# Likelihood calculations for vsn

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## 1 Introduction

This vignette contains the computations that underlie the numerical code of *vsn*. If you are a new user and looking for an introduction on how to **use** *vsn*, please refer to the vignette *Robust calibration and variance stabilization with vsn*, which is provided separately.

# 2 Setup and Notation

Consider the model

$$\operatorname{arsinh}(f(b_i) \cdot y_{ki} + a_i) = \mu_k + \varepsilon_{ki}$$

where  $\mu_k$ , for  $k=1,\ldots,n$ , and  $a_i$ ,  $b_i$ , for  $i=1,\ldots,d$  are real-valued parameters, f is a function  $\mathbb{R} \to \mathbb{R}$  (see below), and  $\varepsilon_{ki}$  are i.i.d. Normal with mean 0 and variance  $\sigma^2$ .  $y_{ki}$  are the data. In applications to  $\mu$ array data, k indexes the features and i the arrays and/or colour channels.

Examples for f are f(b)=b and  $f(b)=e^b$ . The former is the most obvious choice; in that case we will usually need to require  $b_i>0$ . The choice  $f(b)=e^b$  assures that the factor in front of  $y_{ki}$  is positive for all  $b\in\mathbb{R}$ , and as it turns out, simplifies some of the computations.

In the following calculations, I will also use the notation

$$Y \equiv Y(y, a, b) = f(b) \cdot y + a$$

$$h \equiv h(y, a, b) = \operatorname{arsinh}(f(b) \cdot y + a)$$
.

The probability of the data  $(y_{ki})_{k=1...n,\ i=1...d}$  lying in a certain volume element of y-space (hyperrectangle with sides  $[y_{ki}^{\alpha}, y_{ki}^{\beta}]$ ) is

$$P = \prod_{k=1}^{n} \prod_{i=1}^{d} \int_{y_{k_{i}}^{\alpha}}^{y_{k_{i}}^{\beta}} dy_{k_{i}} \ p_{\text{Normal}}(h(y_{k_{i}}), \mu_{k}, \sigma^{2}) \ \frac{dh}{dy}(y_{k_{i}}),$$

where  $\mu_k$  is the expectation value for feature k and  $\sigma^2$  the variance.

With

$$p_{\text{Normal}}(x,\mu,\sigma^2) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(x-\mu)^2}{2\sigma^2}\right)$$
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the likelihood is

$$L = \left(\frac{1}{\sqrt{2\pi\sigma^2}}\right)^{nd} \prod_{k=1}^n \prod_{i=1}^d \exp\left(-\frac{(h(y_{ki}) - \mu_k)^2}{2\sigma^2}\right) \cdot \frac{dh}{dy}(y_{ki}).$$

For the following, I will need the derivatives

$$\frac{\partial Y}{\partial a} = 1$$

$$\frac{\partial Y}{\partial b} = y \cdot f'(b)$$

$$\frac{dh}{dy} = \frac{f(b)}{\sqrt{1 + (f(b)y + a)^2}} = \frac{f(b)}{\sqrt{1 + Y^2}},$$

$$\frac{\partial h}{\partial a} = \frac{1}{\sqrt{1 + Y^2}},$$

$$\frac{\partial h}{\partial b} = \frac{y}{\sqrt{1+Y^2}} \cdot f'(b).$$

Note that for f(b) = b, we have f'(b) = 1, and for  $f(b) = e^b$ ,  $f'(b) = f(b) = e^b$ .

## 3 Likelihood for Incremental Normalization

Here, incremental normalization means that the model parameters  $\mu_1,\dots,\mu_n$  and  $\sigma^2$  are already known from a fit to a previous set of  $\mu$ arrays, i.e. a set of reference arrays. See Section 4 for the profile likelihood approach that is used if  $\mu_1,\dots,\mu_n$  and  $\sigma^2$  are not known and need to be estimated from the same data. Versions  $\geq 2.0$  of the vsn package implement both of these approaches; in versions 1.X only the profile likelihood approach was implemented, and it was described in the initial publication [1].

First, let us note that the likelihood 6 is simply a product of independent terms for different i. We can optimize the parameters  $(a_i,b_i)$  separately for each  $i=1,\ldots,d$ . From the likelihood 6 we get the i-th negative log-likelihood

$$-\log(L) = \sum_{i=1}^{d} -LL_i$$

$$-LL_{i} = \frac{n}{2}\log\left(2\pi\sigma^{2}\right) + \sum_{k=1}^{n} \left(\frac{(h(y_{ki}) - \mu_{k})^{2}}{2\sigma^{2}} + \log\frac{\sqrt{1 + Y_{ki}^{2}}}{f(b_{i})}\right)$$
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$$= \frac{n}{2}\log(2\pi\sigma^2) - n\log f(b_i) + \sum_{k=1}^{n} \left(\frac{(h(y_{ki}) - \mu_k)^2}{2\sigma^2} + \frac{1}{2}\log(1 + Y_{ki}^2)\right)$$
 14

This is what we want to optimize as a function of  $a_i$  and  $b_i$ . The optimizer benefits from the derivatives. The derivative with respect to  $a_i$  is

$$\frac{\partial}{\partial a_i}(-LL_i) = \sum_{k=1}^n \left(\frac{h(y_{ki}) - \mu_k}{\sigma^2} + \frac{Y_{ki}}{\sqrt{1 + Y_{ki}^2}}\right) \cdot \frac{1}{\sqrt{1 + Y_{ki}^2}}$$

$$= \sum_{k=1}^n \left(\frac{r_{ki}}{\sigma^2} + A_{ki}Y_{ki}\right) A_{ki}$$
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and with respect to  $b_i$ 

$$\frac{\partial}{\partial b_i}(-LL_i) = -n\frac{f'(b_i)}{f(b_i)} + \sum_{k=1}^n \left(\frac{h(y_{ki}) - \mu_k}{\sigma^2} + \frac{Y_{ki}}{\sqrt{1 + Y_{ki}^2}}\right) \cdot \frac{y_{ki}}{\sqrt{1 + Y_{ki}^2}} \cdot f'(b_i)$$

$$= -n\frac{f'(b_i)}{f(b_i)} + f'(b_i) \sum_{k=1}^n \left(\frac{r_{ki}}{\sigma^2} + A_{ki}Y_{ki}\right) A_{ki}y_{ki}$$
16

Here, I have introduced the following shorthand notation for the "intermediate results" terms

$$r_{ki} = h(y_{ki}) - \mu_k \tag{17}$$

$$A_{ki} = \frac{1}{\sqrt{1 + Y_{ki}^2}}.$$

Variables for these intermediate values are also used in the C code to organise the computations of the gradient.

#### 4 Profile Likelihood

If  $\mu_1,\ldots,\mu_n$  and  $\sigma^2$  are not already known, we can plug in their maximum likelihood estimates, obtained from optimizing LL for  $\mu_1,\ldots,\mu_n$  and  $\sigma^2$ :

$$\hat{\mu}_k = \frac{1}{d} \sum_{j=1}^d h(y_{kj})$$
 19

$$\hat{\sigma}^2 = \frac{1}{nd} \sum_{k=1}^n \sum_{j=1}^d (h(y_{kj}) - \hat{\mu}_k)^2$$

into the negative log-likelihood. The result is called the negative profile log-likelihood

$$-PLL = \frac{nd}{2}\log(2\pi\hat{\sigma}^2) + \frac{nd}{2} - n\sum_{j=1}^{d}\log f(b_j) + \frac{1}{2}\sum_{k=1}^{n}\sum_{j=1}^{d}\log\sqrt{1 + Y_{kj}^2}.$$
 21

Note that this no longer decomposes into a sum of terms for each j that are independent of each other – the terms for different j are coupled through Equations 19 and 20. We need the following derivatives.

$$\frac{\partial \hat{\sigma}^2}{\partial a_i} = \frac{2}{nd} \sum_{k=1}^n r_{ki} \frac{\partial h(y_{ki})}{\partial a_i}$$

$$= \frac{2}{nd} \sum_{k=1}^n r_{ki} A_{ki}$$
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$$\frac{\partial \hat{\sigma}^2}{\partial b_i} = \frac{2}{nd} \cdot f'(b_i) \sum_{k=1}^n r_{ki} A_{ki} y_{ki}$$
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#### Likelihood calculations for vsn

So, finally

$$\frac{\partial}{\partial a_i}(-PLL) = \frac{nd}{2\hat{\sigma}^2} \cdot \frac{\partial \hat{\sigma}^2}{\partial a_i} + \sum_{k=1}^n A_{ki}^2 Y_{ki}$$

$$= \sum_{k=1}^n \left(\frac{r_{ki}}{\hat{\sigma}^2} + A_{ki} Y_{ki}\right) A_{ki}$$
24

$$\frac{\partial}{\partial b_i}(-PLL) = -n\frac{f'(b_i)}{f(b_i)} + f'(b_i)\sum_{k=1}^n \left(\frac{r_{ki}}{\hat{\sigma}^2} + A_{ki}Y_{ki}\right) A_{ki}y_{ki}$$
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## 5 Summary

Likelihoods, from Equations 12 and 21:

$$-LL_{i} = \underbrace{\frac{n}{2}\log\left(2\pi\sigma^{2}\right)}_{\text{scale}} + \underbrace{\sum_{k=1}^{n}\frac{(h(y_{ki}) - \mu_{k})^{2}}{2\sigma^{2}}}_{\text{residuals}} - n\log f(b_{i}) + \frac{1}{2}\sum_{k=1}^{n}\log(1 + Y_{ki}^{2})$$

$$-PLL = \underbrace{\frac{nd}{2}\log\left(2\pi\hat{\sigma}^2\right)}_{\text{scale}} + \underbrace{\frac{nd}{2}}_{\text{residuals}} + \underbrace{\sum_{i=1}^{d}\left(-n\log f(b_i) + \frac{1}{2}\sum_{k=1}^{n}\log(1+Y_{ki}^2)\right)}_{\text{jacobian}}$$

The computations in the C code are organised into steps for computing the terms "scale", "residuals" and "jacobian".

Partial derivatives with respect to  $a_i$ , from Equations 15 and 24:

$$\frac{\partial}{\partial a_i}(-LL_i) = \sum_{k=1}^n \left(\frac{r_{ki}}{\sigma^2} + A_{ki}Y_{ki}\right) A_{ki}$$
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$$\frac{\partial}{\partial a_i}(-PLL) = \sum_{k=1}^n \left(\frac{r_{ki}}{\hat{\sigma}^2} + A_{ki}Y_{ki}\right) A_{ki}$$

Partial derivatives with respect to  $b_i$ , from Equations 16 and 25:

$$\frac{\partial}{\partial b_i}(-LL_i) = -n\frac{f'(b_i)}{f(b_i)} + f'(b_i)\sum_{k=1}^n \left(\frac{r_{ki}}{\sigma^2} + A_{ki}Y_{ki}\right)A_{ki}y_{ki}$$

$$\frac{\partial}{\partial b_i}(-PLL) = -n\frac{f'(b_i)}{f(b_i)} + f'(b_i) \sum_{k=1}^n \left(\frac{r_{ki}}{\hat{\sigma}^2} + A_{ki}Y_{ki}\right) A_{ki}y_{ki}.$$

Note that the terms have many similarities – this is used in the implementation in the C code.

# References

- [1] W. Huber, A. von Heydebreck, H. Sültmann, A. Poustka, and M. Vingron. Variance stablization applied to microarray data calibration and to quantification of differential expression. *Bioinformatics*, 18:S96–S104, 2002.
- [2] W. Huber, A. von Heydebreck, H. Sültmann, A. Poustka, and M. Vingron. Parameter estimation for the calibration and variance stabilization of microarray data. *Statistical Applications in Genetics and Molecular Biology*, Vol. 2: No. 1, Article 3, 2003. http://www.bepress.com/sagmb/vol2/iss1/art3