.00288)$ and $\mu_N \equiv \mu_2 \sim N(5.39, 0.00280)$.

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- Moreover, we want an idea of the variability of the data on its original scale, where we've got evidence of non-normality.
- The easiest way to elicit a prior on a scale/rate parameter like τ is to ask about percentiles of the underlying data.

Eliciting Priors on τ

- We elicit information from our expert about the 90th (or some other) percentile of the data distribution. The log of this is $\mu + 1.645 \sqrt{1/\tau}$. The elicitation is now conditional on the best guess for μ being $\log(\tilde{m})$.

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- We obtain $\log(u_{0.9}/\tilde{m}) = 1.645 \sqrt{1/\tilde{\tau}}$ or

$$\tilde{\tau} = 1.645^2 / \{\log(u_{0.9}/\tilde{m})\}^2.$$

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- Since we assume a $\text{Gamma}(c, d)$ prior for τ , set $(c - 1)/d = \tilde{\tau}$ or equivalently $c = 1 + \tilde{\tau}d$.
- We can proceed with eliciting an upper limit on $u_{0.90}$ but often the expert wants to stop in which case we introduce the same large variability as in a proper Gamma reference prior by picking $d = 0.001$.

Eliciting Priors on τ

- Our expert provided his best guess for the 90th percentile of Diasorin values in the low ($\mu_{0.90,1} = 170$) and normal ($\mu_{0.90,2} = 280$) bone turnover groups.

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- Our expert provided his best guess for the 90th percentile of Diasorin values in the low ($\mu_{0.90,1} = 170$) and normal ($\mu_{0.90,2} = 280$) bone turnover groups.
- We use gamma priors with modes 170 and 280, and with large variances: $\tau_1 \sim \text{Gamma}(1.0376, 0.001)$ and $\tau_2 \sim \text{Gamma}(1.04653, 0.001)$.

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- At the end of the day, our models are only as good as their ability to represent reality. We want to use them to predict what will happen in the future, or to understand the probability associated with future events.
- We need sensible distributions for any part of the model we’re interested in interpreting after the fact.

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- For me, there are two big reasons: intellectual honesty and understanding the problem.

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- *Intellectual Honesty* – Science doesn’t happen in a vacuum. The very fact that we’re able to formulate scientific hypotheses says a lot about our level of knowledge about natural phenomena. Pretending that we don’t have this information for the sake of “objectivity” is just papering over the truth. It’s better to accept our prior beliefs and incorporate them into our work. Techniques like sensitivity analysis help us confront those beliefs head-on and see whether they’re affecting our results.

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- *Understanding the Problem* – Any high-level modeling work is going to involve a lot of parameters and data vectors, and it’s easy to lose sight of what you really care about in a problem. Eliciting expert information and building informative priors is one way to explore your data and try to understand it better. If you have some sense of what data values you can expect, it’s easier to spot output that doesn’t make sense. More positively, it’s easier to spot meaningful results when you see them.

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- Uniform and (scaled) Beta priors only make sense when you know that there are hard limits for which values you can see, since they have finite support.
- Normal priors are great for anything you think is symmetric.
- If you don’t have hard limits or symmetry, i.e. if you have a skewed distribution without finite support, the Gamma distribution is usually the easiest choice.

We'll start by looking at the posterior distribution for these data under the informative priors, and those priors themselves.

(a) Posterior from Informative Priors					
Parameter	mean	sd	2.50%	median	97.50%
μ_L	4.86	0.05212	4.757	4.86	4.961
μ_N	5.395	0.05143	5.294	5.395	5.496
$\mu_N - \mu_L$	0.5356	0.07315	0.3922	0.5355	0.6793
τ_L	1.275	0.3944	0.6245	1.231	2.161
τ_N	1.285	0.4389	0.5757	1.236	2.274
τ_N/τ_L	1.114	0.5547	0.3873	1.003	2.496

(b) Informative Priors					
Parameter	mean	sd	2.50%	median	97.50%
μ_L	4.87	0.053	4.765	4.87	4.975
μ_N	5.39	0.053	5.286	5.39	5.494
$\mu_N - \mu_L$	0.52	0.07546	0.3724	0.5201	0.668
τ_L	1037	1019	29.45	729.59	3767.5
τ_N	1046	1023	30.48	738.26	3786.03
τ_N/τ_L	10.11	638.7	0.02897	1.01	35.67

Next, let's look at what would happen if we used reference priors (proper or improper).

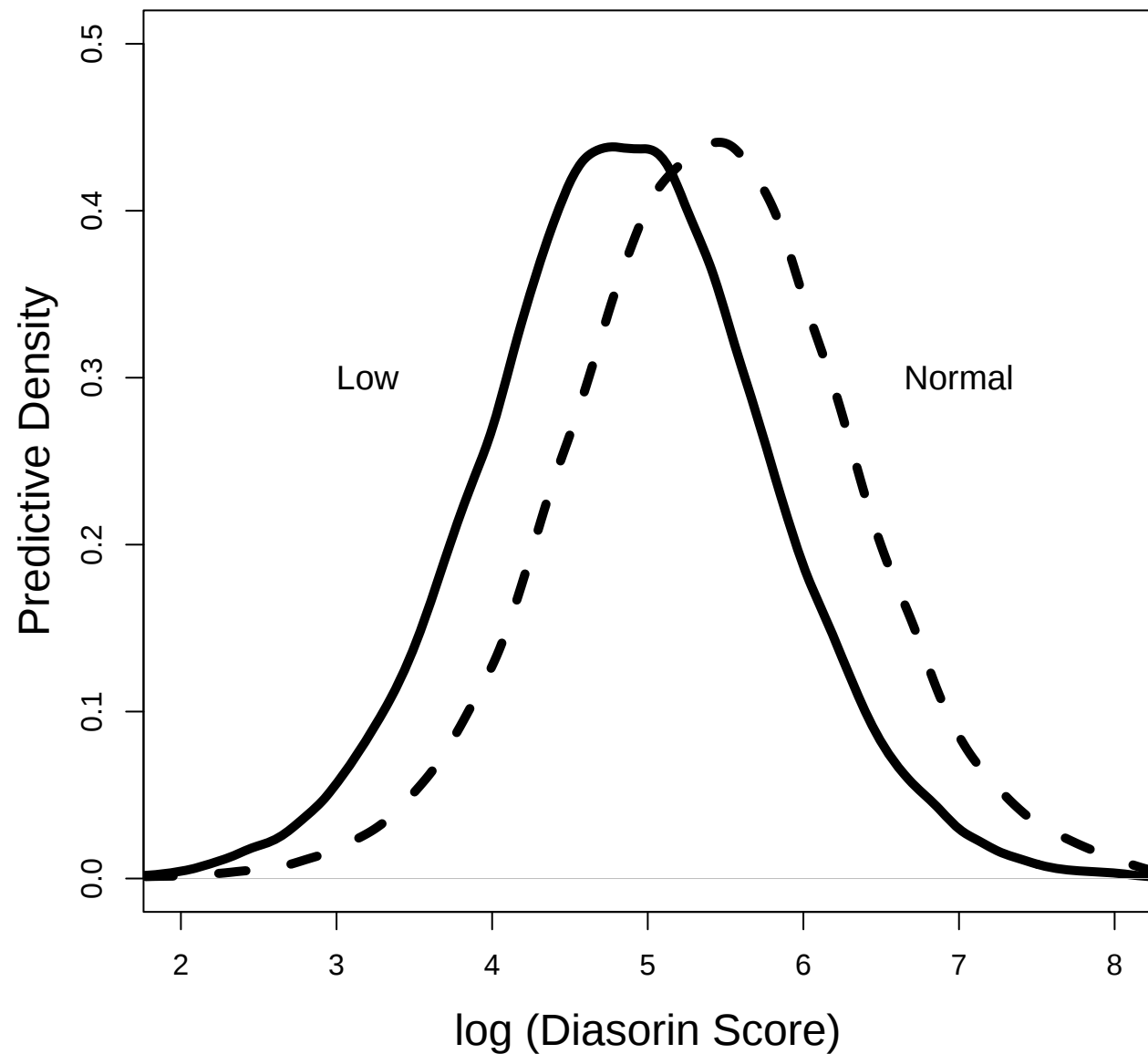
(c) Posterior from Proper Reference Prior for Means

Parameter	mean	sd	2.50%	median	97.50%
μ_L	4.706	0.2167	4.278	4.706	5.131
μ_N	5.49	0.2486	4.997	5.491	5.984
$\mu_N - \mu_L$	0.784	0.3296	0.135	0.7826	1.435
τ_L	1.252	0.3961	0.5991	1.208	2.147
τ_N	1.227	0.4319	0.5332	1.178	2.205
τ_N/τ_L	1.088	0.5596	0.3643	0.9723	2.49

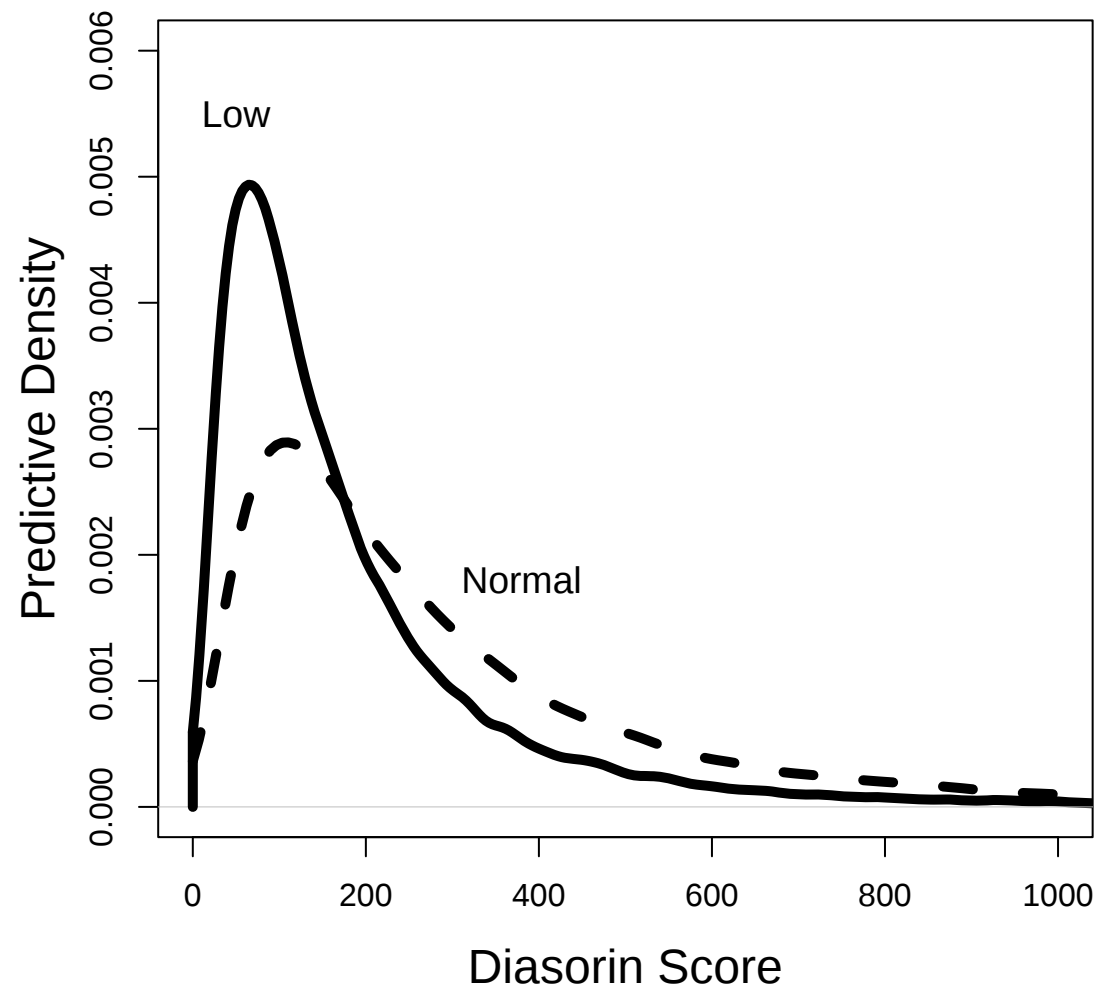
(d) Posterior from Improper Reference Prior

Parameter	mean	sd	2.50%	median	97.50%
μ_L	4.71	0.94	4.257	4.71	5.163
μ_N	5.49	0.97	4.953	5.49	6.027
τ_L	1.13	0.377	0.517	1.089	1.979
τ_N	1.06	0.401	0.427	1.013	1.983

- The next slide gives predictive densities for a future log Diasorin value from the low and normal groups. Note the similarity of the distributional shapes, which is due to the similarity of the precisions. With similar precisions, it becomes clear that the “normal” group has higher scores and that the means characterize the differences between the two distributions.



- If the variances were not the same, the difference in means would not be nearly so meaningful. To illustrate this, the next slide gives the predictive distributions of the Diasorin scores. These densities are much more difficult to interpret relative to one another. In particular, it is not obvious that the difference in the means of the predictive distributions would be a good measure of how the two distributions differ.



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- If we're interested in long-term averages, the mean may still be a reasonable point to consider. But if we're interested in uncommon events (which we sometimes call *tail behavior*), knowing which population has a higher density over a given region of the support becomes important.
- Also, if we consider unbalanced loss functions (where an incorrect decision in one direction is more damaging than an incorrect decision in the other direction – think Type I and Type II error), we will be more concerned about the entire density of the two populations than just the mean of those populations.