

ABSTRACT

OPTIMIZED STRICT MULTISCALE FRANGI PREFILTERING FOR SEGMENTATION: TOWARDS AN AUTOMATED PLACENTAL CHORIONIC SURFACE VASCULAR NETWORK EXTRACTION

By

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Recent statistical analysis of placental features has suggested the usefulness of studying key features of the placental chorionic surface vascular network (PCSVN) as a measure of overall neonatal health [1]. A recent study has suggested that reliable reporting of these features may be useful in identifying risks of certain neurodevelopmental disorders at birth. The necessary features can be extracted from an accurate tracing of the surface vascular network, but such tracings must still be done manually, with significant user intervention. Automating this procedure would not only allow more data acquisition to study the potential effects of placental health on later conditions, but may ideally serve as a real-time diagnostic for neonatal risk factors as well.

Much work has been to develop reliable vascular extraction methods for well-known image domains (such as retinal MRA images) using Hessian-based filters, namely the (multiscale) Frangi filter. It is desirable to extend these technique to study placental images, but this approach is greatly hindered by the comparative irregularity of the placental surface as a whole, which introduces significant noise into the image domain. Prior work [2] has made to apply an additional local curvilinear filter to the

Frangi result in an effort to remove some noise from the final extraction.

Here we provide an in depth mathematical background of the Frangi filter and a reasonable introduction to Gaussian scale space theory. Finally, we discuss an important advancement in implementation–scale space conversion for differentiation (i.e. gaussian blur) via Fast Fourier Transform, which offers a significant speedup. This allows us faster calculation of the eigenvalues of the Hessian, from which we calculate the Frangi filter, a vesselness measure.

We demonstrate the effectiveness of our sped-up implementation of the Frangi filter by performing a large ($N=20$) multiscale Frangi filter on a set of 201 placental images from a private database provided by the National Children’s Study (NCS). We then compare several approaches of merging the multiscale result into an approximation of the PCSVN and compare them to manual tracings of the network. We finally suggest several ways to improve upon our approximation, namely by using the Frangi result as a prefilter for more robust techniques, providing a brief demo using a random walker segmentation.

**OPTIMIZED STRICT MULTISCALE FRANGI PREFILTERING FOR
SEGMENTATION: TOWARDS AN AUTOMATED PLACENTAL CHORIONIC
SURFACE VASCULAR NETWORK EXTRACTION**

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CHAPTER 1

INTRODUCTION

From [1], it is useful to develop a neonatal test for high risk of Autism Spectrum Disorder. There is some evidence as in [3] of correlation between this risk and placental health factors.. Most ASD cases are not diagnosed until the child reaches three or four, so the benefit of an early detection technique would be massive, as the brain may be more receptive to treatment at a young age. In particular, it was shown in [3] that measurements of the placental chorionic surface vascular network (PCSVN) may be useful in identifying such risk. [1] has provided a method of automatically calculating such features from an extracted vascular network, but does so with manual tracing of the PCSVN in order to make these measurements. These manual tracings are labor-intensive, requiring 4 to 8 hours of user intervention to generate each trace. The present work follows several other efforts towards an automated extraction technique, such as [4], [2], and most recently [5]. Automating this procedure would not only allow more data acquisition to study the potential connection between ASD and placental health, but could even potentially serve as the basis of real-time diagnostic for neonatal risk factors as well. We continue the work of developing a procedure to automate extraction of the PCSVN.

Our basic goal of "vascular network extraction" is a common one in image processing. There have been many techniques adapted to extracting vascular networks. However, the placenta in particular poses as a particularly difficult image domain to work with. It is a surface network with much irregularity: there are frequent gaps and crossings, the "background" has a great degree of variation in color intensity

and structure itself, causing many naïve approaches to fail completely.

Reliable vascular extraction methods do exist for well-known image domains (such as retinal MRA images) using Hessian-based filters, namely the (multiscale) Frangi filter. It is desirable to extend this technique to study placental images, but this approach is greatly hindered by the comparative irregularity of the placental surface as a whole, which introduces significant noise into the image domain. Previous attempts to implement the Frangi filter in this context [2] dealt with this noise by passing the Frangi filtered result to an additional local curvilinear filter (a directional filter bank) in an effort to retrieve a partial segmentation. Other more recent efforts [5] are very promising but are considerably more resource-intensive.

Here we provide an in depth mathematical background of the Frangi filter and its justification as an image-processing technique, as well as an introduction to the Gaussian scale space theory common to many multiscale methods. Finally, we discuss an important advancement in implementation–scale space conversion for differentiation (i.e. gaussian blur) via Fast Fourier Transform, which offers a significant speedup. This allows us faster calculation of the eigenvalues of the Hessian, from which we calculate the Frangi filter, a vesselness measure.

We demonstrate the effectiveness of our sped-up implementation of the Frangi filter by performing a large ($N = 20$) multiscale Frangi filter on a set of 201 placental images from a private database provided by the National Children’s Study (NCS). We then appeal to the usefulness of our multiscale output by then demonstrating several approaches to determining a segmentation of the PCSVN. These will range from naive (i.e direct thresholding) to rather viable (scalewise random walks). We compare each of these results to manual tracings of the network. We shall our ability to take many more scales into consideration (by virtue of the sped up Frangi filter) allows us to be pickier about our thresholding, as well as our choice of parameters, which significantly reduces

noise experienced in previous efforts.

CHAPTER 2

MATHEMATICAL METHODS: DIFFERENTIAL GEOMETRY AND SURFACE CURVATURE

Our goal is establish a resource efficient method of finding curvilinear content in 2D grayscale digital images using concepts of differential geometry. We proceed by (i) establishing a standard method of viewing these images as 2D surfaces, (ii) developing a minimal yet rigorous distillation of differential geometry to obtain suitable quantifiers for the study of curvilinear structure in 3D surfaces, (iii) establishing a filter based on these quantifiers, and finally (iv) developing methods necessary for efficient computation of the filter.

Problem Setup in Image Processing

A digital 2D grayscale image is given by a $M \times N$ array of pixels, whose intensity is given by an integer value between 0 and 255.

Definition 2.1 (Image as a pixel matrix).

$$\mathbf{I} \in \mathbb{N}^{M \times N} \quad \text{with} \quad 0 \leq I_{ij} \leq 2^8 - 1$$

For theoretical purposes, we wish to consider any such picture to ultimately be a sampling of a 2D continuous surface. We also require that this surface is sufficiently continuous as to admit the existence of second partial derivatives.

Definition 2.2 (Image as an interpolated surface).

$$h : \mathbb{R}^2 \rightarrow \mathbb{R} \quad \text{with} \quad h \in C^2(\mathbb{R}^2), \quad \text{where} \quad h(i, j) = I_{ij} \quad \forall (i, j) \in \{0, \dots, M\} \times \{0, \dots, N\} \subset \mathbb{N}^2$$

That is, the function h is identical to the pixel matrix I at all integer inputs, and simply a “smooth enough” interpolation of those points for all other values.

It is of course necessary to admit that I is not really a perfect representation of the underlying “content” within the picture. Not only is information lost when I is stored as an integer, there are also elements of noise and anomalies of lighting that would constitute noise to the original signal. There are multiple treatments of image processing that do address this discrepancy in a pragmatic way [6], especially when the goal is noise reduction. However, we will be content to simply represent the pixels of I as the ultimate “cause” of the surface h in definition 2.2, and worry not about how faithfully that sampling corresponds to the real world. Moreover, though our samples in the image domain have been carefully prepared (as outlined in section 8.1), there are numerous shortcomings therein, and improvements to the veracity of our original signal could be made from many angles. Though we shall draw upon the notion of the pixel matrix I as a sampling again to motivate our development of scale space theory in chapter 4, we ultimately use these techniques because we find them successful to our problem.

Differential Geometry

We wish to describe the structure of an image as a surface. To do this, we develop the notion of curvature of a surface in \mathbb{R}^3 in a standard way, following [7] (although any undergraduate text in Differential Geometry should prove satisfactory).

Preliminaries of Differential Geometry

Given an open subset $U \subset \mathbb{R}^2$ and a twice differentiable function $h : U \rightarrow \mathbb{R}$ (as in definition 2.2) we define the graph, f , of h in the following definition.

Definition 2.3. *The surface f is a graph (of the function h) when*

$$f : U \rightarrow \mathbb{R}^3 \quad \text{by} \quad f(u_1, u_2) = (u_1, u_2, h(u_1, u_2)), \quad u = (u_1, u_2) \in U \subset \mathbb{R}^2$$

Since the graph f is clearly one-to-one by definition, we may readily associate any input $u \in U$ with its corresponding output $p \in f[U]$, i.e.

$p = f(u) = f(u_1, u_2) = (u_1, u_2, h(u_1, u_2))$, depending on whether we wish to focus on a point of a graph in terms of its input or in terms of the structure of the graph itself.

Our development of curvature ultimately will hinge upon a careful consideration of the tangent plane of f at a point p , for we will require a concrete definition of both the tangent space within the domain and image of f , as well as the so called "differential" of f , the lattermost of which we will only define for the immediate case required.

Definition 2.4 (Tangent space of U at u).

$$T_u U = \{u\} \times \mathbb{R}^2$$

Definition 2.5 (Tangent space of \mathbb{R}^3 at p).

$$T_p \mathbb{R}^3 = \{p\} \times \mathbb{R}^3$$

It is immediately clear that $T_u U$ and $T_p \mathbb{R}^3$ are isomorphic to \mathbb{R}^2 and \mathbb{R}^3 , respectively, and we can easily visualize elements of $T_u U$ are tangent vectors in \mathbb{R}^2 "originating" at the point u , and elements of $T_p \mathbb{R}^3$ are tangent vectors "originating" at the point p .

Definition 2.6 (The differential of f at a point u). $Df|_u$ is the map from $T_u U$ into \mathbb{R}^3 given by

$$Df|_u : T_u U \rightarrow T_{f(u)} \mathbb{R}^3 \quad \text{by} \quad w \mapsto J_f(u) \cdot v$$

where $J_f(u)$ is the Jacobian of f evaluated at some fixed point $u \in U$, i.e. the matrix

$$J_f(u) = \left[\frac{\partial f_i}{\partial u_j} \right]_{i,j}$$

Although not necessary presently, we could just as easily consider the differential of an arbitrary function as a map between tangent vectors in the function's domain and tangent vectors in its range. We could also just identify this as mapping $U \rightarrow \mathbb{R}^3$ by the obvious isomorphism described above. and then differential of f at x is simply a linear transformation of between the tangent spaces $T_u U$ and $T_p \mathbb{R}^3$ where the transformation in question is given by the Jacobian. We can define such a differential at any point u in the domain.

With these three definitions, we are equipped to give a formal definition of $T_u f$, the tangent plane of f at an input u .

Definition 2.7 (Tangent plane of a graph).

$$T_u f := Df|_u(T_u U) \subset T_{f(u)} \mathbb{R}^3 = T_p \mathbb{R}^3$$

This vectors of this plane can thus be identified as tangent vectors from $T_u U$ that have been passed through the differential mapping $Df|_u$. We shall denote a generic tangent vector $X \in T_u f$ at point p . We may expand any such vector X in terms of the basis $\left\{ \frac{\partial f}{\partial u_i} \right\}_{i=1,2}$; that is, $\text{span} \left\{ \frac{\partial f}{\partial u_1}, \frac{\partial f}{\partial u_2} \right\} = T_u f$.

Given the level of abstraction above, it may be refreshing to explicitly show the linear independence of this set in the case of an arbitrary graph f .

Lemma 2.1. *When f is a graph, for all points $u \in U$, $\left\{ \frac{\partial f}{\partial u_1}, \frac{\partial f}{\partial u_2} \right\}$ is in fact a basis for the tangent plane $T_u f$.*

Quite obviously, we're assuming $(1,0), (0,1) \in U$. If this is not the case, we pick

some α small enough so that $(\alpha, 0)$ and $(0, \alpha)$ are contained and this scaled version would serve as a basis instead.

Proof. Given the definition of a graph f as in definition 2.3, we can directly calculate the partial derivatives of f at a point u .

$$f_{u_1} = (1, 0, h_{u_1}(u)) \quad \text{and} \quad f_{u_2} = (0, 1, h_{u_2}(u))$$

which are obviously linearly independent. Then $Df|_u(1, 0) = f_{u_1}$, and $Df|_u(0, 1) = f_{u_2}$, which shows $\left\{\frac{\partial f}{\partial u_1}, \frac{\partial f}{\partial u_2}\right\} \in T_u f$. Thus $\left\{\frac{\partial f}{\partial u_1}, \frac{\partial f}{\partial u_2}\right\}$ is a linearly independent subset of $T_u f$, and can serve as its basis. \square

The partials derivatives of f are not, in general, orthogonal at any point u , unless it happens that h_{u_1} or h_{u_2} is zero. A visualization of some of the above is given in fig. 1, although note that f_{u_1} and f_{u_2} accidentally appear orthogonal.

We now concern ourselves with developing the notion of curvature on a surface. First, we need to consider an arbitrary regular curve (i.e. differentiable, one-to-one, non-zero derivative) contained within the image of f .

Curvature of a surface and its calculation

In the context of a regular arc-length parametrized curve $c : I \rightarrow \mathbb{R}^3$ parametrized along some closed interval $I \subset \mathbb{R}$ (that is, a differentiable, one-to-one curve where $c'(s) = 1 \quad \forall s \in I$), curvature at a point $s \in I$ is defined simply as the magnitude of the curve's acceleration: $\kappa(s) := \|c''(s)\|$.

To extend the notion of curvature of a surface f , we can consider the curvature of such an arbitrary curve embedded within the surface.

Definition 2.8 (Surface curve). *Given a closed interval $I \subset \mathbb{R}$, we call the regular curve $c : I \rightarrow \mathbb{R}^3$ a surface curve in the event that $\text{image}(c) \subset \text{image}(f)$ entirely. The one-to-one-ness of*



FIGURE 1: Tangent plane of a graph

the graph f ensures that we can define (for the given curve) an intermediary parametrization θ_c so that $c = f \circ \theta_c$. That is,

$$\theta_c : I \rightarrow U \text{ by } \theta(t) = (\theta_1(t), \theta_2(t))$$

so that $c(t) = f(\theta_c(t)) \forall t \in I$, and $c[I] = f[\theta_c[I]]$.

Note as well that the velocity of this particular curve lies within T_{uf} . This can be seen by an elementary application of chain rule:

$$-\frac{dc}{dt} = -\frac{d}{dt}[f(\theta_c(t))] \quad (2.1)$$

$$= -\frac{d}{dt}[f(\theta_1(t), \theta_2(t))] \quad (2.2)$$

$$= \theta'_1(t) \left(\frac{\partial f}{\partial u_1} \right) + \theta'_2(t) \left(\frac{\partial f}{\partial u_2} \right) \in T_{uf}. \quad (2.3)$$

Considering a point $p \in I$ and its associated point $u = \theta_c(p)$, we wish to compare

the curvatures of all (regular) surface curves passing through the point p at some particular velocity.

We now present a main result that provides a notion of curvature of a surface.

Theorem 2.2 (Theorem of Meusnier). *Given a point $u \in U$ and a tangent direction $X \in T_u f$, any regular curve on the surface $c : I \rightarrow \text{image}(f)$ with $p \in I$: $\theta_c(p) = u$ where $c'(p) = X$ will have the same curvature.*

In other words, any two curves on the surface with a common velocity at a given point on the surface will have the same curvature. To prove this, we'll require one final definition.

Definition 2.9 (The Gauss Map). *The Gauss map at a point $p = f(u)$ is the unit normal to the tangent plane*

$$v : U \rightarrow \mathbb{R}^3 \quad \text{by} \quad v(u) := \frac{\frac{\partial f}{\partial u_1} \times \frac{\partial f}{\partial u_2}}{\left\| \frac{\partial f}{\partial u_1} \times \frac{\partial f}{\partial u_2} \right\|}$$

Each partial above understood to be evaluated at the input $u \in U$; that is, we calculate $\frac{\partial f}{\partial u_i} \Big|_u$. The existence of the cross product in its definition makes it clear that $v \perp \frac{\partial f}{\partial u_i}$ each $i = 1, 2$. A simple dimensionality argument of \mathbb{R}^3 implies that these must exist in $T_u f$. However, we can also show it directly:

To show that $\left\{ \frac{\partial v}{\partial u_1}, \frac{\partial v}{\partial u_2} \right\} \subset T_u f$, first note that at any particular $u \in U$, $\langle v, v \rangle = 1 \implies \frac{\partial}{\partial u_i} \langle v, v \rangle = 0$, and so by chain rule $2 \langle \frac{\partial v}{\partial u_i}, v \rangle = 0 \implies \frac{\partial v}{\partial u_i} \perp v$. Since $v \perp \text{span} \left\{ \frac{\partial f}{\partial u_i} \right\}$ as well (since v its outer product), in \mathbb{R}^3 , this implies $\text{span} \left\{ \frac{\partial v}{\partial u_i} \right\} \parallel \text{span} \left\{ \frac{\partial f}{\partial u_i} \right\}$. Thus, we have $\text{span} \left\{ \frac{\partial v}{\partial u_1}, \frac{\partial v}{\partial u_2} \right\} \subset T_u f$ as well and we can also use it as a basis.

We are finally ready to prove theorem 2.2, the Theorem of Meusnier.

Proof. Let $X \in T_u f$ be given and consider some curve where $\frac{dc}{dt}(u) = X$ where $X \in T_u f$. We wish to decompose the curve's acceleration along the orthogonal vectors X and the Gauss

map $\nu = \nu(u_1, u_2) = \frac{\frac{\partial f}{\partial u_1} \times \frac{\partial f}{\partial u_2}}{\|\frac{\partial f}{\partial u_1} \times \frac{\partial f}{\partial u_2}\|}$ as in definition 2.9. Note that X and ν are indeed orthogonal, as $X \in \text{span}\left\{\frac{\partial f}{\partial u_i}\right\} = T_u f$, and $\nu \perp T_u f$. We then have (at this fixed point $u = \theta_c(p)$)

$$c'' = \langle c'', X \rangle X + \langle c'', \nu \rangle \nu \quad (2.4)$$

Because c is a regular curve, we either have $c'' = 0$, or $c' \perp c''$, since $\|c'\| = 1$ implies $0 = \frac{d}{dt} \langle c', c' \rangle = 2 \langle c'', c' \rangle$. Thus

$$\langle c'', X \rangle = \langle c'', c' \rangle = 0$$

and we can rewrite the second coefficient of eq. (2.4) using the chain rule:

$$\langle c'', \nu \rangle = \frac{\partial}{\partial t} [\langle c', \nu \rangle] - \langle c', \frac{\partial \nu}{\partial t} \rangle \quad (2.5)$$

$$= \frac{\partial}{\partial t} [\langle X, \nu \rangle] - \langle c', \frac{\partial \nu}{\partial t} \rangle \quad (2.6)$$

$$= 0 - \langle X, \frac{\partial \nu}{\partial t} \rangle \quad (2.7)$$

Thus, we can express the curvature at this point on our selected curve as

$$\|c''\| = \|\langle c'', X \rangle X + \langle c'', \nu \rangle \nu\| = \|0 + \langle c'', \nu \rangle \nu\| \quad (2.8)$$

$$= -\langle X, \frac{\partial \nu}{\partial t} \rangle \|\nu\| \quad (2.9)$$

$$= -\langle X, \frac{\partial \nu}{\partial t} \rangle \quad (2.10)$$

$$= \langle X, -\frac{\partial \nu}{\partial t} \rangle \quad (2.11)$$

We may compute the quantity $-\frac{\partial v}{\partial t}$ that appears in eq. (2.11) via chain rule:

$$-\frac{dv}{dt} = -\frac{d}{dt}[v(u_1, u_2)] \quad (2.12)$$

$$= -\frac{d}{dt}[v(\theta_1(t), \theta_2(t))] \quad (2.13)$$

$$= \theta'_1(t) \left(-\frac{\partial v}{\partial u_1} \right) + \theta'_2(t) \left(-\frac{\partial v}{\partial u_2} \right) \quad (2.14)$$

Identifying $\text{span}\left\{-\frac{\partial v}{\partial u_i}\right\}_{i=1,2}$ as a subset of $T_u f$, we can define a linear transformation L which maps the basis $\left\{\frac{\partial f}{\partial u_i}\right\}_{i=1,2}$ to this subset:

Definition 2.10 (The Weingarten Map).

$$L : T_u f \rightarrow T_u f \quad \text{given by the composition} \quad L = Dv \circ (Df)^{-1}.$$

That is, $L\left(\frac{\partial f}{\partial u_i}\right) = -\frac{\partial v}{\partial u_i}$ for $i = 1, 2$, where the negative sign comes about from blind adherence to eq. (2.14) and eq. (2.11). This allows us to rewrite the time derivative of the Gauss map eq. (2.12) as

$$-\frac{dv}{dt} = \theta'_1(t) \left(-\frac{\partial v}{\partial u_1} \right) + \theta'_2(t) \left(-\frac{\partial v}{\partial u_2} \right) \quad (2.15)$$

$$= \theta'_1(t) \left(L\left(\frac{\partial f}{\partial u_1}\right) \right) + \theta'_2(t) \left(L\left(\frac{\partial f}{\partial u_2}\right) \right) \quad (2.16)$$

$$= L \left[\theta'_1(t) \left(\frac{\partial f}{\partial u_1} \right) + \theta'_2(t) \left(\frac{\partial f}{\partial u_2} \right) \right] \quad (2.17)$$

$$= L \left(\frac{d}{dt} [f(\theta(t))] \right) = L \left(\frac{d}{dt} [c(t)] \right) = L(X) \quad (2.18)$$

With this, we can re-express the curvature of our curve from eq. (2.11) as the much simplified

$$\|c''\| = \langle X, -\frac{\partial v}{\partial t} \rangle = \langle X, L(X) \rangle \quad (2.19)$$

The linear transformation L from definition 2.10, and thereby the computation of curvature given in eq. (2.19), depends only on the point u and the selected direction X , not on the particular curve c at all. \square

To recap, given a point u on the surface and an arbitrary vector X in the tangent plane, we can calculate the curvature of any surface curve with velocity X there. In fact, we refer to this intrinsic quantity as the normal curvature of the surface.

Definition 2.11. *The normal curvature of a surface, denoted κ_v at point u in the direction X is given by*

$$\kappa_v := \langle X, L(X) \rangle$$

In fact, theorem 2.2 shows that the normal curvature is an intrinsic property of the surface—it depends only on the surface at a point, and no reference to any particular curve on the surface is necessary or implied.

The map L introduced in the proof above is known as the Weingarten map and is implicitly defined at each $u \in U$. We wish to make its existence rigorous as well as find a matrix representation for it, using the standard motivation that $L\left(\frac{\partial f}{\partial u_i}\right) = -\frac{\partial v}{\partial u_i}$.

That is, we may trace any $X \in T_u f$ which has been expanded in terms of the basis $\left\{ \frac{\partial f}{\partial u_1}, \frac{\partial f}{\partial u_2} \right\}$ and map it to the span of $\left\{ -\frac{\partial v}{\partial u_1}, -\frac{\partial v}{\partial u_2} \right\}$.

The Weingarten map can be formally shown to be well-defined, invariant under coordinate transformation in the general case (that is, for surfaces f that are not graphs). We refer to [7] for the general proof. Our present situation is much less delicate, as we're only concerned for cases when f is a graph. In this case, the linear transformation may be simply constructed, and we proceed by simply calculating its matrix representation.

Lemma 2.3. *The Weingarten map as in definition 2.10 is well-defined for graphs.*

To find a matrix representation for L (which we will denote $\widehat{L} \in R^{2 \times 2}$), we simply wish to find a linear transformation such that $\widehat{L} \left. \frac{\partial f}{\partial u_i} \right|_{T_u f} = - \left. \frac{\partial v}{\partial u_i} \right|_{T_u f} \quad \text{for } i = 1, 2 \text{ where}$

$- X|_{T_u f}$ denotes that $X \in T_u f$ is being represented in so-called 'local coordinates' for $T_u f$. (Strictly speaking, of course $T_u f \subset \mathbb{R}^3$ and thus $\frac{\partial f}{\partial u_i} \in \mathbb{R}^3$. Thus when we say $\frac{\partial f}{\partial u_i}|_{T_u f}$ we are referring to this 3-vector expanded with respect to the two-dimensional basis for $T_u f$). In matrix form, we describe this situation as

$$\left[\widehat{\mathbf{L}} \right] \begin{bmatrix} \left. \frac{\partial f}{\partial u_1} \right|_{T_u f} & \left. \frac{\partial f}{\partial u_2} \right|_{T_u f} \\ | & | \end{bmatrix} = \begin{bmatrix} \left. \widehat{\mathbf{L}} \frac{\partial f}{\partial u_1} \right|_{T_u f} & \left. \widehat{\mathbf{L}} \frac{\partial f}{\partial u_2} \right|_{T_u f} \\ | & | \end{bmatrix} \quad (2.20)$$

$$= \begin{bmatrix} | & | \\ -\frac{\partial v}{\partial u_1} \Big|_{T_u f} & -\frac{\partial v}{\partial u_2} \Big|_{T_u f} \\ | & | \end{bmatrix} \quad (2.21)$$

Now, representing each vector in $T_u f$ with respect to the basis $\left\{ \frac{\partial f}{\partial u_i} \right\}$, we have

$$\Rightarrow \left[\widehat{\mathbf{L}} \right] \begin{bmatrix} -\frac{\partial f}{\partial u_1} \\ -\frac{\partial f}{\partial u_2} \end{bmatrix} \begin{bmatrix} | & | \\ \frac{\partial f}{\partial u_1} & \frac{\partial f}{\partial u_2} \\ | & | \end{bmatrix} = \begin{bmatrix} -\frac{\partial f}{\partial u_1} \\ -\frac{\partial f}{\partial u_2} \end{bmatrix} \begin{bmatrix} | & | \\ -\frac{\partial v}{\partial u_1} & -\frac{\partial v}{\partial u_2} \\ | & | \end{bmatrix} \quad (2.22)$$

We can simplify this greatly by defining

$$g_{ij} := \langle \frac{\partial f}{\partial u_i}, \frac{\partial f}{\partial u_j} \rangle \quad \text{and} \quad h_{ij} := \langle \frac{\partial f}{\partial u_i}, -\frac{\partial v}{\partial u_j} \rangle \quad (2.23)$$

so that

$$\left[\widehat{\mathbf{L}} \right] \begin{bmatrix} g_{11} & g_{12} \\ g_{21} & g_{22} \end{bmatrix} = \begin{bmatrix} h_{11} & h_{12} \\ h_{21} & h_{22} \end{bmatrix} \quad (2.24)$$

Then we rearrange to solve for $\widehat{\mathbf{L}}$ as

$$\widehat{\mathbf{L}} = \begin{bmatrix} h_{11} & h_{12} \\ h_{21} & h_{22} \end{bmatrix} \begin{bmatrix} g_{11} & g_{12} \\ g_{21} & g_{22} \end{bmatrix}^{-1} \quad (2.25)$$

where $[g_{ij}]$ is clearly invertible, as the set $\left\{ \frac{\partial f}{\partial u_j} \right\}$ is linearly independent.

It should be noted that this matrix representation is accurate not only for the surface of a graph, but for any *generalized* surface $f : U \rightarrow \mathbb{R}^3$ with $u \mapsto (x(u), y(u), z(u))$ as well. We shall later show that this calculation simplifies (somewhat) in the case that our surface is a graph.

Our final goal is to characterize such normal curvatures. Namely, we wish to establish a method of determining in which directions an extremal normal curvature occurs.

Principal Curvatures and Principal Directions

To do so, we shall consider the relationship between the direction X and the normal curvature κ_v , definition 2.11 in that direction at some specified u .

First, we need the following lemma:

Lemma 2.4. *If $A \in R^{n \times n}$ is a symmetric real matrix, $v \in R^n$ and given the dot product $\langle \cdot, \cdot \rangle$, we have $\nabla_v \langle v, Av \rangle = 2Av$. In particular, when $A = I$ the identity matrix, we have $\nabla_v \langle v, v \rangle = 2v$.*

Proof. The result is uninterestingly obtained by tracking each (the ‘ith’) component of $\nabla_v \langle v, Av \rangle$:

$$(\nabla_v \langle v, Av \rangle)_i = \frac{\partial}{\partial v_i} [\langle v, Av \rangle] = \frac{\partial}{\partial v_i} \left[\sum_{j=1}^n v_j (Av)_j \right] \quad (2.26)$$

$$= \frac{\partial}{\partial v_i} \left[\sum_{j=1}^n v_j \sum_{k=1}^n a_{jk} v_k \right] \quad (2.27)$$

$$= \frac{\partial}{\partial v_i} \left[a_{ii} v_i^2 + v_i \sum_{k \neq i} a_{ik} v_k + v_i \sum_{j \neq i} a_{ji} v_j + \sum_{j \neq i} \sum_{k \neq i} v_j a_{jk} v_k \right] \quad (2.28)$$

$$= 2a_{ii}v_i + \sum_{k \neq i} a_{ik}v_k + \sum_{j \neq i} a_{ji}v_j + 0 \quad (2.29)$$

$$= 2a_{ii}v_i + 2 \sum_{k \neq i} a_{ik}v_k = 2 \sum_{k=1}^n a_{ik}v_k = 2(Av)_i \quad (2.30)$$

$$\implies \nabla_v \langle v, Av \rangle = 2Av. \quad (2.31)$$

□

We are now ready for the major result of this section, which ties the Weingarten map to the notion of normal curvatures.

Theorem 2.5 (Theorem of Olinde Rodrigues). *Fixing a point $u \in U$, a direction $X \in T_u f$ minimizes the normal curvature $\kappa_v = \langle LX, X \rangle$ subject to $\langle X, X \rangle = 1$ iff X is a (normalized) eigenvector of the Weingarten map L .*

Proof. In the following, we will assume that $X \in T_u f$ is expanded, in local coordinates, i.e. along a two dimensional basis (such as $\left\{ \frac{\partial f}{\partial u_i} \right\}_{i=1,2}$) and thus can refer to L freely as the 2×2 matrix \widehat{L} . Using the method of Lagrange multipliers, we define the Lagrangian:

$$\mathcal{L}(X; \lambda) := \langle \widehat{L}X, X \rangle - \lambda(\langle X, X \rangle - 1) \quad (2.32)$$

Extremal values occur when $\nabla_{X,\lambda} \mathcal{L}(X; \lambda) = 0$, which results in the two equations

$$\begin{cases} \nabla_X \langle \widehat{\mathcal{L}}X, X \rangle - \lambda \nabla_X (\langle X, X \rangle - 1) = 0 \\ \langle X, X \rangle - 1 = 0 \end{cases} \quad (2.33)$$

The second requirement is simply the constraint that X is normalized. Using the previous lemma, we can simplify the first result as follows:

$$\begin{aligned} \nabla_X \langle \widehat{\mathcal{L}}X, X \rangle - \lambda \nabla_X (\langle X, X \rangle - 1) &= 0 \\ 2\widehat{\mathcal{L}}X - \lambda(2X) &= 0 \\ \implies \widehat{\mathcal{L}}X - \lambda X &= 0 \\ \implies \widehat{\mathcal{L}}X &= \lambda X \end{aligned} \quad (2.34)$$

which implies that X is an eigenvector of $\widehat{\mathcal{L}}$ with corresponding eigenvalue λ ($X \neq 0$ from the second equation of eq. (2.33)). Thus the two hypotheses are exactly equivalent when X is normalized. It is also worth remarking that the corresponding eigenvalue λ is the Lagrangian multiplier itself. \square

Thus, to find the directions of greatest and least curvature of a surface at a point $u \in U$, we simply must calculate the Weingarten map and its eigenvectors. We refer to these directions as follows.

Definition 2.12 (Principal Curvatures and Principal Directions). *The extremal values of normal curvature of a surface at a point $u \in U$ are referred to as **principal curvatures**. The corresponding directions at which normal curvature attains an extremal value are referred to as **principal directions**.*

Our final goal is to explicitly determine a (hopefully simplified) version of the Weingarten map in the case of a graph $f(u_1, u_2) = (u_1, u_2, h(u_1, u_2))$ and calculate the

principal directions and curvatures in a simple example.

Theorem 2.6 (Relationship between Hessian and Weingarten Map of a Graph). *Given the graph $f : U \rightarrow \mathbb{R}^3$ where $(x, y) \mapsto (x, y, h(x, y))$, the matrix representation of its Weingarten map is given by*

$$\widehat{\mathbf{L}} = \text{Hess}(h)\tilde{G}, \quad \text{where } \tilde{G} := \frac{1}{\sqrt{1+h_x^2+h_y^2}} \begin{bmatrix} 1+h_y^2 & -h_x h_y \\ -h_x h_y & 1+h_x^2 \end{bmatrix} \quad (2.35)$$

In particular, given a point $u = (x, y) \in U \subset \mathbb{R}^2$ where $h_x \approx h_y \approx 0$, we have $\tilde{G} \approx \text{Id}$, and thus $\widehat{\mathbf{L}} \approx \text{Hess}(h)$.

Proof. First, we can (using chain rule) rewrite each component as in eq. (2.23):

$$h_{ij} = \left\langle \frac{\partial f}{\partial u_i}, -\frac{\partial v}{\partial u_j} \right\rangle = \left\langle \frac{\partial^2 f}{\partial u_i \partial u_j}, v \right\rangle$$

Now, given our particular surface f , we can calculate each of these components directly. We have:

$$\begin{aligned} f_x &= (1, 0, h_x), & f_y &= (0, 1, h_y) \\ f_{xx} &= (0, 0, h_{xx}), & f_{xy} &= (0, 0, h_{xy}) = f_{yx}, & f_{yy} &= (0, 0, h_{yy}) \end{aligned} \quad (2.36)$$

and we have the unit normal vector (Gauss map)

$$v(u_1, u_2) = \frac{\frac{\partial f}{\partial x} \times \frac{\partial f}{\partial y}}{\left\| \frac{\partial f}{\partial x} \times \frac{\partial f}{\partial y} \right\|} \quad (2.37)$$

$$= \frac{(1, 0, h_x) \times (0, 1, h_y)}{\|(1, 0, h_x) \times (0, 1, h_y)\|} \quad (2.38)$$

$$= \frac{(-h_x, -h_y, 1)}{\sqrt{h_x^2 + h_y^2 + 1}} \quad (2.39)$$

We then calculate each h_{ij} as

$$\begin{aligned} h_{11} &= \left\langle \frac{\partial^2 f}{\partial x^2}, v \right\rangle = \frac{h_{xx}}{\sqrt{1+h_x^2+h_y^2}} \\ h_{12} &= \left\langle \frac{\partial^2 f}{\partial x \partial y}, v \right\rangle = \frac{h_{xy}}{\sqrt{1+h_x^2+h_y^2}} = h_{21} \\ h_{22} &= \left\langle \frac{\partial^2 f}{\partial y^2}, v \right\rangle = \frac{h_{yy}}{\sqrt{1+h_x^2+h_y^2}} \end{aligned} \quad (2.40)$$

and thus the first matrix in eq. (2.25) is given by

$$[h_{ij}] = \frac{1}{\sqrt{1+h_x^2+h_y^2}} \text{Hess}(h) \quad (2.41)$$

To calcuate the second, we use

$$\begin{aligned} g_{ij} &= \left\langle \frac{\partial f}{\partial u_i}, \frac{\partial f}{\partial u_j} \right\rangle \\ g_{11} &= \langle f_x, f_x \rangle = 1 + h_x^2 \\ g_{12} &= \langle f_x, f_y \rangle = h_x h_y = g_{21} \\ g_{22} &= \langle f_y, f_y \rangle = 1 + h_y^2 \end{aligned} \quad (2.42)$$

and thus

$$[g_{ij}]^{-1} = \begin{bmatrix} 1+h_x^2 & h_x h_y \\ h_x h_y & 1+h_y^2 \end{bmatrix}^{-1} = \begin{bmatrix} 1+h_y^2 & -h_x h_y \\ -h_x h_y & 1+h_x^2 \end{bmatrix} \quad (2.43)$$

Combining $[h_{ij}]$ and $[g_{ij}]^{-1}$ from eq. (2.43) and eq. (2.41) we arrive at eq. (2.35). \square

Thus the matrix of the Weingarten map \widehat{L} is the Hessian matrix exactly at a critical point $u \in U$, where $\nabla h(u) = (h_x(u), h_y(u)) = 0$. Of course this implies that \widehat{L} and $\text{Hess}(h)$ have the same eigenvalues and eigenvectors at these points.

But this observation is more broadly useful than for analyzing critical points alone. If \tilde{G} above is close to identity, then the eigenvalues and eigenvectors of \widehat{L} will be similarly close to the eigenvalues of the Hessian. We can rewrite \tilde{G} from eq. (2.35) as identity plus a small matrix:

$$\tilde{G} = I + [\delta], \quad [\delta] := \begin{bmatrix} h_y^2 & -h_x h_y \\ -h_x h_y & h_x^2 \end{bmatrix} \quad (2.44)$$

We can then rewrite eq. (2.35) as

$$\widehat{L} = \frac{1}{\sqrt{1+h_x^2+h_y^2}} \text{Hess}(h) + \frac{1}{\sqrt{1+h_x^2+h_y^2}} \text{Hess}(h)[\delta] \quad (2.45)$$

We can see that as h_x, h_y are close to zero, $[\delta]$ will be very close to the zero matrix (and the constant $\frac{1}{\sqrt{1+h_x^2+h_y^2}}$ will be very close to 1 as well), and we should not expect the addition of a "close to 0" matrix to have much effect on the eigenvectors or eigenvalues. This intuition is confirmed by a result from Wilkinson [8], which we state without rigorous proof.

Theorem 2.7. *If A, B are matrices such that $|A_{ij}| < 1, |B_{ij}| < 1$ (a condition that can be ignored with scaling) and λ is a simple eigenvalue of A , then given $\epsilon > 0$, there exists a simple eigenvalue $\tilde{\lambda}$ of the matrix $A + \epsilon B$ with $|\lambda - \tilde{\lambda}| = O(\epsilon)$. Similarly, if v is an eigenvector of A , then \tilde{v} is an eigenvector of $A + \epsilon B$ with $|v - \tilde{v}| = O(\epsilon)$.*

The proof ultimately relies on a general result of analysis, that the zeros of a polynomial are continuous with respect to its coefficients. In this case, the polynomial in question is the characteristic polynomial $p(\lambda) = \det(\lambda I - A - \epsilon B)$, whose coefficients will scale with ϵ . Thus $\widehat{L} \approx \text{Hess}(h)$ for any point where the gradient $\nabla h \approx 0$. We shall see that we're only concerned with regions where h_x, h_y is small anyway, and we do not expect

much response anyway when the gradient is large.

From [9], we can bound the perturbation of eigenvalues from \widehat{L} to $\text{Hess}(h)$ by

Theorem 2.8. *Let A be a $n \times n$ normal matrix with eigenvalues $\lambda_1, \dots, \lambda_n$ and E an $n \times n$ arbitrary matrix. If $\hat{\lambda}$ is an eigenvalue of $A + E$, then there is an eigenvalue λ_i of A for which $|\hat{\lambda} - \lambda_i| \leq \|E\|_2$*

In the event that we do wish to rigorously compute the Weingarten map should want to be rigorously computed "without approximation"—that is, without concern for the magnitude of the gradient—we refer to [10] and survey papers mentioned therein.

To make the Weingarten map and its relationship to the Hessian more explicit, we will calculate the Weingarten map for a relatively simple graph.

The Weingarten map and Principal Curvatures of a Cylindrical Ridge

Let f be the graph given by

$$f : \mathbb{R}^2 \rightarrow \mathbb{R}^3 \text{ by } f(x, y) = (x, y, h(x, y)), \text{ with } h(x, y) = \begin{cases} \sqrt{r^2 - x^2} & -r \leq x \leq r \\ 0 & \text{else} \end{cases} \quad (2.46)$$

The graph is shown in fig. 2. We calculate the necessary partial derivatives of f as follows:

$$\frac{\partial f}{\partial x} = \left(1, 0, \frac{-x}{\sqrt{r^2 - x^2}} \right) \quad , \quad \frac{\partial^2 f}{\partial x^2} = \left(0, 0, \frac{-r^2}{(\sqrt{r^2 - x^2})^3} \right) \quad (2.47)$$

$$\frac{\partial f}{\partial y} = (0, 1, 0) \quad , \quad \frac{\partial^2 f}{\partial y^2} = \frac{\partial^2 f}{\partial x \partial y} = 0 \quad (2.48)$$



FIGURE 2: The graph of a cylindrical ridge of radius r

The gauss map is given by

$$\nu(x, y) = \frac{\frac{\partial f}{\partial x} \times \frac{\partial f}{\partial y}}{\left\| \frac{\partial f}{\partial x} \times \frac{\partial f}{\partial y} \right\|} = \left(\frac{x}{r}, 0, \frac{\sqrt{r^2 - x^2}}{r} \right) \quad (2.49)$$

$$\Rightarrow \frac{\partial \nu}{\partial x} = \left(\frac{1}{r}, 0, \frac{-x}{r \sqrt{r^2 - x^2}} \right) , \quad \frac{\partial \nu}{\partial y} = (0, 0, 0). \quad (2.50)$$

We then calculate matrix elements of the Weingarten map's construction as given

in eq. (2.41) and eq. (2.43) :

$$[h_{ij}] = \frac{1}{\sqrt{1+h_x^2+h_y^2}} \text{Hess}(h) = \frac{1}{\sqrt{1+\left(\frac{x^2}{r^2-x^2}\right)}} \begin{bmatrix} \frac{-r^2}{\sqrt{r^2-x^2}} & 0 \\ 0 & 0 \end{bmatrix} = \begin{bmatrix} \frac{-r}{r^2-x^2} & 0 \\ 0 & 0 \end{bmatrix} [g_{ij}]^{-1} = \begin{bmatrix} \frac{r^2-x^2}{r^2} & 0 & 0 \\ 0 & 1 \end{bmatrix} \quad (2.51)$$

$$\implies \widehat{L} = [h_{ij}] [g_{ij}]^{-1} = \begin{bmatrix} \frac{-r}{r^2-x^2} & 0 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{r^2-x^2}{r^2} & 0 & 0 \\ 0 & 1 \end{bmatrix} \quad (2.52)$$

$$= \begin{bmatrix} -\frac{1}{r} & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \quad (2.53)$$

We see that $u_2 = (0, 1)$ and $u_1 = (1, 0)$ are eigenvectors for \widehat{L} with respective eigenvalues $\kappa_2 = -\frac{1}{r}, \kappa_1 = 0$. Given the theorem of Olinde Rodriguez suggests that u_2 points in the direction of maximum curvature of the surface, $-\frac{1}{r}$, which is predictably in the direction directly perpendicular to the trough, whereas the direction of least curvature is along the trough and is 0. The theorem of Meusnier theorem 2.2 suggests that the normal curvature $\kappa_2 = -\frac{1}{r}$ is reasonable—any curve on the trough perpendicular to the ridge should have the curvature of a circle (the negative simply indicates that we are on the “outside” of the surface). Finally, we note that at the ridge of the trough is exactly where $\nabla f = 0$, and the Weingarten map is exactly the Hessian matrix there.

Viewing the surface in \mathbb{R}^3 , we define the Hessian $\text{Hess}(x, y)$ of the surface L at a point (x, y) on the surface as the matrix of its second partial derivatives:

$$\text{Hess}(x, y) = \begin{bmatrix} L_{xx}(x, y) & L_{xy}(x, y) \\ L_{yx}(x, y) & L_{yy}(x, y) \end{bmatrix} \quad (2.54)$$

At any point (x, y) we denote the two eigenpairs of the Hessian matrix of h as

$$\text{Hess}(x, y)u_i = \kappa_i u_i, \quad i = 1, 2 \quad (2.55)$$

where κ_i and u_i are known as the *principal curvatures* and *principal directions* of $L(x, y)$, respectively, and we label such that $|\kappa_2| \geq |\kappa_1|$. Notably, $\text{Hess}(x, y)$ is a real, symmetric matrix (since $L_{xy} = L_{yx}$ and L is a real function) and thus its eigenvalues are real and its eigenvectors are orthonormal to each other, as given by following basic result from linear algebra, [11]:

Lemma 2.9 (Principal Axis Theorem?). *Let A be a real, symmetric matrix. The eigenvalues of A are real and its eigenvectors are orthonormal to each other.*

Proof. Let $x \neq 0$ so that $Ax = \lambda x$. Then

$$\begin{aligned} \|Ax\|_2^2 &= \langle Ax, Ax \rangle = (Ax)^* Ax \\ &= x^* A^* Ax = x^* A^T Ax = x^* A A x \\ &= x^* A \lambda x = \lambda x^* A x \\ &= \lambda x^* \lambda x = \lambda^2 x^* x = \lambda^2 \|x\|_2^2 \end{aligned}$$

Upon rearrangement, we have $\lambda^2 = \frac{\|Ax\|_2^2}{\|x\|_2^2} \geq 0 \implies \lambda$ is real.

To prove that a set of orthonormalizable eigenvectors exists, let A be real, symmetric as above and consider the eigenpairs $Av_1 = \lambda_1 v_1, Av_2 = \lambda_2 v_2$ with $v_1, v_2 \neq 0$.

5 In the case that $\lambda_1 \neq \lambda_2$, we have

$$\begin{aligned} (\lambda_1 - \lambda_2)v_1^T v_2 &= \lambda_1 v_1^T v_2 - \lambda_2 v_1^T v_2 \\ &= (\lambda_1 v_1)^T v_2 - v_1^T (\lambda_2 v_2) \\ &= (Av_1)^T v_2 - v_1^T (Av_2) \\ &= v_1^T A^T v_2 - v_1^T A v_2 \\ &= v_1^T A v_2 - v_1^T A v_2 = 0 \end{aligned}$$

Since $\lambda_1 \neq \lambda_2$, we conclude that $v_1^T v_2 = 0$.

In the case that $\lambda_1 = \lambda_2 =: \lambda$, we can define (as in Gram-Schmidt orthogonalization) $u = v_2 - \frac{v_1^T v_2}{v_1^T v_1} v_1$. This is an eigenvector for $\lambda = \lambda_2$, as

$$\begin{aligned} Au &= A \left(v_2 - \frac{v_1^T v_2}{v_1^T v_1} v_1 \right) \\ &= Av_2 - \frac{v_1^T v_2}{v_1^T v_1} Av_1 \\ &= \lambda v_2 - \frac{v_1^T v_2}{v_1^T v_1} \lambda v_1 \\ &= \lambda \left(v_2 - \frac{v_1^T v_2}{v_1^T v_1} v_1 \right) = \lambda u \end{aligned}$$

and is perpendicular to v_1 , since

$$\begin{aligned} v_1^T u &= v_1^T \left(v_2 - \frac{v_1^T v_2}{v_1^T v_1} v_1 \right) \\ &= v_1^T v_2 - \left(\frac{v_1^T v_2}{v_1^T v_1} \right) v_1^T v_1 \\ &= v_1^T v_2 - v_1^T v_2 (1) = 0. \end{aligned}$$

□

Thus we see that the two principal directions form an orthonormal frame at each point (x,y) within the continuous image $L(x,y)$.

CHAPTER 3

THE UNISCALE FRANGI FILTER

We now seek to harness the ideas of this section to the task at hand: identifying curvilinear content within images.

The Frangi Filter: Uniscale

The Frangi filter, first described by Alejandro Frangi et al. in [12] is a widely used Hessian-based filter within image processing. Hessian-based filters make use of the logical “proximity” of the Hessian to notions of curvature of surfaces, as developed in section 2.2. Several such Hessian-based filters exist—see [13] and [14], as well as a comparison given in [15]. These filters use information about the principal curvatures, approximated as eigenvalues of the Hessian) at each point in the image to identify regions of significant curvature within an image.

Frangi’s filter was originally developed for vascular segmentation in images such as MRIs and it excels in that context.

The procedure for a single scale in a 2D image is as follows: Let λ_1, λ_2 be the two eigenvalues of the Hessian of the image at point (x, y) , ordered such that $|\lambda_1| \leq |\lambda_2|$, and define the Frangi vesselness measure as:

$$\mathcal{V}_o(x_0, y_0) = \begin{cases} 0 & \text{if } \lambda_2 > 0 \\ \exp\left\{-\frac{A^2}{2\beta^2}\right\} \left(1 - \exp\left\{-\frac{S^2}{2c^2}\right\}\right) & \text{otherwise} \end{cases} \quad (3.1)$$

where

$$A := |\lambda_1/\lambda_2| \quad \text{and} \quad S := \sqrt{\lambda_1^2 + \lambda_2^2} \quad (3.2)$$

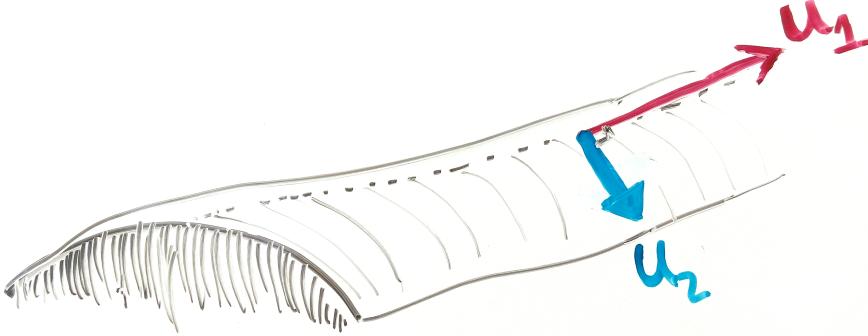


FIGURE 3: The principal eigenvectors at a ridge like structure

and β and c are tuning parameters. Before we discuss appropriate values for β and c , we first seek to highlight the significance of eq. (3.1), and in particular, the ratios defined in eq. (3.2). A and S are known as the anisotropy measure and structureness measure, respectively. Consequently, we'll refer to the two factors in eq. (3.1) as the anisotropy factor and structureness factor, respectively.

Anisotropy Measure

The anisotropy (or directionality) measure A is simply the ratio of magnitudes of λ_1 and λ_2 . Since at a ridge point of a tubular structure, we should have $\lambda_1 \approx 0$ and $|\lambda_2| \gg |\lambda_1|$, a very small value of A would be present at a ridge of a tubular structure.

In fig. 3, this situation is demonstrated. Here, u_1, u_2 form the orthogonal set of Hessian eigenvectors with corresponding eigenvalues λ_1 and λ_2 . At such a ridgelike structure, we could predict the largest change in curvature to be straight down the ridge (in the direction of u_2), and the direction of least curvature to be directly along the ridge (in the direction of u_1). $\lambda_1 \approx 0$ and λ_2 is large and negative.

Of course, if the the ridge is perfectly circular along its cross section (as was in section 2.2.4, it is of course apparent that λ_2 would be the same value at any place along the ridge (not just at its crest), and λ_1 would likewise be 0 at any such point. One could

also imagine a similar situation in which the dropoff from crest to bottom gets increasing steep. In such a case, λ_2 as a function of x would in fact be largest nearest to the bottom. This thought experiment should dispel a naïve misunderstanding of the power of a Frangi filter: a high anisotropy measure (and a large structureness measure) will not in general identify the crests of a ridge-like structure—it only will highlight that such a pixel is on a ridge-like structure at all. Thus, the anisotropy measure will not necessarily be at a maximum at the crest of the ridge, but instead, somewhere along it.

Similarly, the vessel we wish to identify can not be reasonably expected to behave as perfectly as our toy example. There will likely be small aberrations in a ridgelike structure, such as small divots or depressions in an overall ridge-like structure. Of importance in our data set later (section 8.1), there will be points where we seem to "lose" our ridgelike structure, but this is simply due to an error in the sample.

Importantly, this formulation does not require λ_1 to be approximately zero, just that the curvature in the downward direction is much more significant than in the transverse direction.

Also the crest could be really flat ("hangar shaped"), in which case both are around zero. At the crest of the ridge, we would actually expect both u_1 and u_2 to be around 0, whereas a point somewhere between the crest and the "foot" of the ridge to contain the maximum u_2 . We will fix this issue specifically by casting this as a multiscale problem in ??.

Two other ideas that could fix some other discrepancies mentioned above is to identify these ridges on their own, or also where the 'feet are'. We will discuss these ideas in section 12.1.

Structureness measure

There is another concern with using the pure ratio $S := |\lambda_1/\lambda_2|$ as an identifying feature of ridgelike structures apart from the ones listed above. We could have $|\lambda_2| \gg |\lambda_1|$

in a relative sense, but still have $\lambda_2 \approx 0$. As a rather extreme example, we should certainly wish to differentiate a point on the surface where $\lambda_2 \approx 10^{-5}$ and $\lambda_1 \approx 10^{-10}$ from another point where $\lambda_2 \approx 10000$ and $\lambda_2 = 0.1$.

A natural fix to differentiate these points is to introduce a “structureness” measure to insure that there is in fact significant curvilinear activity at the point in question. Frangi used $S := \sqrt{(\lambda_1)^2 + (\lambda_2)^2}$, which is in fact the Frobenius norm of the Hessian matrix. Thus the Frangi filter should also prefer areas of great curvilinear content in the image first of all.

The Frangi vesselness measure

Our goal then is to attach a numerical measure to each pixel in the image (at a particular scale σ) that is large when the anisotropy measure A and the structureness measure S is sufficiently large.

The form Frangi arrived at in eq. (3.1) in which a factor of $\exp\{\dots\}$ and $(1 - \exp\{\dots\})$ are multiplied together are simply to ensure that the final vesselness measure V is largest when A is small and S is large enough, with rapid decay in other situations.

Frangi further strengthened the filter by adding an additional case to in eq. (3.1), ensuring that λ_2 is not positive. If we are indeed at a curvilinear ridge, we need the second derivative of the surface in the maximal direction to be negative, which hasn't been accounted for as yet in our formulation of A and S – we wish (for our purposes) to only identify when we are finding crests. A will still be small and S will still be large however if we identify a “trough”.

The only perceivable difference is that the maximum normal curvature will be positive—we are at a local minimum in the direction of u_2 . In situations where we wish to only identify ridges (as is the case here) we simply exclude any points where there is not a negative curvature in the maximal direction. Conversely, we could only seek to find valley, or local minima, as thus require $\lambda_2 > 0$, and set the vesselness measure to zero

when $\lambda_2 < 0$.

Choosing parameters β and c

The parameters β and c are meant to scale so that the peaks of the anisotropy factor $\exp\left\{\frac{-A^2}{2\beta^2}\right\}$ and the structureness factor $(1 - \exp\left\{\frac{-S^2}{2c^2}\right\})$ coincide enough to be statistically significant at highly curvilinear structures, but rapidly decay in areas not associated with curvilinear content. What values of these parameters are appropriate is ultimately dependent on the context of the problem.

Frangi suggested for c that half of (the Frobenius norm of the) Hessian matrix is appropriate, simply because the minimum value of S is zero, and its maximum value is exactly the max Frobenius norm. With this in mind we would like to introduce the scaling factor γ , so that $c = \gamma S_{\max}$. This creates a minor annoyance though: although the anisotropy factor can certainly attain a value of 1, if c is to take this “appropriate” value, the maximum value of the structureness factor is somewhat smaller than 1. In fact,

$$\begin{aligned} \max\{\mathcal{V}_\sigma\} &\leq \max\left(\exp\left\{\frac{-A^2}{2\beta^2}\right\}\right) \max\left(\left(1 - \exp\left\{\frac{-S^2}{2(\gamma S_{\max})^2}\right\}\right)\right) \\ &\leq \max\left\{\left(1 - \exp\left\{\frac{-S^2}{2(\gamma S_{\max})^2}\right\}\right)\right\} \\ &= \left(1 - \exp\left\{\frac{-(S_{\max})^2}{2(\gamma S_{\max})^2}\right\}\right) = \left(1 - \exp\left\{\frac{-1}{2\gamma^2}\right\}\right) \end{aligned} \tag{3.3}$$

Thus, when γ takes the suggested value of $\gamma = 1/2$, the above calculation suggests that the maximum theoretical value that the Frangi filter could attain at any scale is $\max\{\mathcal{V}_\sigma\} \leq 1 - \exp\{-1\} \approx .8647$. This (among other obvious reasons) certainly justifies Frangi’s description of the vesselness measure as only “probability-like.” Still, we would like the filter’s sensitivity to relative structureness to not have the effect of dampening the Filter as a whole, so we will introduce a rescaling factor a_γ , which is a explicit function of γ that rescales \mathcal{V}_σ so that the structureness factor has a maximum output score of 1 regardless of choice of γ . Our final Frangi vesselness measure is thus

$$\mathcal{V}_\sigma(x_0, y_0) = \begin{cases} 0 & \text{if } \lambda_2 > 0 \\ a_\gamma \exp\left\{\frac{-A^2}{2\beta^2}\right\} \left(1 - \exp\left\{\frac{-S^2}{2(\gamma S_{\max})^2}\right\}\right) & \text{otherwise} \end{cases} \quad (3.4)$$

where, as before,

$$A := |\lambda_1/\lambda_2|, S := \sqrt{\lambda_1^2 + \lambda_2^2} \text{ and } a_\gamma = \left(1 - \exp\left(\frac{-1}{2\gamma^2}\right)\right)^{-1}$$

and

$$|\lambda_1| \leq |\lambda_2| \text{ are eigenvalues of } \text{Hess}_\sigma(I(x_0, y_0))$$

For β , Frangi suggested an innocuous intermediate point, $\beta = 1/2$ (and thus $2\beta^2 = 1/2$). As we will show later, choosing the structureness parameter γ is rather important for the context especially if the background (non-ridgelike structure) is significant and noisy. β should be strengthened/relaxed depending on how “flat” the ridgelike structure is. We shall show empirically that contexts in which more ‘bloblike’ structures are known to be present than that for which the Frangi filter was originally designed, we will benefit from a smaller choice of β .

Considering as the anisotropy measure $|\lambda_1/\lambda_2| \in [0, 1]$ (simply since $|\lambda_1| \leq |\lambda_2|$), we can actually visualize how much the anisotropy factor varies depending on our choice of β , as seen in fig. 4.

We can theoretically choose any values $0 < \beta, \gamma < \infty$ for the two parameters. Two particular limits are of theoretical interest: as $\beta \rightarrow \infty$, the anisotropy factor tends to 1, and as $\gamma \rightarrow 0$, the structureness factor tends to 1, making the that measure entirely irrelevant. (Of course, in the limit that $\beta \rightarrow 0$ or $\gamma \rightarrow \infty$, their respective factors become 0, making the entire filter irrelevant). We will

We make a similar presentation of the dependence of the structureness kernel on its parameter γ , as you can see in fig. 5.



FIGURE 4: Dependence of the Anisotropy Factor on its Parameter

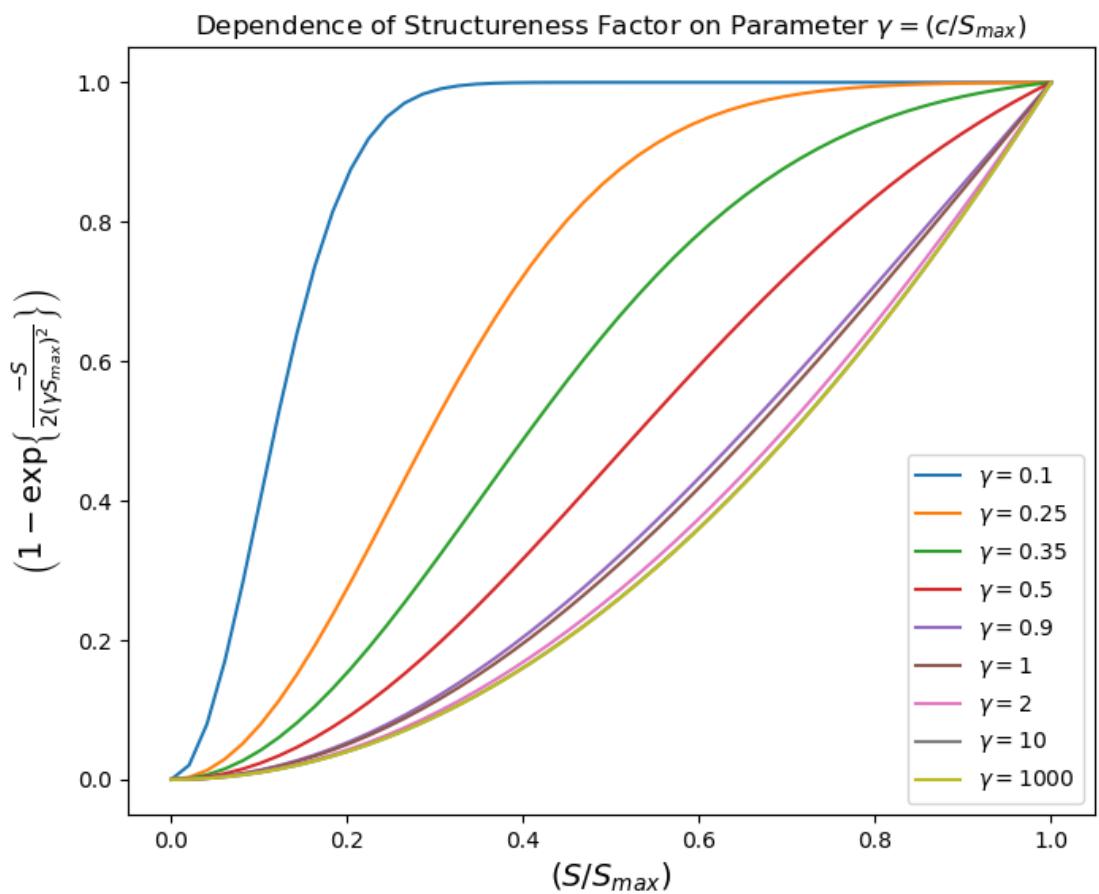


FIGURE 5: Dependence of the Structureness Factor on its Parameter

The ultimate choice of these parameters β and γ have the overall effect of tuning the selectivity of the Frangi filter itself. In the figures in appendix B, we plot the Frangi vesselness measure itself as a function of S and A while sweeping through different choices of β and γ .

We now take a quick tangent from our description of the Frangi filter to develop and justify our “multiscale” approach.

CHAPTER 4

LINEAR SCALE SPACE THEORY

Although the ideas presented above require differentiation of continuous surfaces, our image is in fact composed of discrete pixels. That is, our previous discussions have been in terms of an image as the continuous surface in definition 2.2, rather than the more realistic discrete pixel matrix as in definition 2.1. The present section seeks to address this disconnect. Divided differences can serve as an analogue of differentiation in discrete contexts, but our "derivative" and any use of it is then completely dependent on the bias of our limited sampling of the "true" 3D surface. Our main goal is to counter against some of the bias of our particular sampling. In particular, we wish to not over-represent structures that are clear at our resolution without giving appropriate weight to larger structures as well. Ideally, we would like statements we make about higher order phenomena to be stable enough at least that we would arrive at the same conclusions from analyzing a higher resolution image of the same surface. Koenderink [16] argued that "any image can be embedded in a one-parameter family of derived images (with resolution as the parameter) in essentially only one unique way" given a few of the so-called scale space axioms. He (and others) showed that a small set of intuitive axioms imply that any such family of images $\{K_\sigma\}$ must satisfy the heat equation

$$\begin{cases} \Delta K(x, y; \sigma) = \frac{\partial K}{\partial \sigma}(x, y; \sigma) \text{ for } \sigma \geq 0 \\ K(x, y, 0) = u_0(x, y) \end{cases} \quad (4.1)$$

where $u_0 : \mathbb{R}^2 \rightarrow \mathbb{R}$ is the original image (viewed as a continuous surface), σ is the resolution parameter, and $K : \mathbb{R}^2 \rightarrow \mathbb{R}$ for each fixed σ .

This result is intuitive and desirable—we would anticipate a lower-resolution version of our original image to represent a diffusion or “blurring” of the initial scales information. Much work has been done to formalize this approach [17]. This has resulted in various formulations of a minimal set of axioms from which all other desirable properties of the scale space can be derived, culminating eventually in the necessity and sufficiency of eq. (4.1) itself. We will refrain from such an exhaustive development in the present text, but rather list some desirable properties and outline the approach.

Properties/Axioms of Linear Scale Space Theory

To make matters manageable, we require the one-parameter family to be generated by an operator on the original image:

$$\{ K(x, y; \sigma) = T_\sigma u_0 \mid \sigma \geq 0, K(x, y; 0) = u_0 \} \quad (4.2)$$

The following axioms are then requirements on what sort of operation T_σ should be.

Axiom 4.1 (Linear-shift and Rotational Invariance). *We require that no position in the original signal is favored. This is intuitive, as our operation should apply to any image fairly, regardless of where content is found in the image, and cropping or rotating our initial image should not affect resolution of the content.*

Axiom 4.2 (Semigroup property). *The semigroup property is simply that transforming the original image by some resolution σ should have the same overall effect of two successive transformations σ_1 and σ_2 , i.e.*

$$T_\sigma u = T_{\sigma_1 + \sigma_2} u \quad (4.3)$$

Axiom 4.3 (Continuity of Scale Parameter). *There is no reason for the scale parameter to be discrete; we may alter the resolution with whatever precision we desire. That is, we take the*

resolution parameter σ to be any nonzero real number. Moreover, we require that the operator behaves continuously with respect to the scale parameter.

The following requirement has great implication, and is also very successful in encoding our intuitive sense of resolution.

Axiom 4.4 (Causality Condition). *The causality condition is the one that, as resolution decreases, no finer detail is introduced into the image. That is, as the scale increases, there will be no creation of local extrema that did not exist at a smaller scale.*

To make this more precise, if $K(x_0, y_0; \sigma_0)$ (that is, a point (x_0, y_0) at some particular resolution σ_0) is a local maximum at that resolution, then an increase in scale cannot make this maximum more prominent, i.e.

$$\begin{cases} \nabla K(x_0, y_0; \sigma_0) = 0 \\ \Delta K(x_0, y_0; \sigma_0) < 0 \end{cases} \implies K(x_0, y_0; \sigma_1) \leq K(x_0, y_0; \sigma_0) \forall \sigma_1 \geq \sigma_0 \quad (4.4)$$

Similarly, if $K(x_0, y_0; \sigma_0)$ is a local minimum (with respect to space), then an increase in scale cannot make such a valley more profound, i.e.

$$\begin{cases} \nabla K(x_0, y_0; \sigma_0) = 0 \\ \Delta K(x_0, y_0; \sigma_0) > 0 \end{cases} \implies K(x_0, y_0; \sigma_1) \geq K(x_0, y_0; \sigma_0) \forall \sigma_1 \geq \sigma_0 \quad (4.5)$$

This encodes our intuition that no image feature should be sharpened by a decrease in resolution. The only result is a (non-strictly) monotonic blurring of the image as scale parameter σ tends to infinity.

Sufficiency of the Gaussian Kernel

Although we will omit it here, the above requirements are actually sufficient in proving not only that the operator T_σ is a convolution, but that the heat equation described in eq. (4.1) must hold. This has been shown in various ways, both by

Koenderink [16], Babaud [18], as well as Lindeberg in [17]. Of course, once eq. (4.1) has been established, it is straightforward to show that

$$K(x, y; \sigma) = T_\sigma u_0 = G_\sigma \star u_0 \quad \text{where} \quad G_\sigma := \frac{1}{2\pi\sigma^2} e^{(-|x|^2/(2\sigma^2))} \quad (4.6)$$

is a solution. That is, the family can be generated by convolution with a Gaussian kernel. Lindeberg and others furthered this by arguing that fT_σ 's continuity as σ approaches zero ultimately implies that convolution by a Gaussian is the *unique* operator that generates this scale space.

Scale Spaces over Discrete Structures

The above developments from scale space axioms have (since their first appearance) been recast in terms of discrete structures (rather than continuous surfaces) as in [19]. However, we've chosen to present the above in their original continuous surface for clarity of argument. The discrete case is not much different— we still have the same axioms, and it can be shown that the family of scaled images must simply satisfy a discrete version of the heat equation. However, viewing our actual image definition 2.1 as a sample of a continuous surface definition 2.2, we might expect our convolution by the Gaussian to “commute” with our supposed sampling of the continuous signal, or even that we could simply convolve our discrete signal with a discretely sampled Gaussian kernel. The latter in fact, seems to be an often implemented interpretation of scale space theory.

To be clear, the “sampled” 1D Gaussian Kernel we have in mind might be given by:

Definition 4.1 (Sampled Gaussian Kernel and Generated Family).

$$g(n; \sigma) = \frac{1}{2\pi\sigma} e^{-n^2/2\sigma}, \quad -\infty < n < \infty$$

and the resulting (1D) convolution would be given by

$$K(x, \sigma) = \sum_{n=-\infty}^{\infty} g(n; \sigma) f(x-n) \quad \text{for } x \in \mathbb{Z}, \sigma > 0$$

In [19] and in particular [20], Lindeberg demonstrated that the sampled Gaussian kernel violates not only semigroup property (axiom 4.2), but—much less forgivably—the causality property (axiom 4.2). There is absolutely no guarantee that convolution with a sampled Gaussian kernel will not create “spurious” structures as resolution increases.

Fortunately, Lindeberg was immediately able to remedy this by providing a discrete analogue of the Gaussian kernel, which does satisfy axiom 4.4 and axiom 4.2:

Definition 4.2 (Discrete Gaussian Kernel). *The discrete Gaussian kernel, which can be shown to be a suitable generator for scale space, is given by*

$$T(n; \sigma) = e^{-\alpha\sigma} I_n(\alpha\sigma), \quad I_n(\sigma) = I_{-n}(\sigma) = (-1)^n J_n(i\sigma) \quad n \geq 0, \sigma, \alpha > 0 \quad (4.7)$$

where I_n are the modified Bessel functions of integer order based on the ordinary Bessel functions J_n , i.e.

$$I_n(x) = \sum_{m=0}^{\infty} \frac{1}{m!(m+n)!} \left(\frac{x}{2}\right)^{2m+n}, \quad n \geq 0$$

where we have taken the liberty of simplifying the typical definition [21] (which involves the gamma function), since we only desire Bessel functions of integer order. The parameter α above is simply an optional scaling parameter which is simply set to 1 hereforth.

The derived family of 1D signals is then given by

$$K(x, \sigma) = \sum_{n=-\infty}^{\infty} T(n; \sigma) f(x-n) \quad \text{for } x \in \mathbb{Z}, \sigma > 0 \quad (4.8)$$

The compatibility of scale space theory and derivatives on discrete structures and extension to two dimensions was also demonstrated by Lindeberg in [22] and [23]. In particular, we may take derivatives of the convolutions of our discrete images using, say, a local central difference. Lastly, the 2D version of the family given in eq. (4.8) can be obtained by independent convolution of its dimensions (i.e. it is separable). We will make these ideas explicit in ??.

CHAPTER 5

THE MULTISCALE FRANGI FILTER AND SIGNED FRANGI FILTER

With the ideas of scale established, we may return to our discussion of the Frangi filter. Our ideas of scale developed in the previous section imply that, if the ridgelike structures we wish to detect are more prominent at different scales, then a multiscale approach is the natural one. Considering the dependence of the Frangi filter's response on choice of scale (as demonstrated in section 3.1), we wish to probe at multiple scales regions that would receive a high vesselness score at any range and somehow merge the result. Frangi [12] approached this problem by simply taking the maximum vesselness measure over all scales. Thus the multiscale Frangi vesselness score at the pixel (x_0, y_0) would be

$$\mathcal{V}_{\max}(x_0, y_0) = \max_{\sigma \in \Sigma} \{\mathcal{V}_\sigma(x_0, y_0)\} \quad (5.1)$$

where $\Sigma := \{\sigma_0, \sigma_1, \dots, \sigma_N\}$ is the set of scales at which to probe, and \mathcal{V}_σ is the Frangi vesselness measure at scale σ for the pixel (x_0, y_0) . The set of scales Σ should be chosen to be representative enough of all scales where meaningful content is expected to be found.

Rudimentary Thresholding

After the maximization in eq. (5.1), we are left with a matrix with as many pixels as the original image, all with a vesselness measure between 0 and 1 for each pixel in the image.

At this point, Frangi [12] refrained from explicitly interpreting the score assigned by eq. (5.1); that is—whether a particular pixel (x_0, y_0) in the image definitely represents a vessel or not based on its Frangi score. Instead, he cautioned that the result should not

be used as a segmentation method alone, and moreover that the width of the vasculature cannot be determined rigorously from the Frangi filter (as discussed in chapter 3).

Nonetheless, we wish to demonstrate the usefulness of the Frangi filter within our image domain towards segmentation. We should at least expect that a well-tuned Frangi filter (on an appropriately registered and denoised sample) should assign its highest scores to vessel pixels. We can select these strong Frangi responses and use them as seeds for some subsequent algorithm. A straightforward enough approach would be to simply threshold at some fixed value α . Such thresholding was used in [2].

$$\mathcal{V}_{\Sigma\alpha}(x_0, y_0) = \begin{cases} 1 & \text{if } \mathcal{V}_{\max}(x_0, y_0) \geq \alpha \\ 0 & \text{else} \end{cases}, \quad \alpha > 0 \text{ for } \alpha \text{ fixed.} \quad (5.2)$$

If we insist on such a performing such a thresholding, the “correct” choice of α unfortunately seems to depend on the image domain, so user intervention when dealing with the problem domain seems to be the best strategy. We would hope that some normalization of our data set would permit a single choice of α across all samples, but unfortunately we cannot guarantee this. Without prior knowledge of an appropriate choice of α , we may have to simply select α by trial and error.

A good alternative method of thresholding would be to simply select the highest scores from each responses: we calculate a high percentile score and threshold at that value. Due to the large number of zeros outputted by the filter, we opt instead to take the q th percentile of only nonzero values of V_{Σ} . We briefly demonstrate this in fig. 32 on a particularly well-behaved sample. The top left value image is the base image, the top right is \mathcal{V}_{\max} , the bottom left is \mathcal{V}_{\max} thresholded at the 95th percentile, and the bottom left is thresholded at the 98th percentile.

Of course, the downside of this method is that we do not know in general the size of the network, and we may miss entire branches of the vascular network if there is a

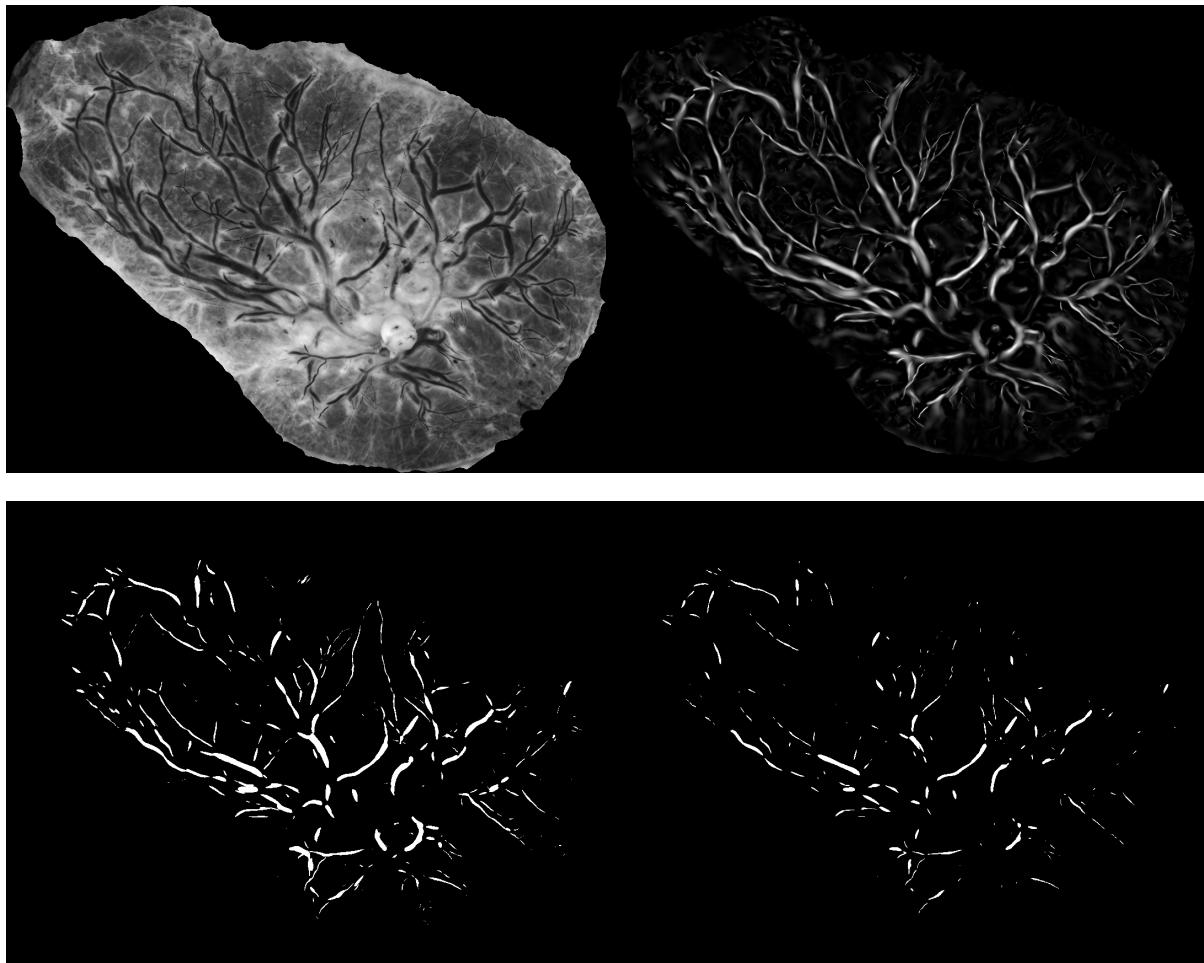


FIGURE 6: Nonzero-percentile thresholding of \mathcal{V}_{\max} (95th and 98th percentile)

large amount of curvilinear content elsewhere in the image.

We will discuss alternatives methods of aggregating results from our multiscale method, as well as optimal values for parameters and scales in chapter 10. As a final note, we admit that any future extensions of this work (as will be discussed in chapter 12) need not proceed from either of these thresholdings; analyzing the raw vesselness score \mathcal{V}_{\max} , or even the un-merged scale-wise scores may prove far more rewarding.

The Signed Frangi Filter

We finally introduce the novel (yet straightforward) notion of the signed Frangi filter. As will be shown in chapter 10, we can benefit from simultaneously calculate for a dark background and a light background. Since the Frangi filter normally throws away any response where $\lambda_2 < 0$ (if dark curvilinear features are targeted) or $\lambda_2 > 0$ (if light curvilinear features are targeted), we lose no computation time at all (although we must store more results). After computing the multiscale result, we can easily separate these into a positive and a negative strain, which we will denote $\mathcal{V}_{\max}^{(+)}$ and $\mathcal{V}_{\max}^{(-)}$. Our $\mathcal{V}_{\max}^{(+)}$ is the same as our \mathcal{V}_{\max} before, and $\mathcal{V}_{\max}^{(-)}$ is the same result as if we had taken the Frangi filter while only looking for the opposite type (light/dark) curvilinear feature. Plotting \mathcal{V}_{\max} over a scale of $[-1, 1]$ demonstrates an interesting effect. Whereas the Frangi filter generally is not reliable in terms of accurately predicting widths of through-like (or ridge-like) curvilinear features, by somehow combining the results of our positive and negative strains. We *can* get a sense of the width by looking at where there is a relatively strong response of opposite sign.

All that remains to describe mathematically is how to actually calculate the derivatives of our images and deal with the ultimately discrete nature of our samples.

CHAPTER 6

FFT-BASED DISCRETE DERIVATIVES

According to section 4.0.3, we may calculate derivatives of our structure by calculating a gradient on our convolved image. Our method of calculating the gradient of a matrix uses a second-order accurate central difference, as in [24].

We note in passing that we may take the derivative of the Gaussian kernel and then convolve it, and the effect will be the same as if we had taken the derivative subsequently [6]. This could offer some computational speedup if we wish to run this procedure on many samples and fixed scale sizes, although we have implemented our scale spaces in the conventional way, as discussed in ??.

Convolution Speedup via FFT

In practice, the convolutions described above are very slow for large scales (σ), as the size of the kernel is very large. Instead, we will perform a fast Fourier transform, which requires only $\mathcal{O}(N \cdot \log_2 N)$ operations for a one dimension signal of length N , as compared to the N^2 operations required of a conventional discrete Fourier transform [6]. We will briefly outline the theory of Fourier transforms.

Fourier Transform of a continuous 1D signal .

A periodic signal (real valued function) $f(t)$ of period T can be expanded in an infinite basis as follows:

$$f(t) = \sum_{-\infty}^{\infty} c_n e^{i \frac{2\pi n}{T} t}, \quad c_n = \frac{1}{T} \int_{-T/2}^{T/2} f(t) e^{-i \frac{2\pi n}{T} t} dt \quad (6.1)$$

The Fourier transform of a 1D continuous function is defined by

$$F(\mu) := \mathcal{F}\{f(t)\} = \int_{-\infty}^{\infty} f(t)e^{j2\pi\mu t} dt \quad (6.2)$$

An inverse transform will then recover our original signal:

$$f(t) = \mathcal{F}^{-1}\{F(\mu)\} = \int_{-\infty}^{\infty} F(\mu)e^{j2\pi\mu t} dt \quad (6.3)$$

Together, eq. (6.2) and eq. (6.3) are referred to as the *Fourier transform pair* of the signal $f(t)$.

Fourier Transform of a Discrete 1D signal .

We wish to develop the Fourier transform pair for a discrete signal., following [6].

We frame the situation as follows: a continuous function $f(t)$ is represented as the sampled function $\tilde{f}(t)$ by multiplying it by a sampling (or impulse) function, an infinite series of discrete impulses with equal spacing ΔT :

$$s_{\Delta T}(t) := \sum_{n=-\infty}^{\infty} \delta[t - n\Delta T], \quad \delta[t] = \begin{cases} 1, & t = 0 \\ 0, & t \neq 0 \end{cases} \quad (6.4)$$

where $\delta[t]$ is the discrete unit impulse.

The discrete sample $f(t)$ is then constructed from $f(t)$ by

$$\tilde{f}(t) = f(t)s_{\Delta T}(t) \quad (6.5)$$

From this we can calculate $\tilde{F}(t)$. Given the discrete signal \tilde{f} , we construct the transform $\tilde{F}(\mu) = \mathcal{F}\{\tilde{f}(t)\}$. by expanding \tilde{f} in the same infinite basis as the continuous

case.

$$\tilde{F}(\mu) = \sum_{n=-\infty}^{\infty} f_n e^{-i2\pi\mu n \Delta T}, \quad f_n = \tilde{f}(n) = f(n\Delta T) \quad (6.6)$$

The transform is a continuous function with period $1/\Delta T$.

2D DFT Convolution Theorem .

Theorem 6.1 (2D DFT Convolution Theorem). *Given two discrete functions are sequences with the same length. $f(x, y)$ and $h(x, y)$ for integers $0 < x < M$ and $0 < y < N$, we can take the discrete fourier transform (DFT) of each:*

$$F(u, v) := \mathcal{D}\{f(x, y)\} = \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} f(x, y) e^{-2\pi i (\frac{ux}{M} + \frac{vy}{N})} \quad (6.7)$$

$$H(u, v) := \mathcal{D}\{h(x, y)\} = \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} h(x, y) e^{-2\pi i (\frac{ux}{M} + \frac{vy}{N})} \quad (6.8)$$

and given the convolution of the two functions

$$(f \star h)(x, y) = \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} f(m, n) h(x - m, y - n) \quad (6.9)$$

then $(f \star h)(x, y)$ and $MN \cdot F(u, v)H(u, v)$ are transform pairs, i.e.

$$(f \star h)(x, y) = \mathcal{D}^{-1}\{MN \cdot F(u, v)H(u, v)\} \quad (6.10)$$

The proof follows from the definition of convolution, substituting in the inverse-DFT of f and h , and then rearrangement of finite sums.

Proof.

$$(f \star h)(x, y) = \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} f(m, n)h(x-m, y-n) \quad (6.11)$$

$$= \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} \left(\sum_{p=0}^{M-1} \sum_{q=0}^{N-1} F(p, q) e^{2\pi i (\frac{mp}{M} + \frac{nq}{N})} \right) \left(\sum_{u=0}^{M-1} \sum_{v=0}^{N-1} H(u, v) e^{2\pi i (\frac{u(x-m)}{M} + \frac{v(y-n)}{N})} \right) \quad (6.12)$$

$$= \left(\sum_{u=0}^{M-1} \sum_{v=0}^{N-1} H(u, v) e^{2\pi i (\frac{ux}{M} + \frac{vy}{N})} \right) \left(\sum_{p=0}^{M-1} \sum_{q=0}^{N-1} F(p, q) \left(\sum_{m=0}^{M-1} e^{2\pi i (\frac{m(p-u)}{M})} \right) \left(\sum_{n=0}^{N-1} e^{2\pi i (\frac{n(q-v)}{N})} \right) \right) \quad (6.13)$$

$$= \left(\sum_{u=0}^{M-1} \sum_{v=0}^{N-1} H(u, v) e^{2\pi i (\frac{ux}{M} + \frac{vy}{N})} \right) \left(\sum_{p=0}^{M-1} \sum_{q=0}^{N-1} F(p, q) (M \cdot \hat{\delta}_M(p-u)) (N \cdot \hat{\delta}_M(q-v)) \right) \quad (6.14)$$

$$= \left(\sum_{u=0}^{M-1} \sum_{v=0}^{N-1} H(u, v) e^{2\pi i (\frac{ux}{M} + \frac{vy}{N})} \right) \cdot MNF(u, v) \quad (6.15)$$

$$= MN \cdot \sum_{u=0}^{M-1} \sum_{v=0}^{N-1} F(u, v) H(u, v) e^{2\pi i (\frac{ux}{M} + \frac{vy}{N})} \quad (6.16)$$

$$= MN \cdot \mathcal{D}^{-1} \{ FH \} \quad (6.17)$$

where

$$\hat{\delta}_N(k) = \begin{cases} 1 & \text{when } k = 0 \pmod{N} \\ 0 & \text{else} \end{cases} \quad (6.18)$$

□

Above, we make use of the following lemma

Lemma 6.2. Let j and k be integers and let N be a positive integer. Then

$$\sum_{n=0}^{N-1} e^{2\pi i \left(\frac{n(j-k)}{N} \right)} = N \cdot \hat{\delta}_N(j-k) \quad (6.19)$$

Proof. Consider the complex number $e^{2\pi i(j-k)/N}$. Note first that this is an N -th root of unity, since

$$\left(e^{2\pi i(j-k)/N}\right)^N = e^{2\pi i(j-k)} = \left(e^{2\pi i}\right)^{(j-k)} = 1^{(j-k)} = 1$$

In other words, $e^{2\pi i n(j-k)/N}$ is a root of $z^N - 1 = 0$, which we can factor as

$$z^N - 1 = (z - 1)(z^{n-1} + \dots + z + 1) = (z - 1) \sum_{n=0}^{N-1} z^n. \quad (6.20)$$

thus giving us

$$0 = \left(e^{2\pi i(j-k)/N} - 1\right) \sum_{n=0}^{N-1} e^{2\pi i n(j-k)/N} \quad (6.21)$$

To prove the claim in eq. (6.19), we consider two cases: First, if $j - k$ is a multiple of N , we of course have $e^{2\pi i n(j-k)/N} = \left(e^{2\pi i}\right)^{n(j-k)/N} = 1$ and thus the left side of eq. (6.19) reduces to

$$\sum_{n=0}^{N-1} \left(e^{2\pi i}\right)^{n(j-k)/N} = \sum_{n=0}^{N-1} (1) = N$$

In the case that $j - k$ is *not* a multiple of N , we refer to eq. (6.21). The first factor is not zero since, $\left(e^{2\pi i(j-k)/N}\right) \neq 1$ (simply since $(j - k)/N$ is not an integer), and thus it must be that the second factor is 0:

$$\sum_{n=0}^{N-1} \left(e^{2\pi i(j-k)/N}\right)^n = 0$$

We can combine these two cases by invoking the definition of eq. (6.18), giving us the result. \square

FFT

As noted, the above result applies to the Discrete Fourier Transform. We actually achieve a convolution speedup using a Fast Fourier Transform (FFT) instead. We follow the developments of [6]. For clarity, we present the following theorems which allow a

framework to calculate a 2D Fourier transforms quickly.

First, a 2D DFT may actually be calculated via two successive 1D DFTs, which can be seen through a basic rearrangement, as follows:

$$F(\mu, \nu) = \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} f(x, y) e^{-i2\pi(\mu x/M + \nu y/N)} \quad (6.22)$$

$$= \sum_{x=0}^{M-1} e^{-i2\pi\mu x/M} \left[\sum_{y=0}^{N-1} f(x, y) e^{-i2\pi\nu y/N} \right] \quad (6.23)$$

$$= \sum_{x=0}^{M-1} e^{-i2\pi\mu x/M} \mathcal{F}_x\{f(x, y)\} \quad (6.24)$$

$$= \mathcal{F}_y\{\mathcal{F}_x\{f(x, y)\}\} \quad (6.25)$$

where $\mathcal{F}_{x'}$ refers to the 1D discrete Fourier transform of the function with respect to the variable x' only.

Thus, to calculate the fourier transform $F(u, v)$ at the point u, v requires the computation of the transform of length N for each iterated point $x \in 0, \dots, M-1$. Thus there are MN complex multiplications and $(M-1)(N-1)$ complex additions in this sequence required for each point u, v that needs to be calculated. Overall, for all points that need to be calculated, the total order of calculations is on the order of $(MN)^2$. We'll also mention that the values of $e^{-i2\pi m/n}$ can be provided by a lookup table rather than ad-hoc calculation.

We now show that a considerable speedup can be achieved through elimination of redundant calculations. In particular, we wish to show that the calculation of a 1D DFT of signal length $M = 2^n, n \in \mathbb{Z}_+$ can be reduced to calculating two half-length transforms and an additional $M/2 = 2^{n-1}$ calculations.

To "simplify" our notation we will use a new notation for the Fourier kernels/basis

functions. Let the 1D Fourier transform be given by

$$F(u) = \sum_{x=0}^{M-1} f(x) W_M^{ux}, \quad \text{where} \quad W_m := e^{-i2\pi/m} \quad (6.26)$$

We'll define $K \in \mathbb{Z}_+ : 2K = M = 2^n$ (i.e. $K = 2^{n-1}$).

We use this to rewrite the series in eq. (6.26) and split it into odd and even entries in the summation

$$F(u) = \sum_{x=0}^{2K-1} f(x) W_{2K}^{ux} \quad (6.27)$$

$$= \sum_{x=0}^{K-1} f(2x) W_{2K}^{u(2x)} + \sum_{x=0}^{K-1} f(2x+1) W_{2K}^{u(2x+1)} \quad (6.28)$$

We'll get a few identities out of the way (where $m, n, x \in \mathbb{Z}_+$ arbitrary).

$$W_{(2m)}^{(2n)} = e^{\frac{-i2\pi(2m)}{2m}} = e^{\frac{-i2\pi m}{n}} = W_m^n \quad (6.29)$$

$$W_m^{(u+m)x} = e^{\frac{-i2\pi(u+m)x}{m}} = e^{\frac{-i2\pi unx}{m}} e^{\frac{-i2\pi mx}{m}} = e^{\frac{-i2\pi ux}{m}} (1) = W_m^{ux} \quad (6.30)$$

$$W_{2m}^{(u+m)} = e^{\frac{-i2\pi(u+m)}{2m}} = e^{\frac{-i2\pi ux}{2m}} e^{-i\pi} = W_{2m}^u e^{-i\pi} = -W_{2m}^u \quad (6.31)$$

Thus we can rewrite eq. (6.28) as

$$F(u) = \sum_{x=0}^{K-1} f(2x) W_{2K}^{2ux} + \sum_{x=0}^{K-1} f(2x+1) W_{2K}^{2ux} W_{2K}^u \quad (6.32)$$

$$\implies F(u) = \left(\sum_{x=0}^{K-1} f(2x) W_K^{ux} \right) + \left(\sum_{x=0}^{K-1} f(2x+1) W_K^{ux} \right) W_{2K}^u \quad (6.33)$$

The major advance comes via using the identities eq. (6.29) to consider the

Fourier transform K frequencies later :

$$F(u+K) = \left(\sum_{x=0}^{K-1} f(2x) W_K^{(u+K)x} \right) + \left(\sum_{x=0}^{K-1} f(2x+1) W_K^{(u+K)x} \right) W_{2K}^{(u+K)} \quad (6.34)$$

$$\implies F(u+K) = \left(\sum_{x=0}^{K-1} f(2x) W_K^{ux} \right) - \left(\sum_{x=0}^{K-1} f(2x+1) W_K^{ux} \right) W_K^u \quad (6.35)$$

Comparing eq. (6.33) and eq. (6.35), we see that the expressions within parentheses are identical. What's more, these parenetical expressions are functionally identical to discrete fourier transforms themselves. Let's notate them as follows:

$$\mathcal{D}_u\{f_{\text{even}}(t)\} := \sum_{x=0}^{K-1} f(2x) W_K^{ux} \quad (6.36)$$

$$\mathcal{D}_u\{f_{\text{odd}}(t)\} := \sum_{x=0}^{K-1} f(2x+1) W_K^{ux} \quad (6.37)$$

If we're calculating an M point transform (i.e. we're wishing to calculate $F(1), \dots, F(M)$), once we've calculated the first K discrete frequencies (i.e. $F(1), \dots, F(K)$) we may simply reuse the two values we've calculated in eq. (6.36) to calculate the next $F(K+1), \dots, F(K+K) = F(M)$. Since each expression in parentheses involves K complex multiplications and $K-1$ complex additions, we are effectively saving $K(2K-1)$ calculations in computing the entire spectrum $F(1), \dots, F(M)$. When M is large, the payoff is undeniable.

In fact, through counting calculations and then doing a proof by induction, we can show that the effective number of calculations is given by $M \log_2 M$.

Of course, since eq. (6.36) are DFTs themselves, there's nothing stopping us from reiterating this procedure; if M is substantially large, we can just as easily repeat this process a few times.

Of course, our development was for 1D. We can extend this to 2D by taking note

of eq. (6.22).

The one caveat is that the above development was for transforming sequences whose lengths are perfect powers of 2. Since our inputs have no reason to be this, we need to adjust for this. The explanation is that you just do the part that's a power of 2 and then do the rest manually or pick a different power.

Finally we note the inverse DFT can actually be found via a DFT of the complex conjugate of the original signal, and of course we may translate that operation to a FFT.

Calculating the Hessian via FFT: A demonstration

Efficient implementation of the Frangi filter ultimately relies on performing a 2D Gaussian blur in frequency space. Here we demonstrate that our FFT implementation of Gaussian blur is commensurate with other implementations.

In fig. 7, we demonstrate the compatibility of standard convolution and FFT convolve. Each row corresponds to a different scale at which Gaussian blurring occurs. Column (a) is standard convolution with a sampled Gaussian kernel, column (b) is FFT-convolution with a Gaussian kernel, and column (c) is a FFT-convolution with the “discrete Gaussian kernel”. In column (d), the 1D discrete Gaussian kernel (in green) is plotted against the sampled continuous Gaussian kernel (in black). Note that each of the images in the first three columns are scaled the same.

In fig. 8, we show these same three methods of Gaussian blur but for a large scale ($\sigma = 45$). For each method of taking the Gaussian blur ((a) - standard convolution with sampled kernel, (b) fft with sampled kernel, (c) FFT with discrete kernel), the top row is one round of Gaussian blur with $\sigma = 45$ and the bottom row is two progressive passes of Gaussian blur ($\sigma_1 = 10, \sigma_2 = 35$). The mean squared error and mean absolute error between the one-pass and two-pass versions are outputted below. Code for this demo can be found in `hfft.semigroup_demo`. The discrete kernel performs very slightly better than the sampled versions. We originally attempted this demonstration with a much

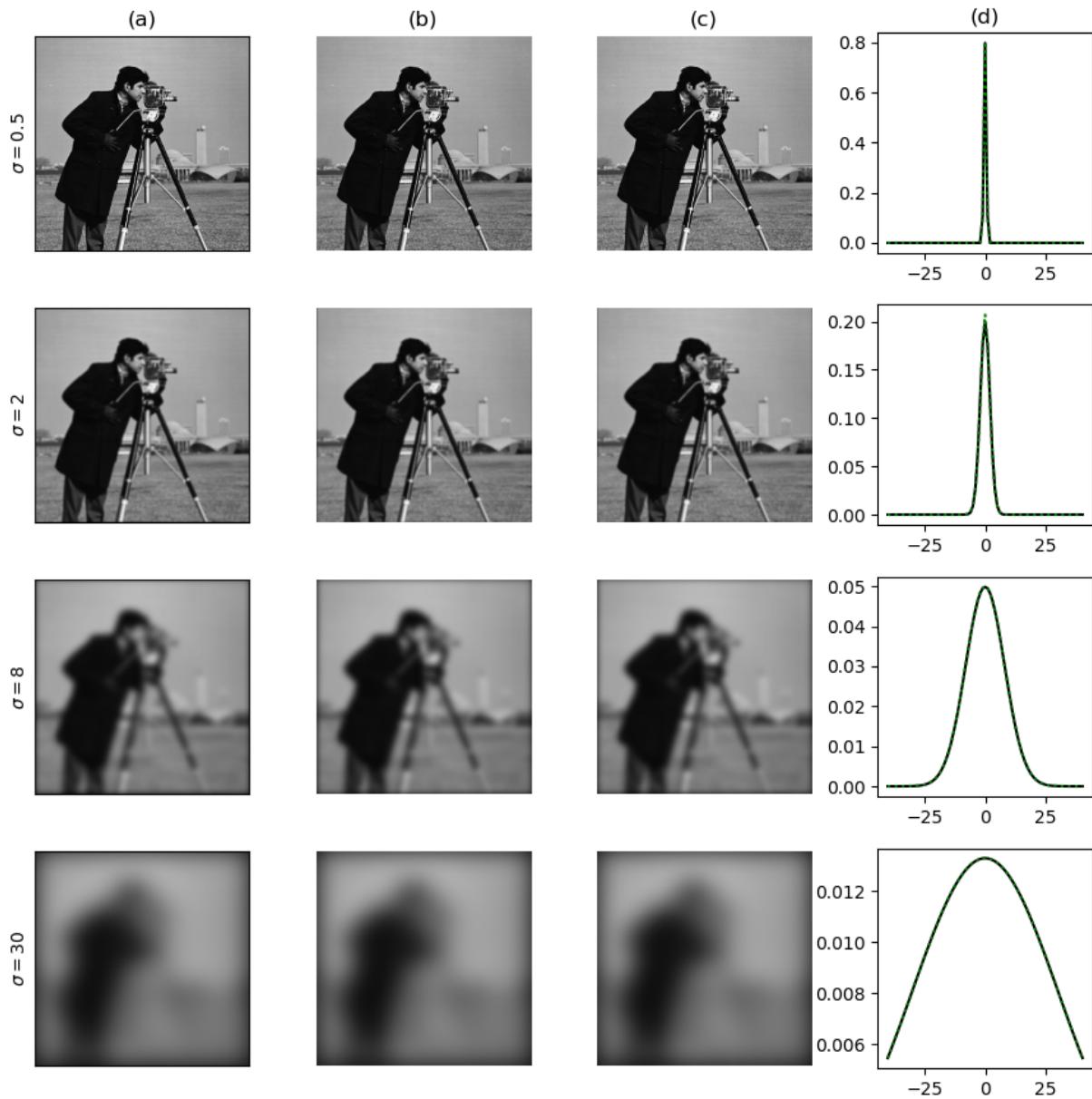


FIGURE 7: Compatibility of Gaussian convolution strategies

blurring method			MSE	MAE
spatial convolution, sampled kernel (A)			0.00054426	0.02015643
FFT convolution, sampled kernel (B)			0.00055205	0.02029916
FFT convolution, discrete kernel (C)			0.00054406	0.02015336

	A	B	C
A	-	1.296e-03	6.772e-06
B	-	-	1.247e-03
C	-	-	-

TABLE 1: MSE of Gaussian blurs ($\sigma = 0.3$) **TABLE 2:** MSE of Frangi scores $\sigma = 0.3$

	A	B	C
A	-	4.256e-06	5.537e-08
B	-	-	4.337e-06
C	-	-	-

larger sigma (say $\sigma = 150$) and multiple iterations, but unfortunately multiple passes cause the “noise” from zeroing out around the boundaries to become very noticeable after several iterations (here, we’ve opted to crop out a radius of pixels from around the edges equal to the standard deviation of the Gaussian before we calculated the MAE or MSE), which is an honest concern in image processing.

We further confirm the commensurate nature of Gaussian blur techniques by comparing the three techniques on a placental image and using each to calculate Frangi targets. The code can be found in `hfft_accuracy.py`. In table 1, table 2, table 3 and table 4 we compare the mean squared error of a single image blurred (A) with standard spatial convolution, (B) with FFT sampled Gaussian kernel, and (C) with the discrete kernel. We see that the standard convolution and discrete convolution are very similar, while the sampled discrete Gaussian is off by two orders of magnitude, but still reasonably small. We further confirm these by viewing the intensity of the images and the Frangi targets themselves across an arbitrarily chosen horizontal cross section of the image. As seen in fig. 9, fig. 10, fig. 11, fig. 12, the peaks of the Gaussian blurred image all still occur at the same places, as do the Frangi responses. We repeated this procedure up to $\sigma = 90$ and found a situation similar to $\sigma = 5$; it was only in very small scales where there was any noticeable difference at all.

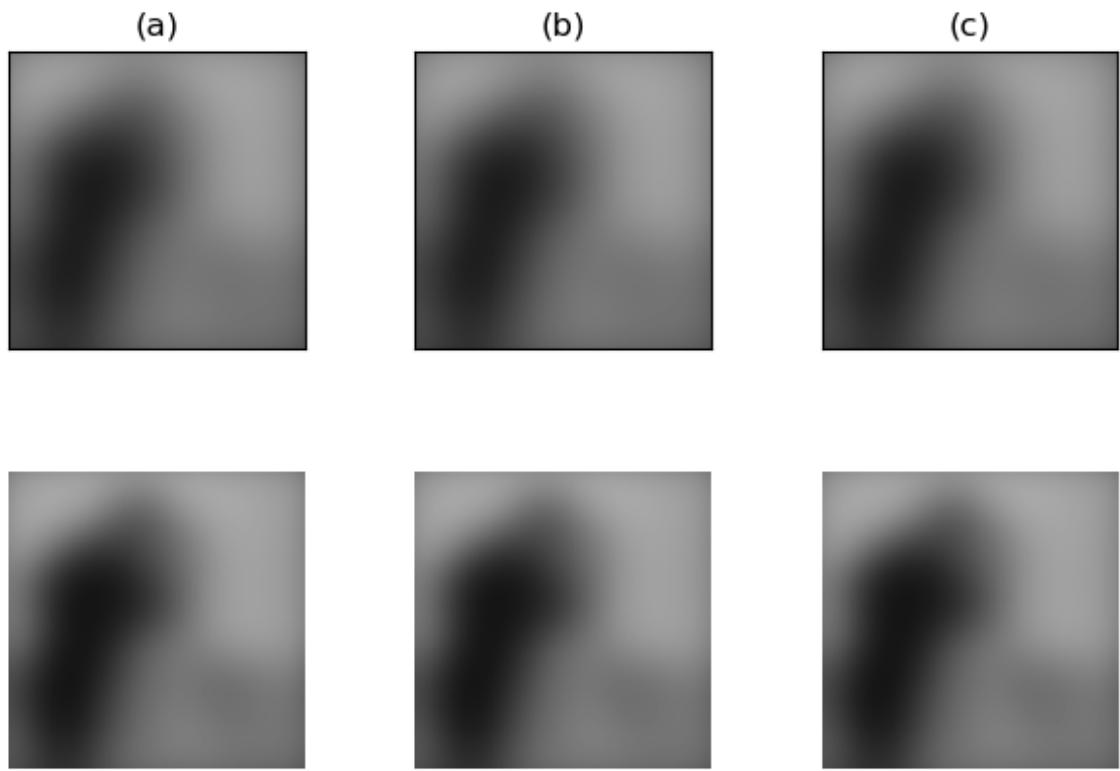


FIGURE 8: Iterative Gaussian blur

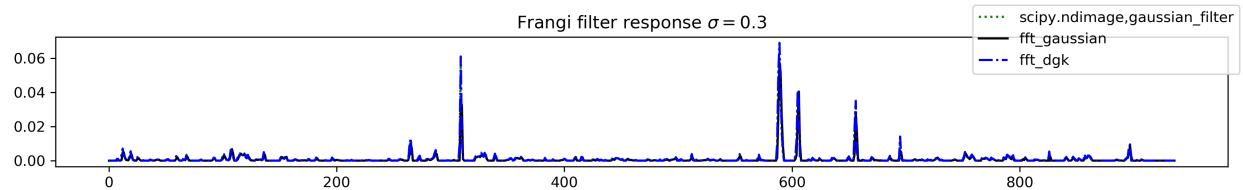


FIGURE 9: Image cross-section of Gaussian blurred images

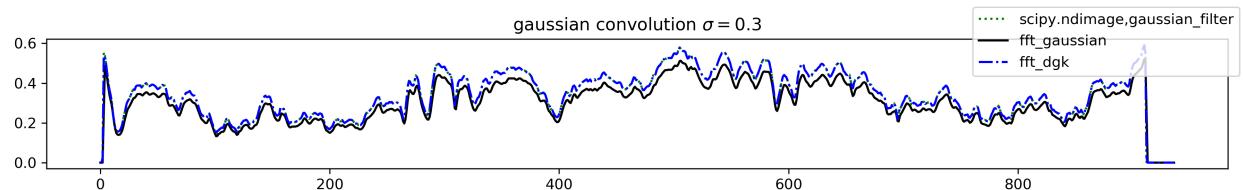


FIGURE 10: Image cross-section of Frangi targets images

	A	B	C
A	-	9.012e-06	8.629e-09
B	-	-	9.031e-06
C	-	-	-

TABLE 3: MSE of Gaussian blurs of an image ($\sigma = 5$)

	A	B	C
A	-	9.388e-05	8.383e-07
B	-	-	9.599e-05
C	-	-	-

TABLE 4: MSE of Frangi scores $\sigma = 5$

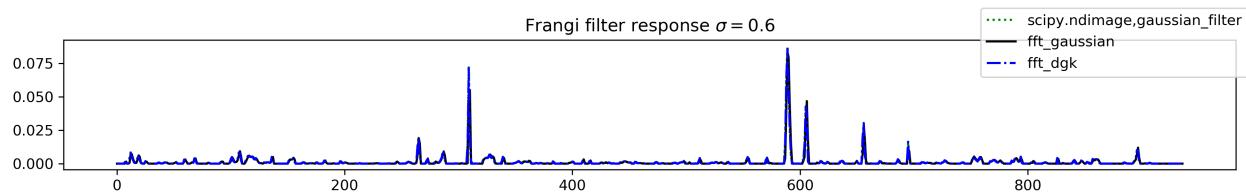


FIGURE 11: Image cross-section of Gaussian blurred images $\sigma = 5$

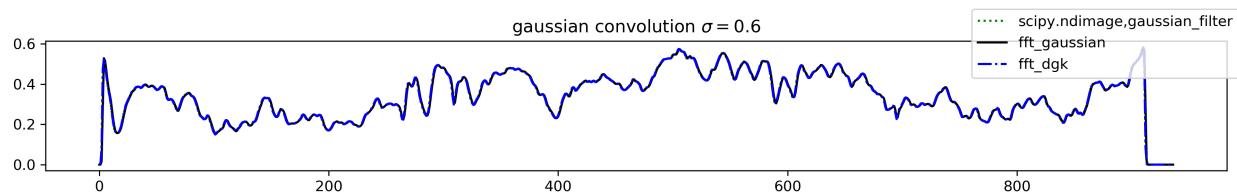


FIGURE 12: Image cross-section of Frangi targets images $\sigma = 5$

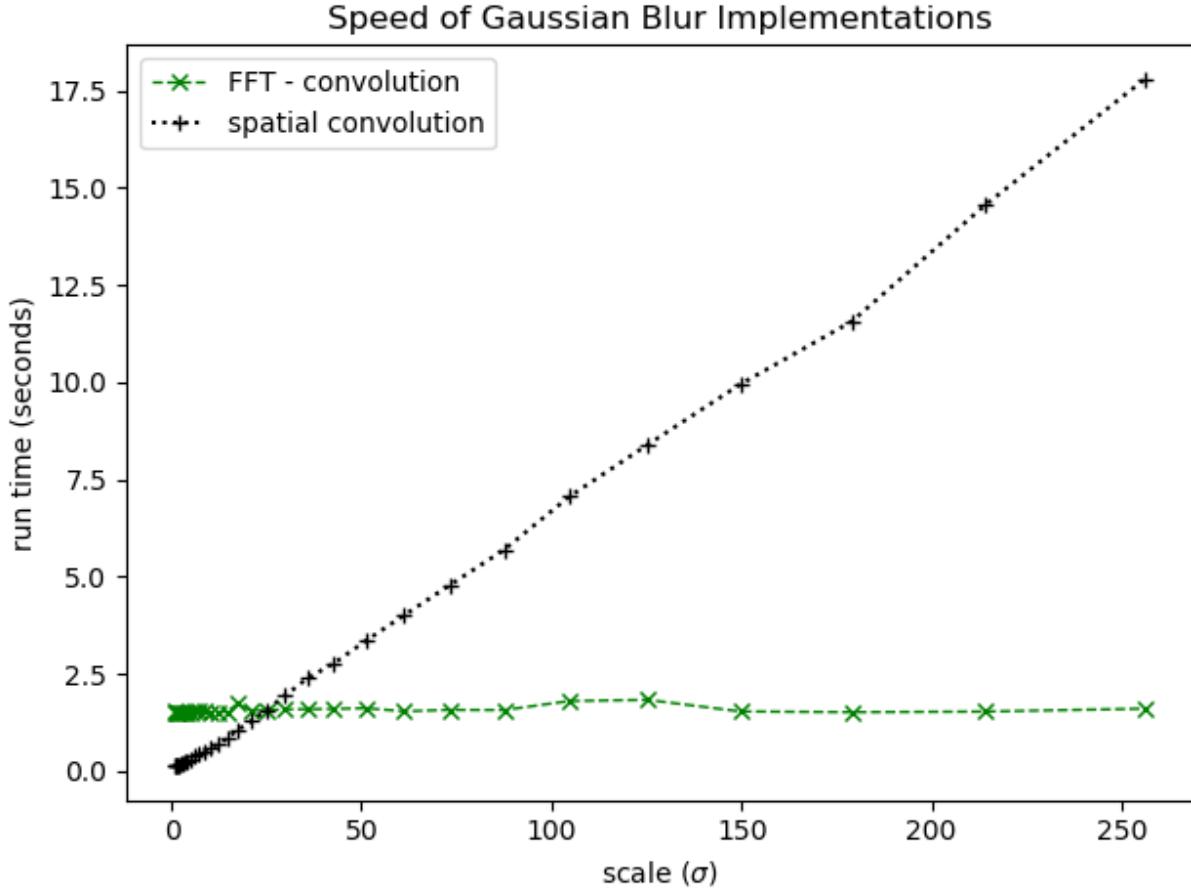


FIGURE 13: Time required

Finally, we wish to demonstrate the point of this comparison—that *FFT – based* convolution is much faster than spatial convolution. We took a much larger sample (2200×2561) and timed each method of convolution (average of three trials) for a large number of samples: logarithmic between $\sigma = 1$ and $\sigma = 128$ with 32 steps. The result shows that the convolution time seems to at least linearly increase with the size of the kernel, whereas FFT is independent of choice of scale.

CHAPTER 7

MORPHOLOGICAL IMAGE PROCESSING

We describe some of the morphological methods in a really basic way and then briefly mention the thinning algorithm.

CHAPTER 8

RESEARCH PROTOCOL

Samples / Image Domain

We ultimately perform a multiscale Frangi prefilter on a subset of 201 color images of placental samples from a private database provided by the National Children’s Study, which had been prepared for a different study. A detailed description of the data set is given in [1], and a description of the cleaning and fixing procedure is given in [4]. The samples are provided as XCF files (the native project file for GIMP) and contain four major layers.

A representative sample

The layers together give a hand tracing of the vascular network and perimeter. A sample of overlaid layers in a representative sample (with ID number “BN0164923”) is given in fig. 14.

Each layer is roughly 1954x1200 pixels (with some occasional variation). In fig. 14, we see these four layers of a characteristic sample. fig. 14a is the base image. A cleaned, fixed placenta is placed on a table with a camera a fixed distance away, and a ruler and penny (presumably for redundancy) are placed nearby to aid registration and calibration of the resolution. The resolution of each sample is roughly 46 pixels per centimeter. fig. 14b is a tracing (in green) of the perimeter of the placenta. The point of umbilical cord insertion is notated in yellow. Two cyan marks are placed on consecutive centimeter markings on the ruler (the dots are enlarged and shown as a darker blue here for clarity). fig. 14c and fig. 14d are each hand traces of the PCSVN, with a layer for each the arteries and veins. These layers are simultaneously overlain on the base image in fig. 14e. The

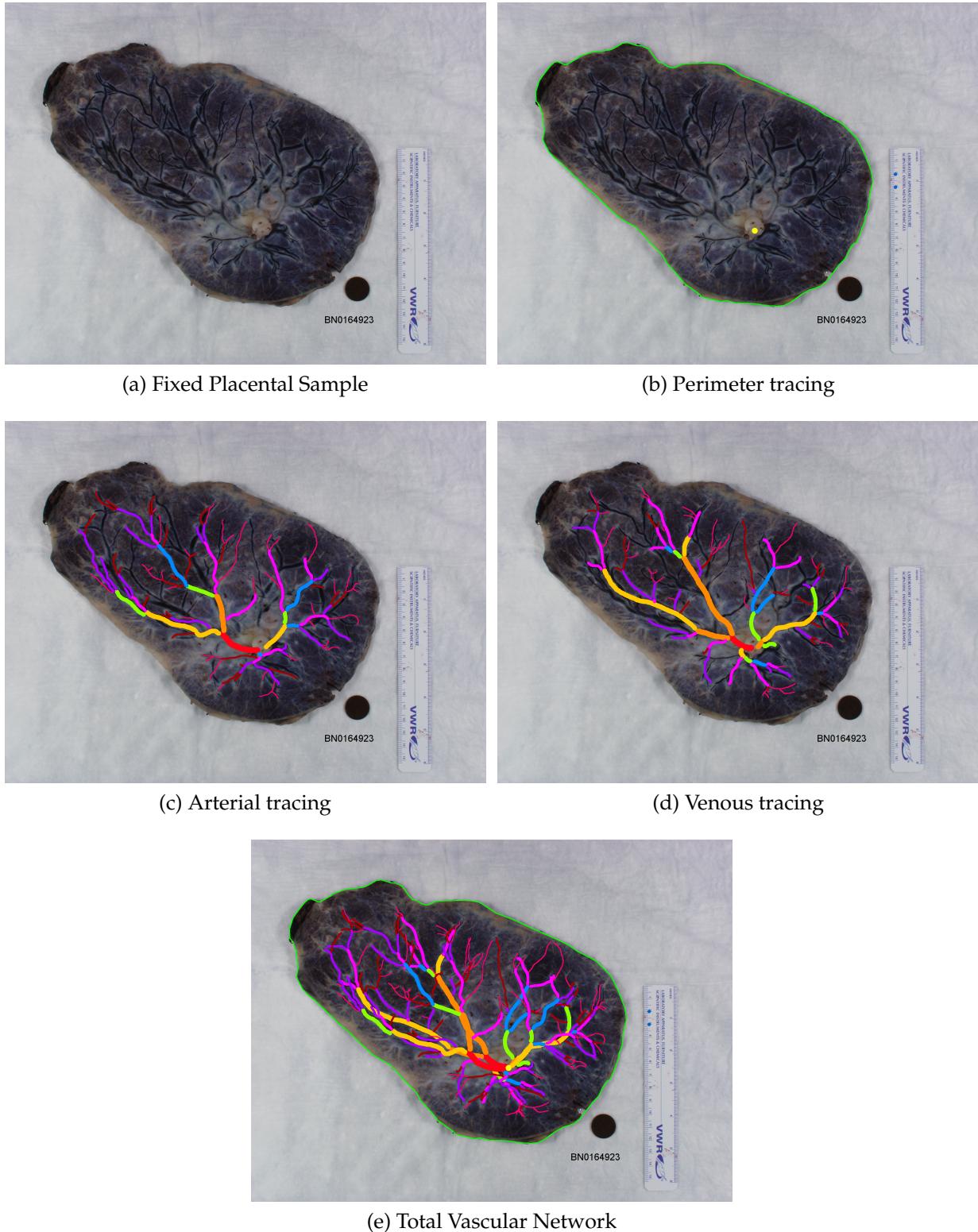


FIGURE 14: A representative placental sample and tracing

vessel width	color (hex value)	color name
3 pixels	#ff006f	magenta
5 pixels	#a80000	dark red
7 pixels	#a800ff	purple
9 pixels	#ff00ff	light pink
11 pixels	#008aff	blue
13 pixels	#8aff00	green
15 pixels	#ffc800	gold
17 pixels	#ff8a00	orange
19 pixels	#ff0015	bright red

TABLE 5: Vessel width color code for manual tracing protocol

coloration is meant to indicate the diameter of each vessel. The diameters are binned into 9 discrete widths, odd integers from 3 to 19 pixels. Vessels of smaller diameter are either binned to three or (quite frequently) left untraced. The correspondence between pencil color and (binned) vessel width used in the tracing protocol is given in table 5.

As stated in the introduction, the task of creating these samples, in particular the tracing and estimation involved in creating fig. 14c and fig. 14d is very labor intensive—requiring between 4 and 8 hours to trace a single sample. A closer look at many of the samples often reveals that a great deal of subjectivity in providing this “ground truth,” as it is not often clear what the underlying truth really is. Often it’s hard to see where the vein is, vascular networks are obscured by the umbilical stem, the blood in the vessels dries unevenly or ruptures, and the vessel seems to disappear momentarily. These situations and more will be showcased in fig. 22, where we will demonstrate how the Frangi filter reacts to these problem areas. Our efforts at the eventual task of network completion must deal with these shortcomings and, in some circumstances, make subjective decisions like the manual tracer did.

Knowns and Unknowns

Since our final goal is a fully automated procedure, we wish to simply operate on the placental sample itself, without any understanding of its provided tracing (except for judging the strength of our algorithm); our goal is to develop an algorithm that can produce a “ground truth” tracing similar to fig. 14e or fig. 15d without any user intervention.

For our purposes however, we will concede and provide a limited amount of information from the tracings, namely the provided placental perimeter (shown in green in fig. 14). In developing a fully automated algorithm, it would be relatively straightforward to obtain this boundary ourselves using various techniques, such as an Active Contour Model [25] or, or even a simple edge finding algorithm followed by watershedding and largest object selection. In fact, we have implemented this later algorithm, but unfortunately we achieve a subpar result on several images, and therefore we currently use it to improve upon the perimeter by removing “cuts”, which were previously reported as being inside the plate and sometimes led to large false positives.

Finally, we will consider the location of the umbilical insertion point as a “known”, as the vessels around it are frequently impossible to see and we wish to exclude them from consideration. It is not unreasonable, however, to consider this to be a known—in future preparations of samples, we could simply require that this point be centered in image in a predictable location. Furthermore, we use its location as a convenience in data analysis—knowledge of this point does not inform our algorithm at the present time.

Data Cleaning and Preprocessing

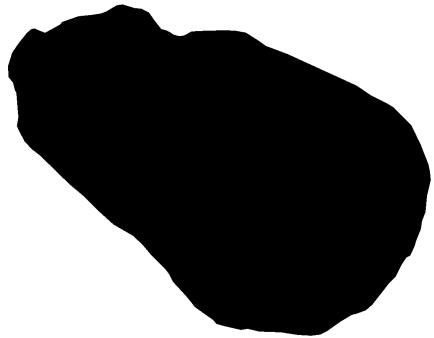
Building a sample suitable for use in our algorithm from fig. 14 is relatively simple. We zero outside the boundary of the plate (so as to not waste computational time calculating the differential geometry of a ruler, say), and also generate a binary mask to identify the plate. Finally, our vessel layers are combined and given as a binary trace, which we will use later for scoring. An example of the preprocessed samples used by the algorithm are given in section 8.2.

These procedures are performed automatically on the 201 images in our data set using a custom GIMP plug-in, which performs various “bucket fill” operations, layer mergings, and thresholdings. For completeness sake, this plug-in (and an associated Scheme script which turns it into a batch operation) can be found in the Appendix.

As a point of technicality, the grayscale image in fig. 15c is not actually produced directly by the extractor plug-in, but created when the 3 channel RGB image fig. 15b is imported at the start of the algorithm. This grayscale conversion is simply done for ease of analysis on the sample: although the Frangi filter is designed for arbitrary N-dimensional input [12], an image with three color channels does not have 3 spatial dimensions. We therefore simply combine the information in three channels using the well-known and oft-implemented ITU-R 601-2 luma [26], or “luminance” transform:

$$L = \frac{299}{1000} R + \frac{587}{1000} G + \frac{114}{1000} B \quad (8.1)$$

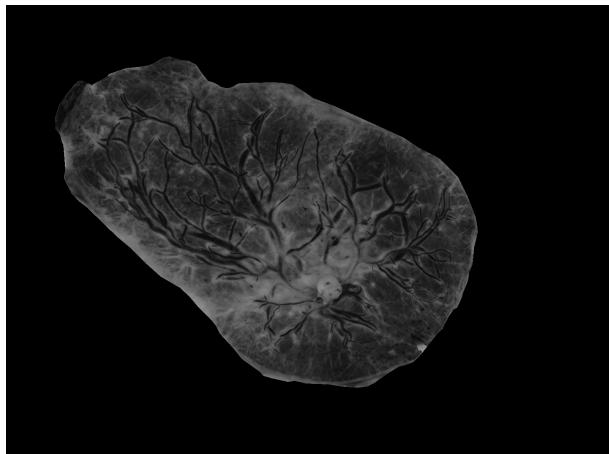
It should be noted that this choice is not a given—several other attempts have used the green channel unmodified, as in [4] and [2]. Preliminary and periodical rechecking has not indicated that such a conversion has any benefit over the luminance transformation for our image domain, although other placental samples with a different preparation method might benefit from it.



(a) Background Mask (in white)



(b) Sample with BG removed



(c) Grayscale

FIGURE 15: Preprocessed files from an NCS sample



(d) Trace / “Ground Truth”

Boundary Dilation

All images are grayscale, M, N pixels as a masked array (of type `numpy.ma.MaskedArray`), where pixels outside of the placental region are masked so they will not be considered by the algorithm. However, some standard implementations of algorithms, namely `numpy.gradient` and `scipy.signal.convolve2d` are not designed to handle masked regions. Although it would be potentially useful to adapt such methods in a way to, say, calculate a gradient or perform a convolution by a “reflection” across an arbitrary closed boundary (as opposed to the edge of the image matrix), we opted instead to “zero out” unwanted background pixels and simply exclude affected areas from consideration. This exclusion could be achieved by simply dilating the mask, but we opt to achieve it in a much more resource efficient manner: we iterate through an array of indices for the image where the boundary occurs and simply extend the mask R pixels in each direction (like a giant plus sign). Since the boundary of the placental plate forms a closed loop, the effect is very similar to convolving with a disk of radius R , but is much faster.

fig. 16 shows the effect of this so-called “boundary dilation.” In the image above, $\sigma = 3$ and border radius is 25 to exaggerate the effect. The first row shows the unaltered boundary of the sample (left) and the sample after boundary dilation (with radius dilation of 25 pixels). The second row shows the Frangi vesselness measure at single scale ($\sigma = 3$) where `DARK_BG=False` to target dark curvilinear structures performed on the altered sample (left) and the boundary dilated sample (right). Removing an unnecessary part of the placental plate prevents a small response to a non-vascular yet mildly curvilinear background feature from appearing. The third row of fig. 16 shows the Frangi vesselness measure at the same scale ($\sigma = 3$) when we are probing for bright curvilinear structures (i.e. `DARK_BG=True`). Here, wherever the very edge of the placental plate is *any* brighter than adjacent interior, a very large Frangi response will occur, as

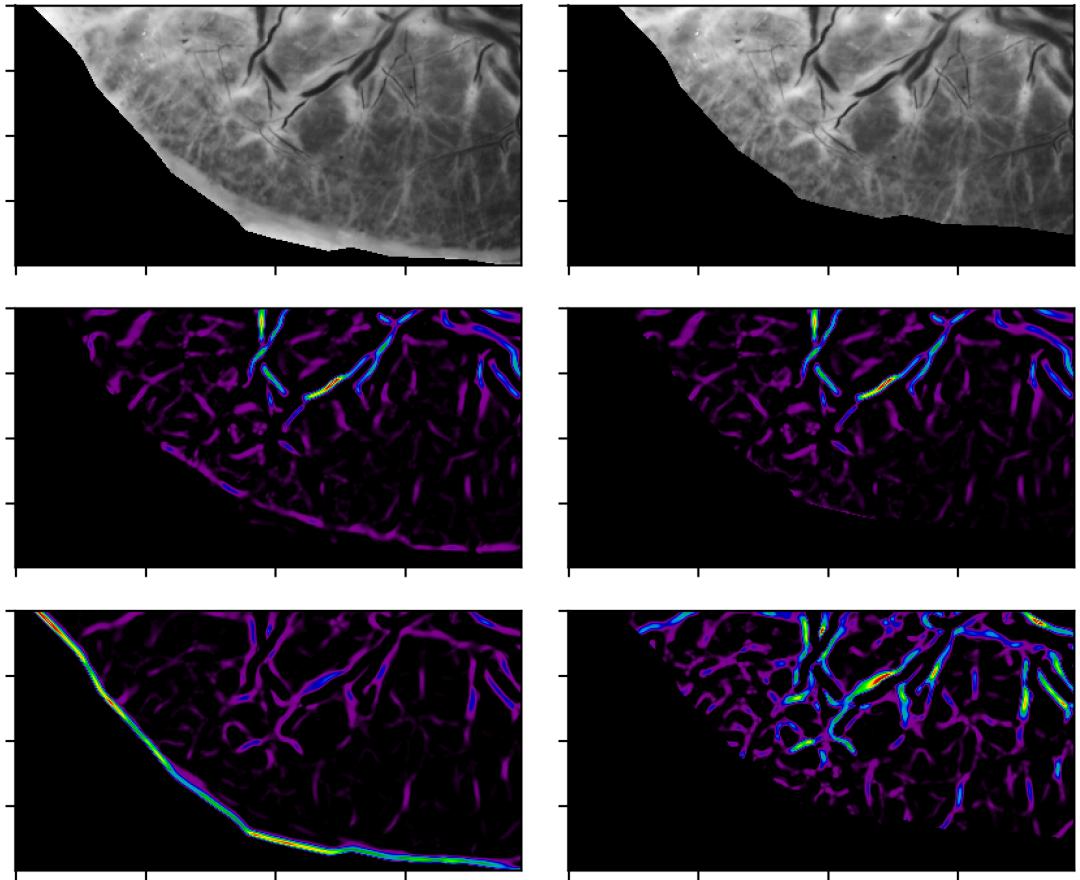


FIGURE 16: Effect of boundary dilation on Frangi responses

seen on the left. Dilating the boundary completely avoids this issue, as seen by the figure on the right. Thus we prevent a visual artifact that is present in much prior work on this problem (see [2], [4]). It should be noted that, while the figure on the right shows a much larger interior response, this is simply because the intensity of the output in each of these images is being independently scaled between the minimum and maximum intensity in the image. However, we argue that this is an appropriate and desired depiction of the situation, as we will frequently consider only the relative maxima of Frangi response per scale in our analysis.

We end our discussion by noting that we perform this boundary dilation within the Frangi algorithm itself when we set the structureness parameter γ as half of the maximum Hessian norm found at that scale—this ensures that the maximum occurs sufficiently away from the boundary of the plate, and does not occur from a noise phenomenon.

The code for generating fig. 16 is found in the within the “`if __name__ == __main__`” block of the file `plate_morphology.py`, (so the figure will be generated when running `plate_morphology.py` as a top-level script from the command line). See appendix.

Deglaring

Despite best efforts when harvesting samples, a select number of the placental samples exhibit substantial glare, which leads to inaccuracies in identifying curvilinear content. Our protocol for deglaring is analogous to that performed in [4] and [2]. Unfortunately, the method relied upon by those previous papers (MATLAB’s `imfill`, which relies on inpainting by solving the Dirichlet problem for masked regions) was not immediately available in a Python environment. Instead, we used an already implemented inpainting algorithm, `scikit-image`’s `inpaint_biharmonic()`, which should be expected to achieve similar results, albeit at the expense of processing time.

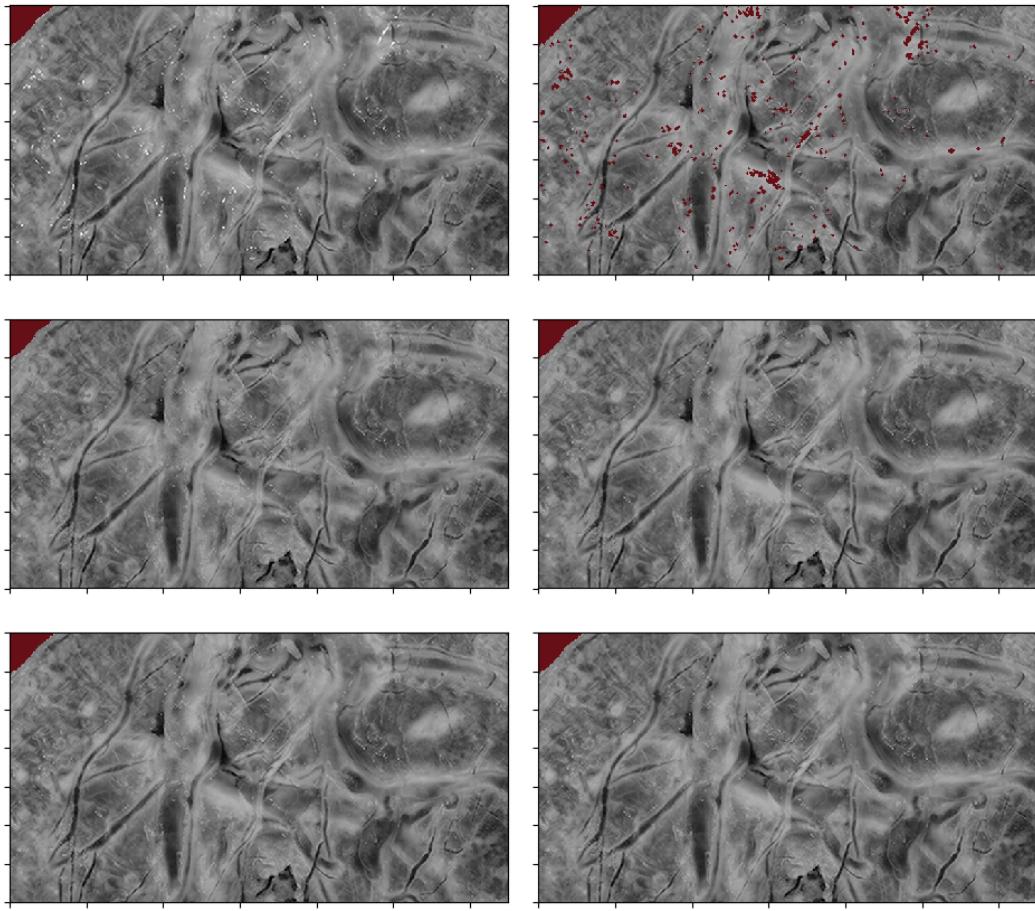


FIGURE 17: Deglaring a sample using a hybrid inpainting method

The function `inpaint_biharmonic` is based on [27], and relies on solving a biharmonic equation i.e. $\nabla\nabla f = 0$ for the surface f subject to boundary conditions (as compared to `imfill`'s solving the Laplace equation $\nabla f = 0$ in regions marked as glare).

The method for deciding what is considered glare is similar to [4], in which we consider any intensities close the maximum intensity in the image (Almoussa et al. used 80% of max intensity, and we use $175/255 \approx 68\%$). This threshold is unfortunately dependent on the image domain.

Inpainting in the above way is rather resource intensive, so we implemented two faster and less precise methods of inpainting that work well enough for removing small

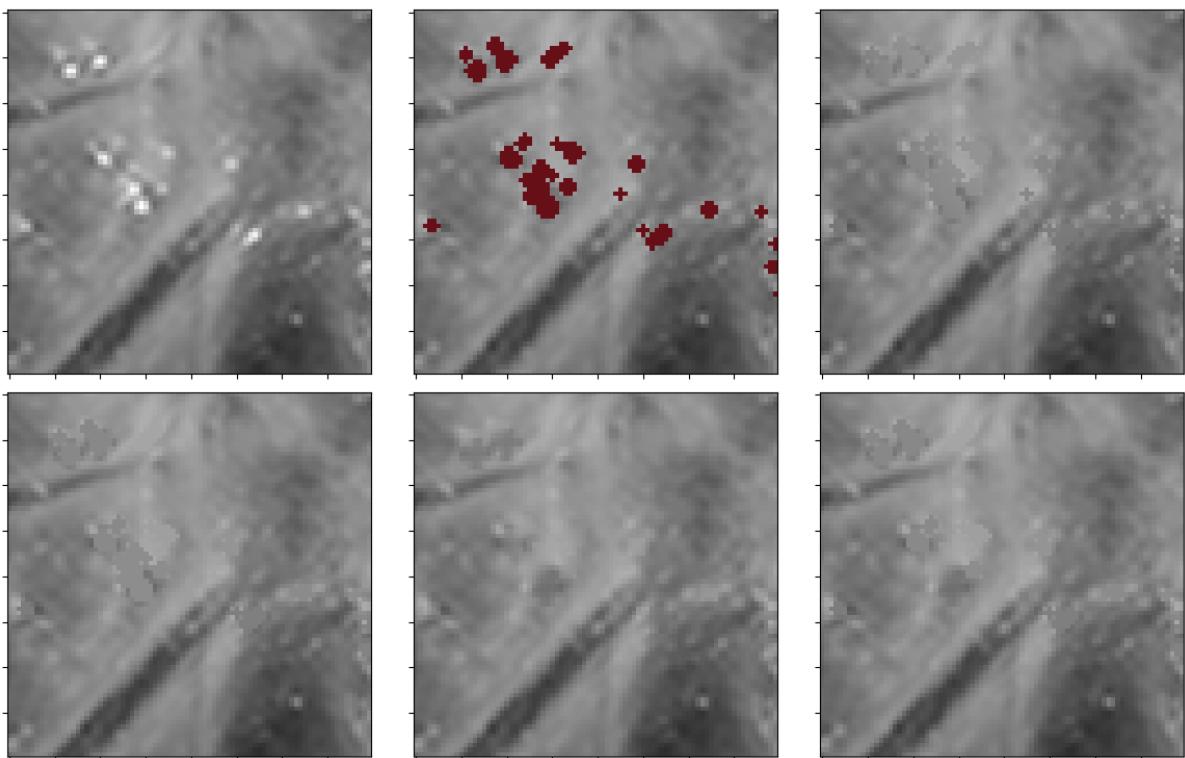


FIGURE 18: Comparison of glare inpainting methods (detail)

regions of glare. can be found in `preprocessing.py`. The first, called `inpaint_glare()` replaces any masked pixel with the average of all non-masked values within a certain distance (default 15 pixels). The second, called `inpaint_with_boundary_median` calculates the median value of the (non-masked) boundary and fills any masked region with that value. We argue that these less-exact methods are adequate for smaller regions, while larger regions of glare deserve a more thoughtful application of inpainting. Our final method of inpainting, `inpaint_hybrid` implements this idea—smaller glare regions are inpainted with a boundary median, while larger areas are inpainted with the more expensive but more accurate biharmonic inpainting.

A comparison of these methods is shown in fig. 17, and a zoomed in portion is shown in fig. 18. In the top left, the glary image is shown. In the top middle, regions above the threshold intensity are masked (shown in dark red, along with the background). In the top right, the strategy is “mean window” with a window size of 15 pixels. The bottom left uses “boundary median” strategy. The middle is the more expensive “biharmonic inpainting” strategy, and the bottom right uses a “hybrid” strategy.

The following timing demonstrates that the “hybrid” strategy is over 3 times faster than biharmonic inpainting, and that biharmonic painting takes 22 seconds, even when only 1% of the placental plate is to be inpainted.

```

1 In [1]: %timeit inpaint_with_boundary_median(img)
2 1 loop, best of 3: 3.99 s per loop
3
4 In [2]: %timeit inpaint_with_biharmonic(img)
5 1 loop, best of 3: 22.3 s per loop
6
7 In [3]: %timeit inpaint_hybrid(img)
8 1 loop, best of 3: 6.49 s per loop
9
10 In [4]: px_inpainted = np.sum(np.logical_and(masked.mask, np.invert(img.mask)))
11 In [5]: px_plate = np.sum(np.invert(img.mask))
12 In [6]: px_inpainted / px_plate # ratio of inpainted pixels to total plate
13 Out[6]: 0.011444460505513942
14

```

We stress again that only a small subset our image domain exhibits disruptive amounts of glare. Future improvements in this direction should probably seek to implement more robust method such as [28] that are not dependent on an arbitrary global threshold for deciding what regions exhibit glare.

Multiscale Setup

Our multiscale Frangi filter requires a list of scales at which to probe. Each scale is chosen to accentuate features (i.e. vessel diameter) of a particular size. This set of scales at which to probe will be denoted as $\Sigma := \{\sigma_1, \sigma_2, \dots, \sigma_N\}$, where each scale is indexed by increasing order.

Although we cannot expect *a priori* that there is an direct proportionality between our scale size σ and (even some function of) the width of a particular vessel [12], we generally expect to isolate narrower curvilinear structures at smaller scales, and thicker curvilinear structures at larger scales. The smallest one should be an effective size where details are expected to be isolated, and the largest should be an effective size as well. In fact, following [16], it is reasonable and natural to select these logarithmically; that is, for some selected inputs $m < M$ we have

$$\sigma_1 = 2^m, \sigma_j = 2^{(m + \frac{M-m}{N-1}j)}, \sigma_N = 2^M \quad (8.2)$$

That is, the exponents are spaced linearly from m to M . This is achieved by the command `np.logspace(m, M, num=N)`. The idea is that the curvilinear content of the image will respond better at some particular scale, but there are diminishing returns as σ increases; while the filter's response may vary substantially between, say $\sigma = 1$ and $\sigma = 2$, we would not expect a substantial difference in response between, say, $\sigma = 46$ and $\sigma = 47$. Historically, there was another benefit of using a logarithmic scale space: computing the vesselness measure was very expensive, and thus it was simply not feasible to collect so many large scale readings. This is much less of an issue with the present

implementation, although we still obviously wish to avoid frivolous, redundant calculations no matter the speed of the implementation.

The optimal choice of scale sizes to probe at is intuitively dependent on the resolution of the image. If there is no particular care taken in selecting a minimum and maximum scale at which to probe, then we must assure that our Frangi filter is “normalized” in such a way that there is a decay in response past certain values. That is, probing at a unreasonably large (or small) scale (say $\sigma = 1000$ or $\sigma = .0001$ should result in an almost null response throughout the image. We will approach this issue in our discussion of “variable thresholding.”

The Research Protocol

Once we have chosen this set of scales Σ , we simply convolve the image with a discrete Gaussian kernel with that standard deviation, then take gradients enough to get a matrix of partial second derivatives, the Hessian. We calculate the eigenvalues of each (2x2) Hessian matrix and then compute the Frangi filter according to section 3.1 and ???. We use these to provide a couple examples of estimating the PCSVN network. The entire decision tree can be shown in the outline below. Indentations with “+” and “.” characters are lists of options at that point, where “+” is the default and “.” is for alternatives discussed elsewhere in the text.

```
% DECISIONTREE  
For each sample:
```

A) Preprocessing

- 1) RGB to single channel via Luminance Transform
- 2) Cut removal
- 3) Remove glare
 - a) Mask glare
 - + Threshold (*175/255*)
 - . Threshold at *80%* of max intensity (Almoussa)
 - . Lange (2005) (multistep procedure, done in RGB space actually)
 - b) Post-process mask
 - + Dilate with radius *2*
 - . Do nothing

- c) Inpaint glare
 - + Hybrid inpainting, with size threshold *32*
 - . Biharmonic inpainting
 - . Mean value of boundary
 - . Median value of boundary
 - . Windowed mean (radius: *15*)
- B) Multiscale Frangi filter
 - 1) Define parameters
 - a) Scales
 - = n_scales (default: *40*)
 - = scale_range (default *[-2, 3.5]*)
 - = scale_type (*logarithmic base 2* or linear or custom)
 - > build scales
 - b) Betas
 - = *0.5* each scale or custom range
 - c) Gammas
 - = strategy: (half L2 hessian norm or *half hessian frobenius norm*)
 - or custom value each scale
 - = redilate plate per scale (?)
 - d) Dilate per scale
 - + Custom function of scale
 - (default *max{10, int(4sigma)} if (sigma < 20) else int(2*sigma))*
 - . No dilation
 - e) Scale space convolution method
 - + Discrete Gaussian kernel with FFT
 - . Sampled gaussian kernel with FFT
 - . Sample gaussian kernel, standard convolution
 - 2) For each sigma: do Uniscale Frangi Filter
 - a) gauss blur image with method from (1e)
 - b) take gradient across each axis, take gradient across each axis of gradient to get Hxx, Hxy, Hyy
 - c) find eigenvalues of hessian at each point (using np.eig) and sort by magnitude
 - d) zero out principal directions according to Dilate Per Scale
 - e) zero out hessian according to max(ceil(sigma),10)
 - f) Calculate Frangi Vesselness Measure
- C) Estimate PCSVN
 - 1) Approximate using strategy
 - a) Calculate Fmax and Fmax.where -> Fmax
 - b) Threshold at 95th percentile -> approx
 - c) Threshold at fixed alpha
 - d) Margin adding to one of the above
 - e) Random walker after margin adding
 - 2) Compare to Trace
 - 3) Calculate Network Coverage and MCC score

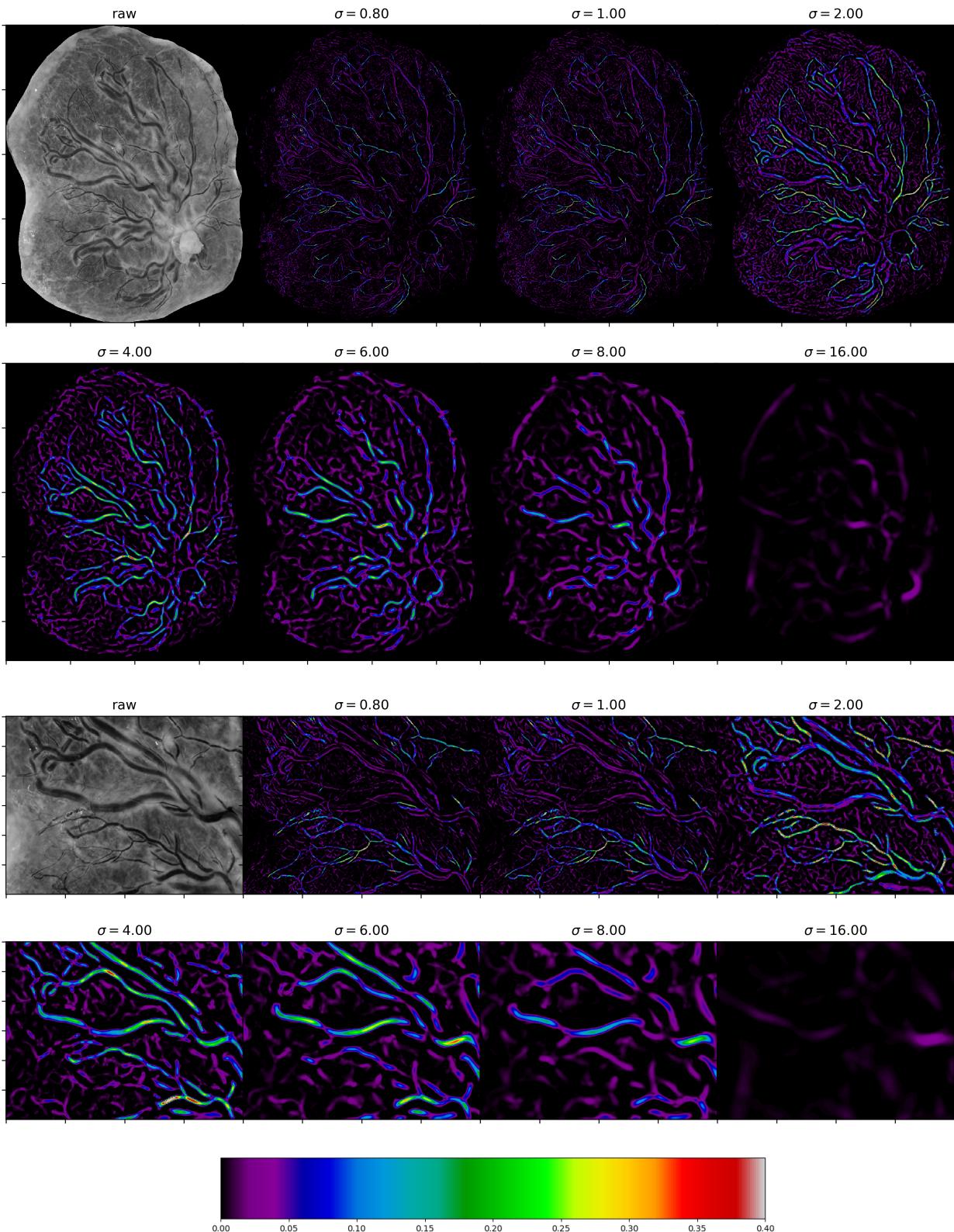


FIGURE 19: Example scalewise Frangi output (plate and inset) (Example 1)

We will discuss our various demonstrations of merging techniques in the Results section.

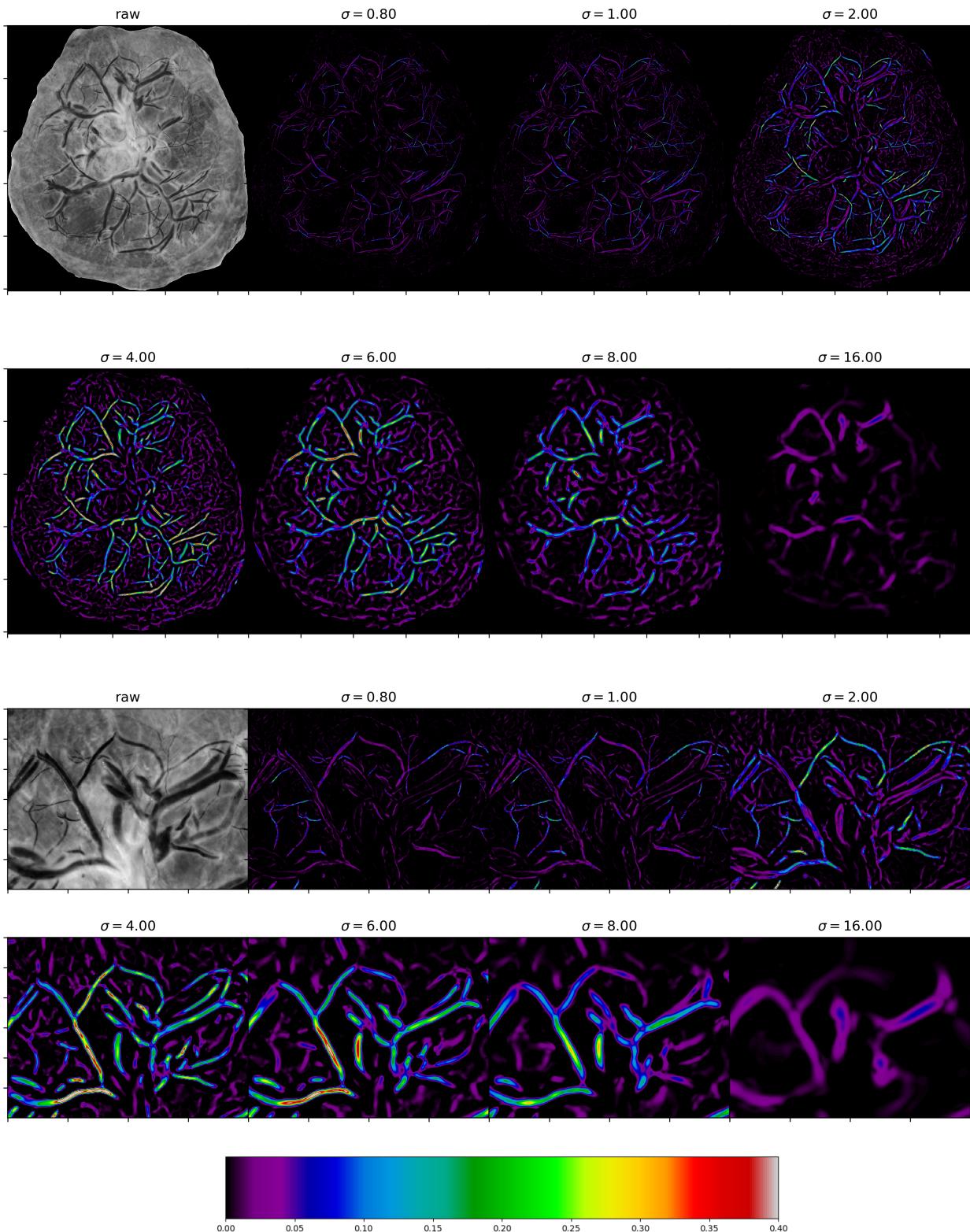


FIGURE 20: Example scalewise Frangi output (plate and inset) (Example 2)

CHAPTER 9

RESULTS AND ANALYSIS

We demonstrate the output of the Frangi filter on our samples after running a multiscale technique with $N = 20$ scales with a stricter anisotropy parameter $\beta = 0.35$ and standard structureness parameter $\gamma = 0.5$, with scales spaced logarithmically from $\sigma_1 = 2^{-1}$ to $\sigma_N = 2^{3.5}$, performing glare and cut removal in preprocessing, and using a discrete gaussian kernel and dilation border of 20. Our goal in this section is to provide a close up look at the Frangi filter on two samples, and then provide some measures of the Frangi output's correspondence with the "ground truth" network tracings across all 201 images, without explicitly performing segmentation. However, for visual demonstration, we will employ both simple thresholding techniques (arbitrary fixed and nonzero-percentile) described in chapter 5. In chapter 10 we will develop and analyze more sophisticated Frangi-based segmentation techniques and compare their performance to these rudimentary thresholding techniques across the entire dataset. For this chapter we will content ourselves with analysis of the raw Frangi vesselness measure within our image domain, and use our simple thresholded results for visual demonstration alone.

Sample visual output

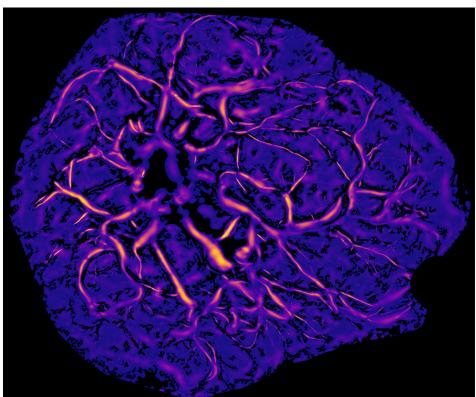
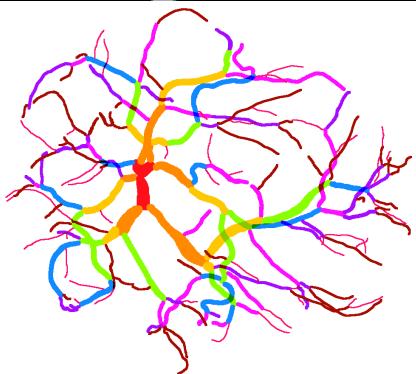
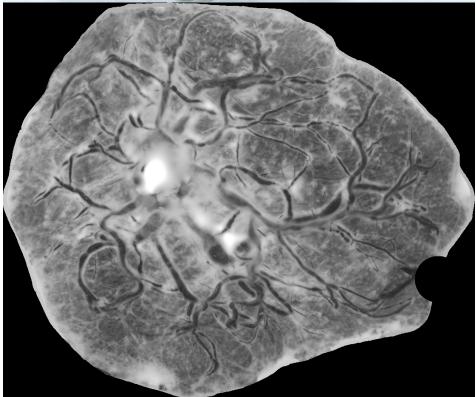
In fig. 21 we take a look at the Frangi output (\mathcal{V}_{\max}) for a well-behaved sample. In the left column we have (from top to bottom) the un-preprocessed placental sample, the preprocessed sample, the color trace(ground truth), and \mathcal{V}_{\max} . In the top-right, we have for each $n = 0, \dots, 19$ scales, we have the size of the scale σ_n , the 95th percentile score at that scale α_p where $p = 95$, and the maximum vesselness score at that scale ($\max(V_\sigma)$). The

bottom-right set of images are two rudimentary thresholds of the Frangi result. The top is the scalewise nonzero percentile threshold (95th percentile) and the bottom is a strict threshold of 0.4. left and right images are two rudimentary thresholds of \mathcal{V}_{\max} . The bottom left is nonzero percentile filtering (thresholded at the 95th percentile, and the right image is a simple threshold at $\alpha = 0.4$. For each pixel that passes the threshold, each of these graphs is color coded to indicate from which scale the maximum value at that pixel occurs, colored according to the scale on the left.

Variations in the Data Set and Imperfections of the Ground Truth

We must qualify our binary classification. There are limitations intrinsic to the image domain and tracing protocol that make our ground truth tracing somewhat inaccurate. In fig. 22 we demonstrate a few common issues with the samples. The four figures show (top left) the original colored raw sample, (top right) the ground truth tracing, (bottom left) \mathcal{V}_{\max} , and (bottom right) the confusion matrix after some segmentation strategy. The green arrow points to the umbilical stump. You can see there is circular noise around this point, and in general perfusion around this point is very low—many of these vessels have been estimated by the tracer. The orange arrows represent points where perfusion is very low, perhaps caused by a clot in the blood vessel. The pink arrows point to vessels that were not traced, although they are clearly visible. The blue arrows point to where the shape of the vessel and the trace clearly do not agree. There are many more examples of these in the frame, and many more across all samples.

The red arrow points to an issue unrelated to the ground truth, but an issue that arises when selecting scales in our multiscale methodology—this is a point of dark curvature that represents noise at larger scales. As you can see from the \mathcal{V}_{\max} of this inset, there is a positive response in this dead space between vessels, and there is another one that appears in the bottom left between two close vessels of similar size.



n	σ_n	α_p	$\max(V_\sigma)$
0	0.3535	0.0547	0.986
1	0.4243	0.0590	0.979
2	0.5092	0.0654	0.970
3	0.6110	0.0765	0.973
4	0.7333	0.0892	0.988
5	0.8801	0.0962	0.991
6	1.0562	0.1082	0.991
7	1.2676	0.1308	0.970
8	1.5212	0.1669	0.973
9	1.8256	0.2232	0.978
10	2.1909	0.2925	0.984
11	2.6294	0.3196	0.968
12	3.1555	0.3269	0.994
13	3.7869	0.3558	0.998
14	4.5447	0.4058	0.999
15	5.4542	0.3764	0.963
16	6.5456	0.3184	0.950
17	7.8553	0.3047	0.958
18	9.4272	0.3287	0.916
19	11.3137	0.3524	0.916

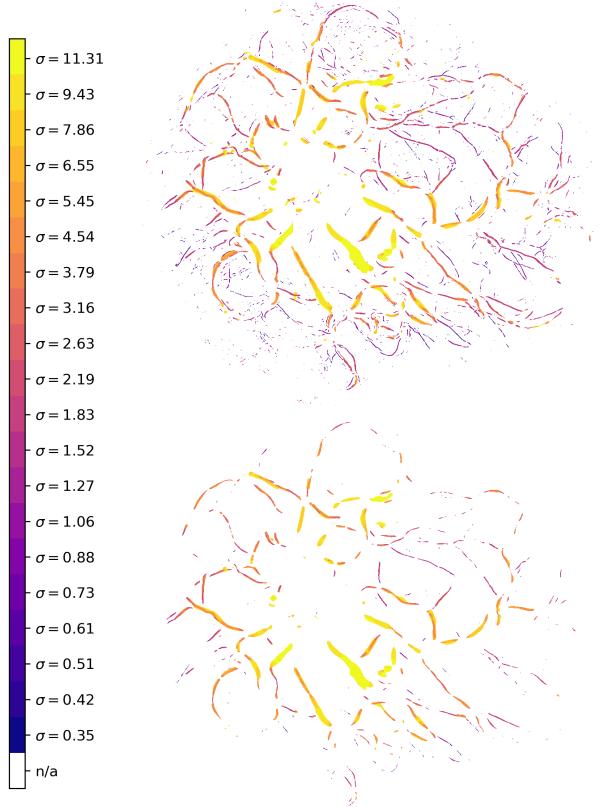


FIGURE 21: Example vesselness score, percentile thresholds, and simple thresholds

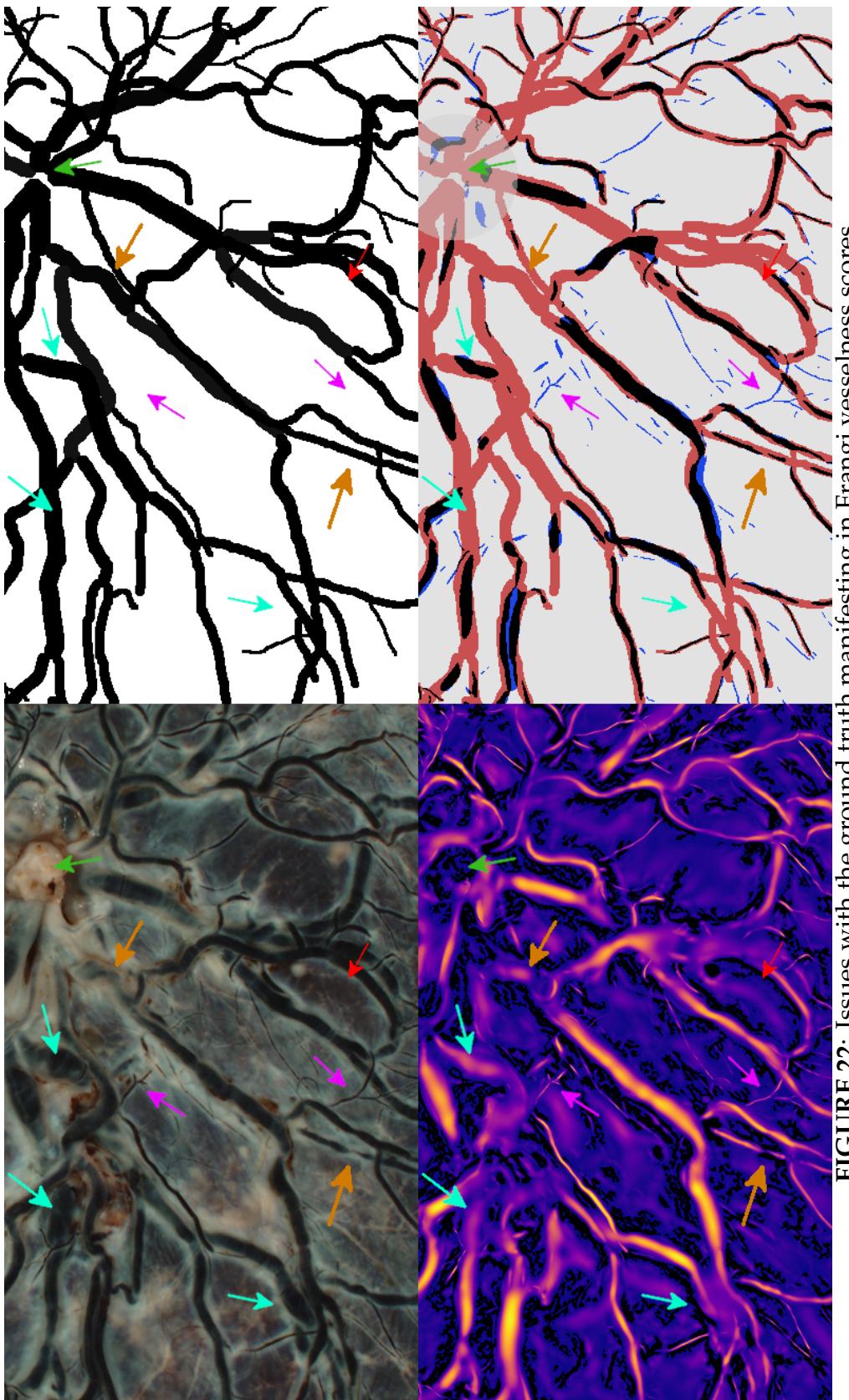


FIGURE 22: Issues with the ground truth manifesting in Frangi vesselness scores

rf

As seen in ??, there are several issues with the samples that will cause trouble in our efforts toward segmentation. Our representative sample is BN0392644. The top left is the original (color) image, the top right is the full vessel width trace. The bottom left is a smaller skeletonization (sketch), where arteries are shown in red and veins are shown in blue. The bottom right figure contains some annotations. At the top, a blue arrow indicates a large curvilinear patch of dried blood that is not part of the vascular network. The green arrow in the middle indicates some vessels that are too small for the diameter binning and are thus not reported. We will see later that our Frangi result perfectly captures these, yet they will be reported as a false positive since they are not part of the tracing. However, there are other vessels of similar visual width in this same inset that are traced. In blue boxes (and in many other spots) the vessels cross each other. The border around these will prevent us from being able to extract the vessel directly. In the green dotted box, a major arterial and a major venous branch each connect to the umbilical cord insertion point. Whereas the arterial branch (on the right) can be seen, it will not be reported by the Frangi filter, since those points are not darker relative to the background. You can also see how much variation there is as you look along a blood vessel. There are some areas where the Frangi filter will have a very limited response.

1. Collar is stupid and should really be considered like a error in marking the perimeter. Throw these away or edit. Maybe make a section called discarded samples that's stupid but yeah.
2. Vessels suck sometimes. In the portion above, 1602443, there's a random blood clot which gets identified at large σ . But also the small forked shaped thing which is obviously a vessel doesn't get defined.
3. Too much blood (not enough?? no idea) is left in the vessels. leading to the weird

white border around some vessels. you could identify these along with black center and combine them somehow. no idea. Also, holy shit, some of the white vessel "sleeves" ARE identified in the tracing, and some aren't. Find an example of this and whine about it.

4. Umbilical cord insertion point is stupid and obscures a lot. The tracer guesses but there's no real guiding principle AFAIK..
5. Small vessels aren't accounted for at all. Not sure how to coincide measurement in terms of scale space anymore, but should figure out how to cut off those values before running MCC metric.

An example of bad samples that performed comparatively poorly across all segmentation methods can be found in the [??](#). You can see that there is a lot of "noise" on the sample itself, and in some cases the vessels are much larger than other samples and therefore weren't picked up.

Results

In fig. 24, we demonstrate the usefulness of stricter parameters for the Frangi filter. Since the Frangi vesselness measure is a "probability-like" score, we should be interested—without doing any actual segmentation yet—to what extent this score aligns with the ground truth in a cumulative sense. We should hope at least that larger values of V_{\max} define the cumulative vesselness ratio by “integrating” the max vesselness score over pixels in the ground truth and over the entire image and considering the ratio:

Definition 9.1. *The cumulative vesselness ratio for a particular parametrization of the multiscale Frangi filter is given by*

$$CVR(V_{\max}) := \frac{\sum_{G \subset I} V_{\max}(x_0, y_0)}{\sum_I V_{\max}(x_0, y_0)} \quad (9.1)$$

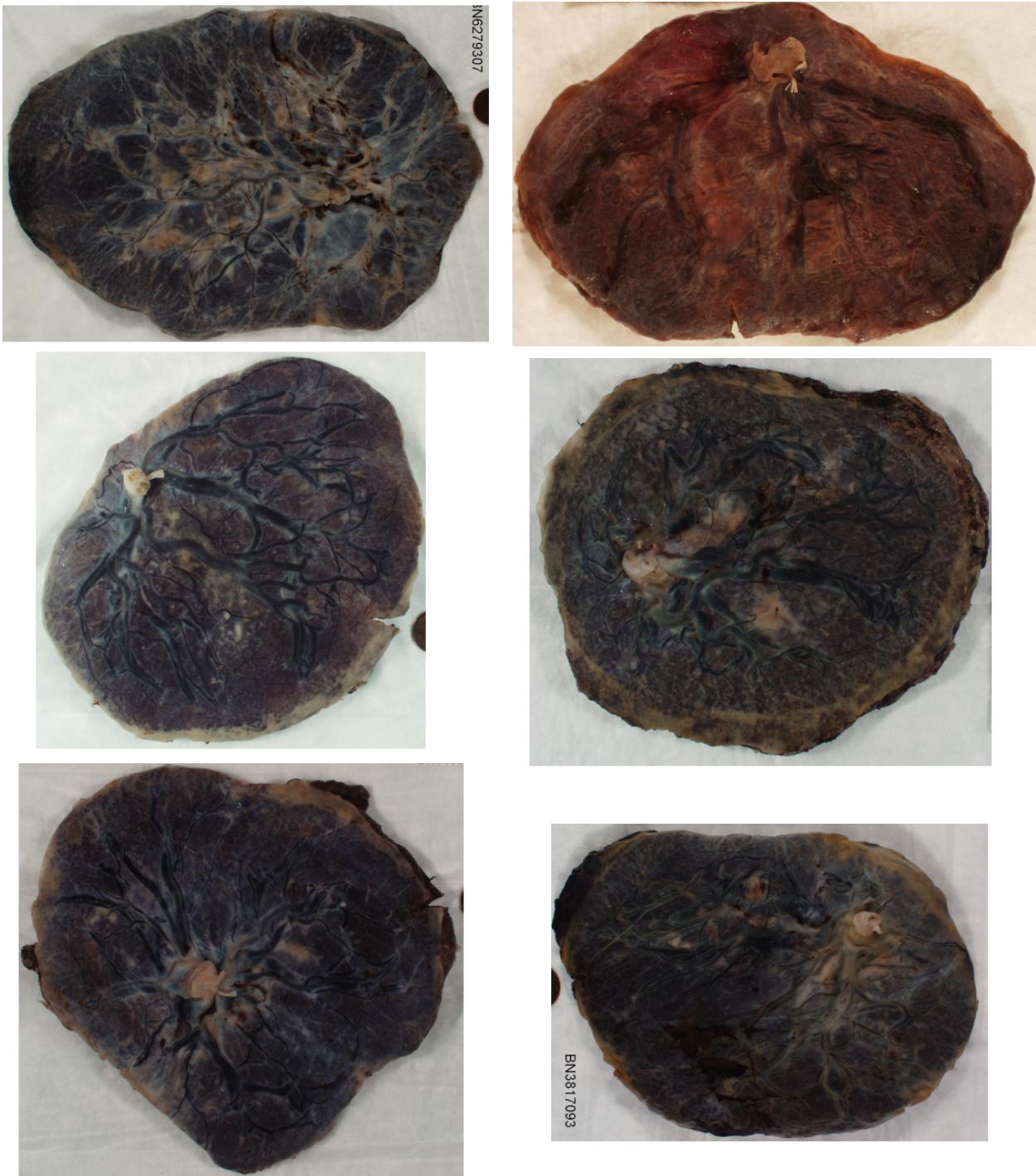


FIGURE 23: Bad samples

where the sums on top and bottom are being carried out for all pixels (x_0, y_0) in the "ground truth" subset G in the image \mathbf{I} and over the entire image \mathbf{I} itself, respectively.

fig. 24 shows \mathcal{V}_{\max} for two well-behaved samples with reported CVR. We see in both cases that stricter parameters (smaller β and larger γ) correspond to an increased CVR. Each of these sample was run over the same scales (logarithmically spaced from $2^{-1.5}$ to $2^{3.5}$ with $N = 20$ and the color output of each \mathcal{V}_{\max} is normalized between 0 and 1.

In fig. 28 we show how the CVR is affected for 25 of the "best" samples, that is, those that generally fared better for segmentation techniques. This shows that the results of fig. 26 and fig. 27 hold in general for all "well-behaved" samples in our image domain.

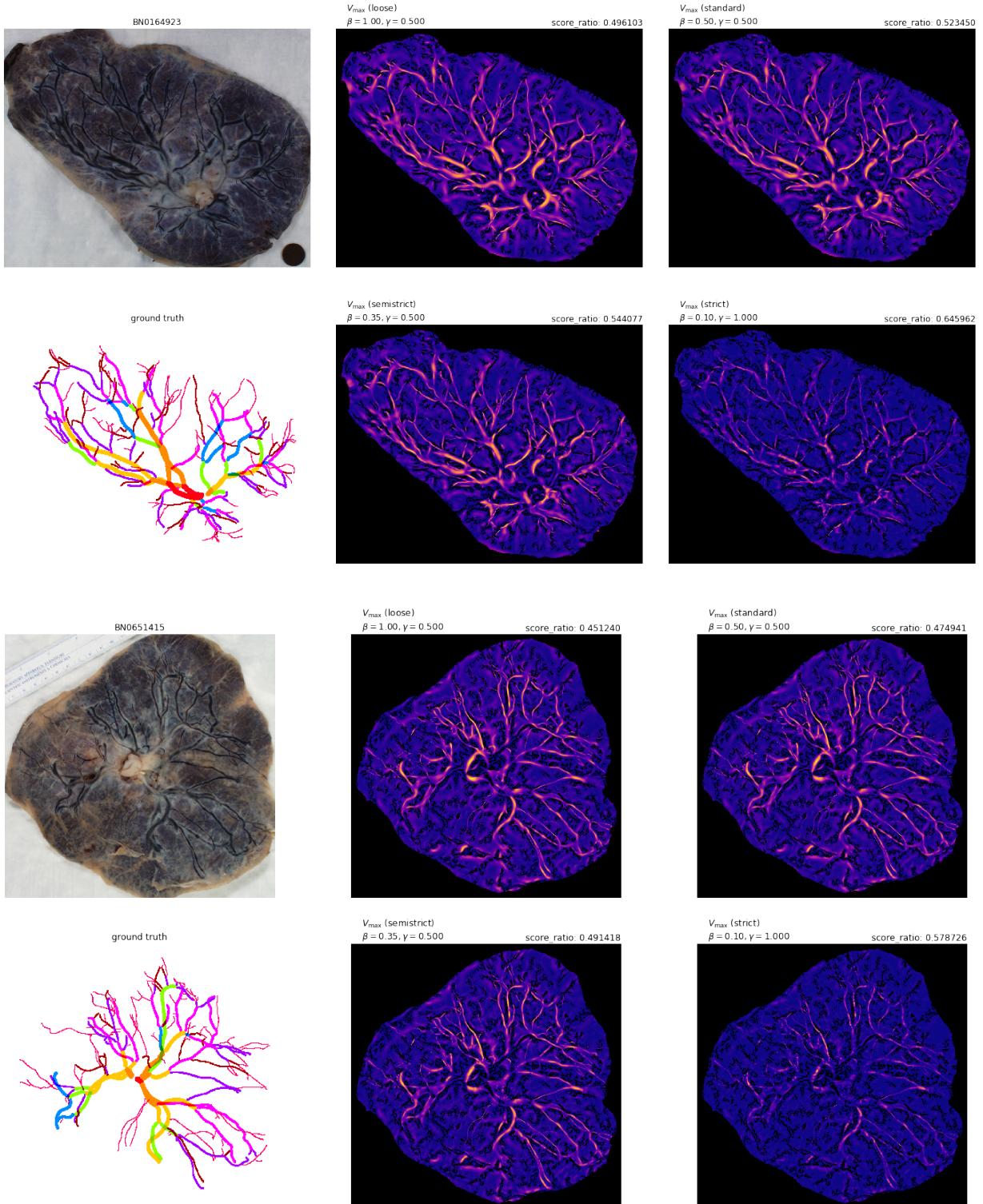


FIGURE 24: \mathcal{V}_{\max} and CVR for different parameter choices

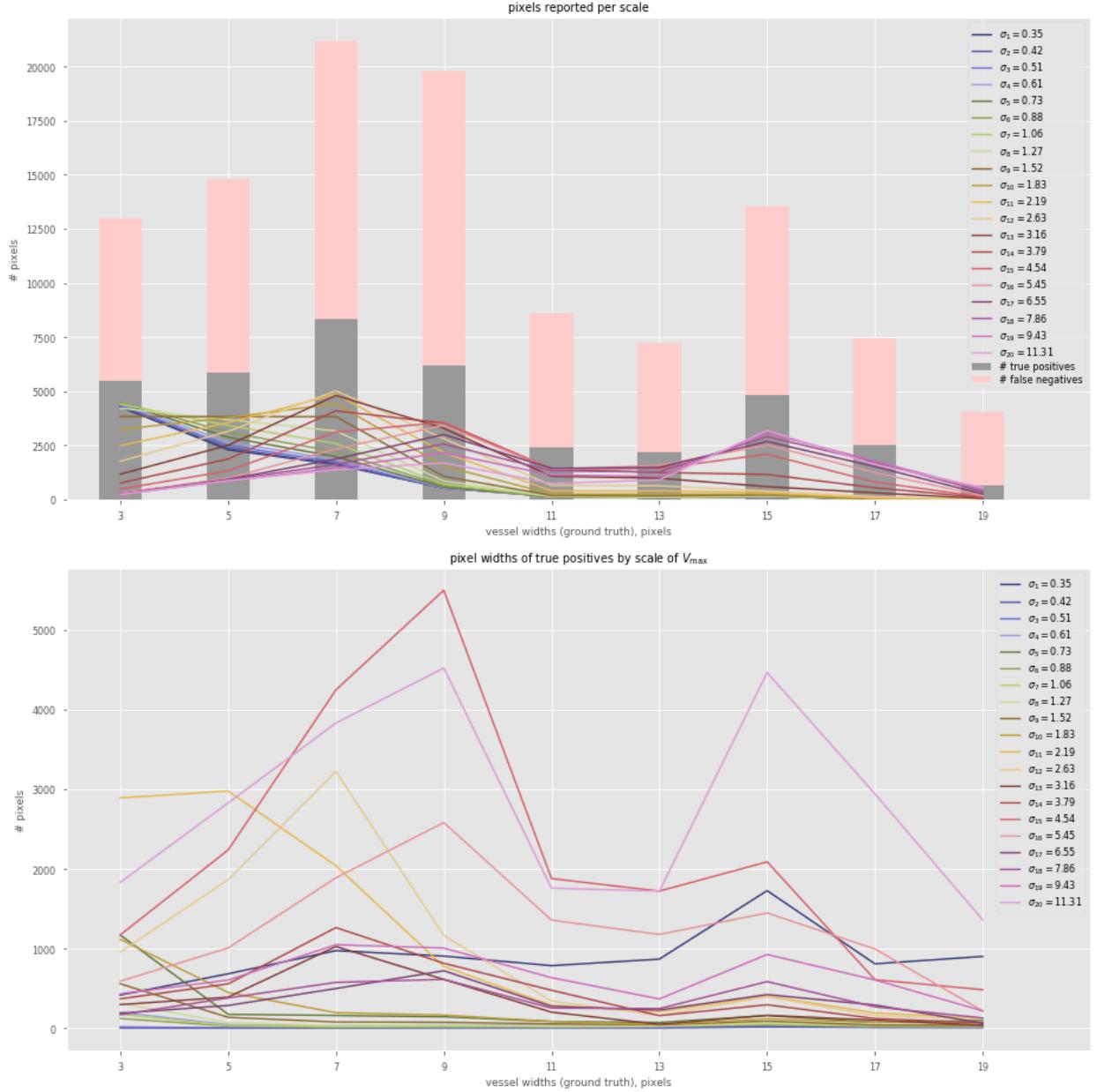


FIGURE 25: Pixel Width of Ground Truth vs. Scale Length for True Positives

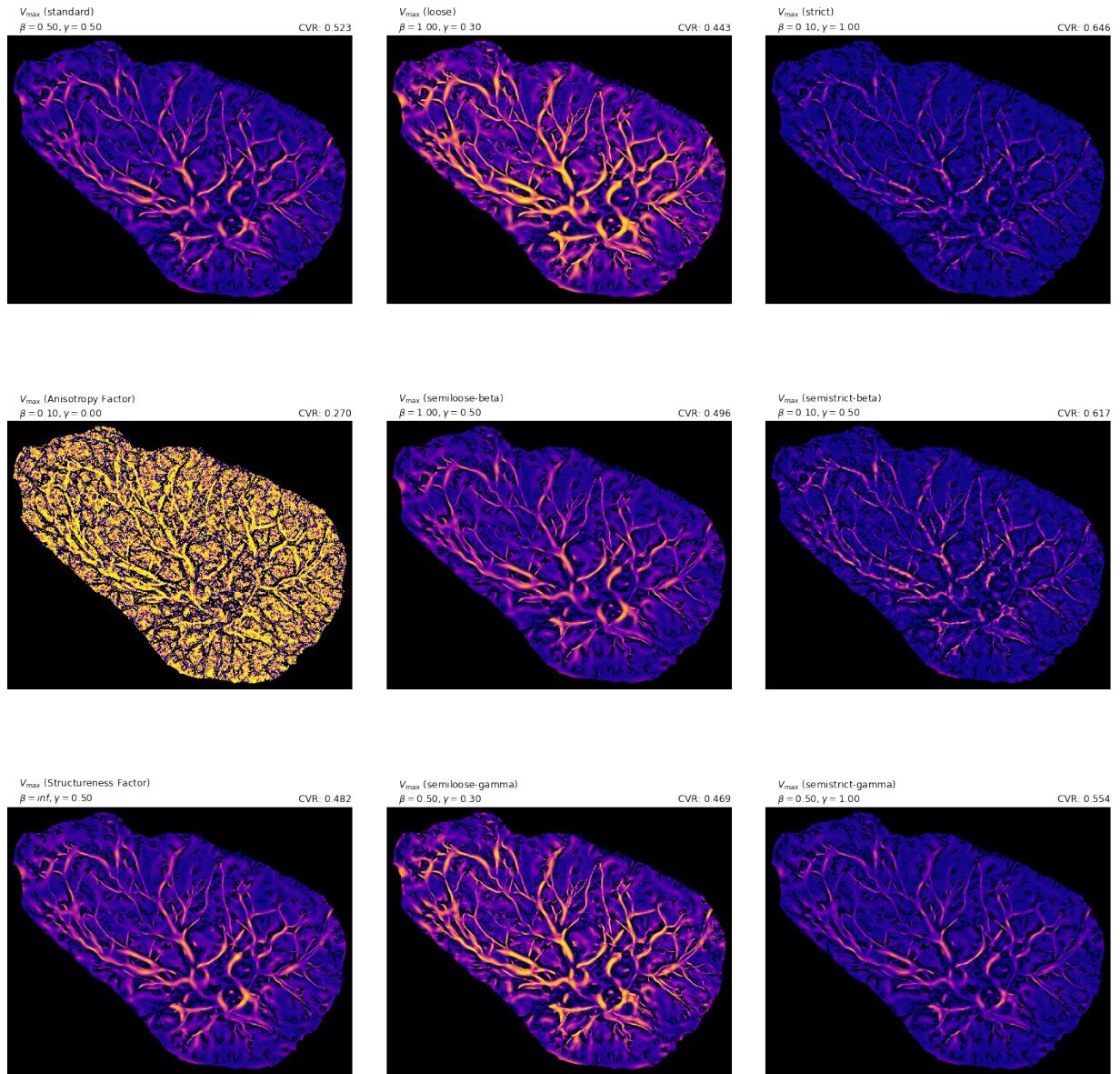


FIGURE 26: V_{\max} and CVR for varying multiscale Frangi parametrizations (Example 1)

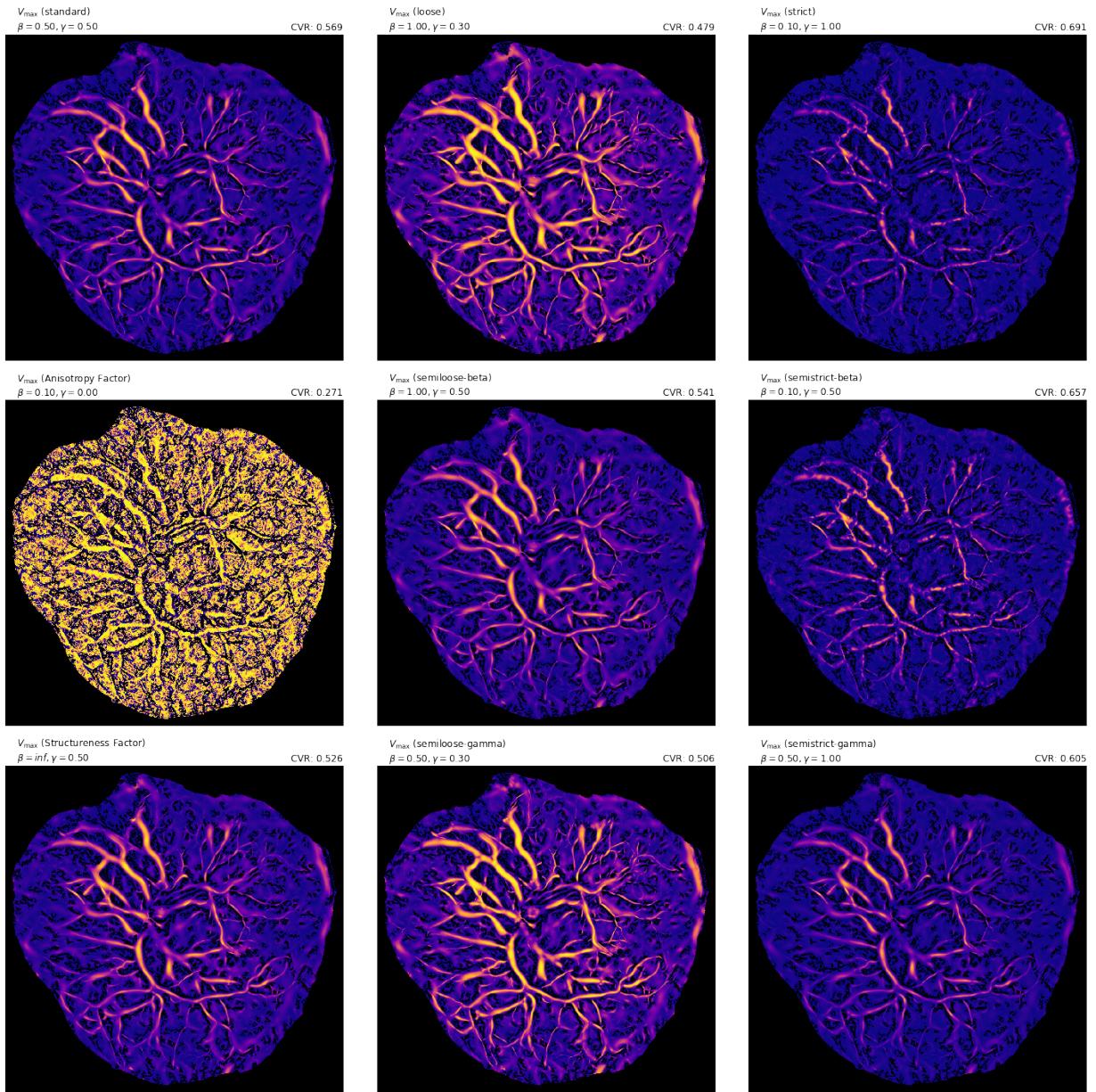


FIGURE 27: V_{\max} and CVR for varying multiscale Frangi parametrizations (Example 2)

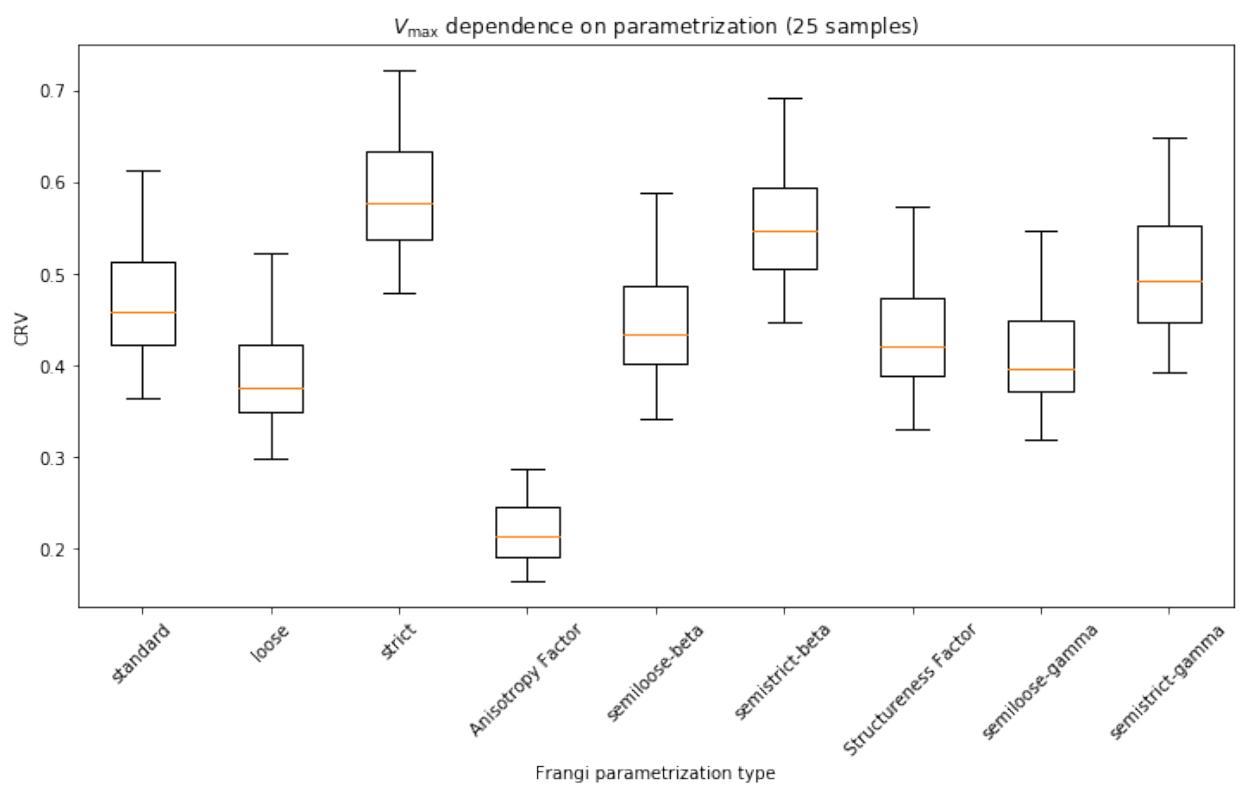


FIGURE 28: CVR scores of 25 samples under varying parametrizations

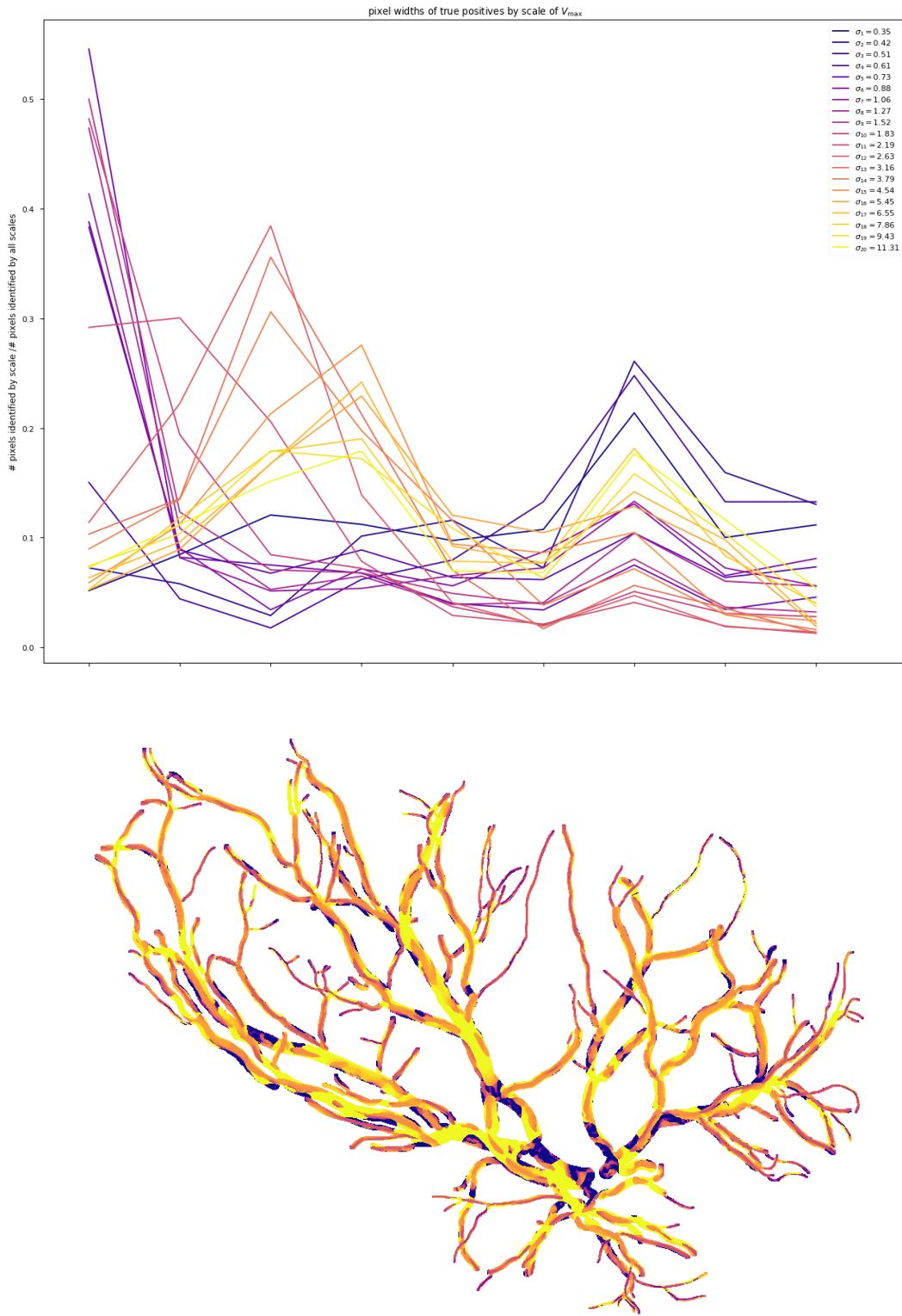


FIGURE 29: Scale of maximum Frangi score for true positives and false negatives

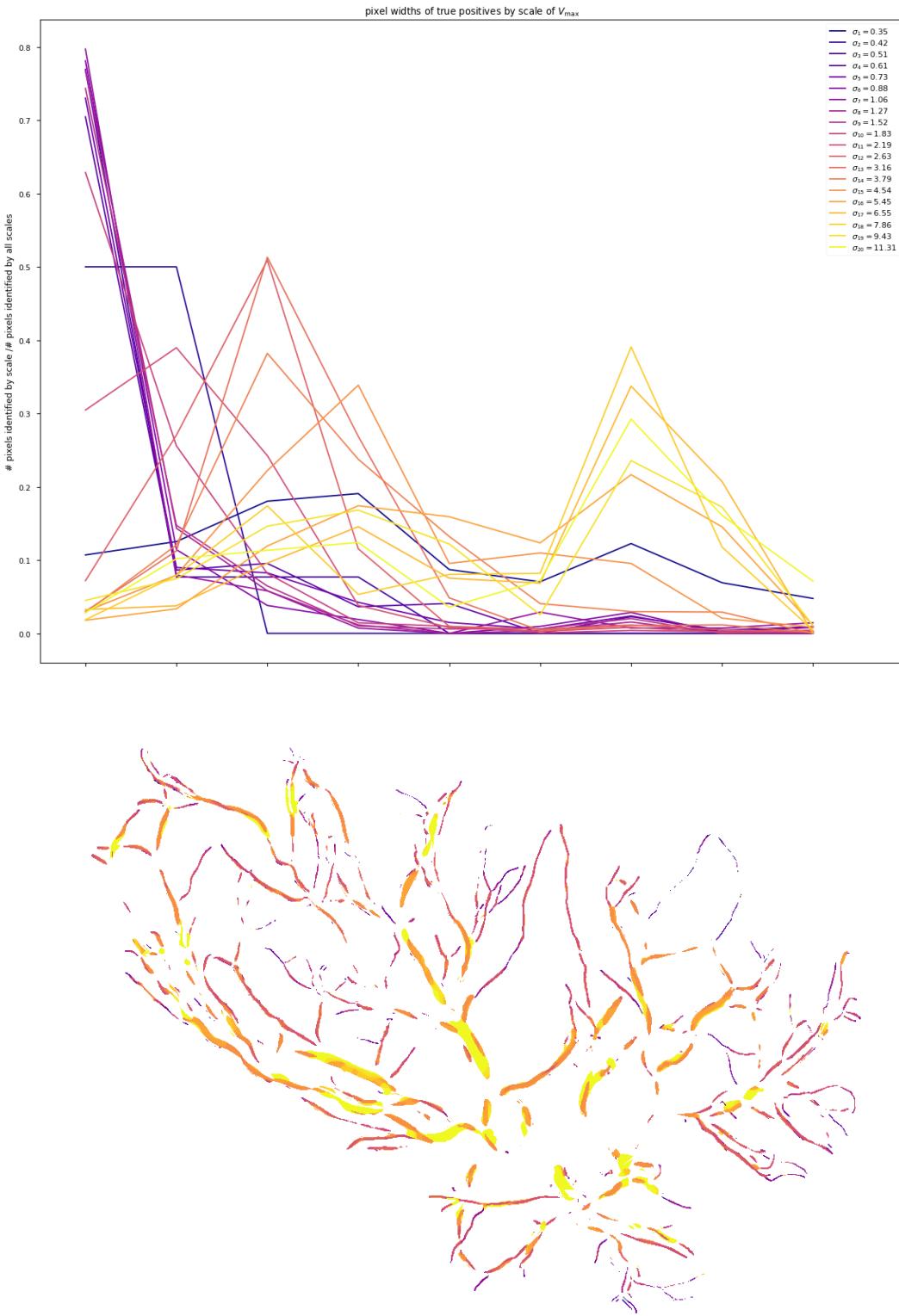


FIGURE 30: Scale of maximum Frangi score for true positives only (percentile filtering)

CHAPTER 10

SEGMENTATION

We discuss how we use the Frangi as a prefilter and discuss several different segmentation strategies, and describe our "strawman" which is the ISODATA threshold. First, we define some standard quantitative measures of success for segmentation methods.

Binary Classifications and the confusion matrix

We wish to come up with a means of gauging the success of an arbitrary segmentation and will adopt a binary classification model to do so. We end up with a boolean matrix the size of the image, and compare it to the ground truth, the trace, and then compare them to get the number of true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN). We demonstrate these four labels visually with a confusion matrix, as in fig. 31. The lighter gray represents true negatives (TN), red represents false negatives (FN), blue represents false positives (FP), and black represents true positives. The darkest gray area is the background mask (pixels are not considered at all in gauging the success of segmentation).

Although there are many measures to gauge the success of binary classification, we will focus on two that we find particularly illustrative. The first is precision, given by

$$\text{precision} = \frac{TP}{TP + FP} \quad (10.1)$$

and the second is the Matthews Correlation Constant (MCC), given by

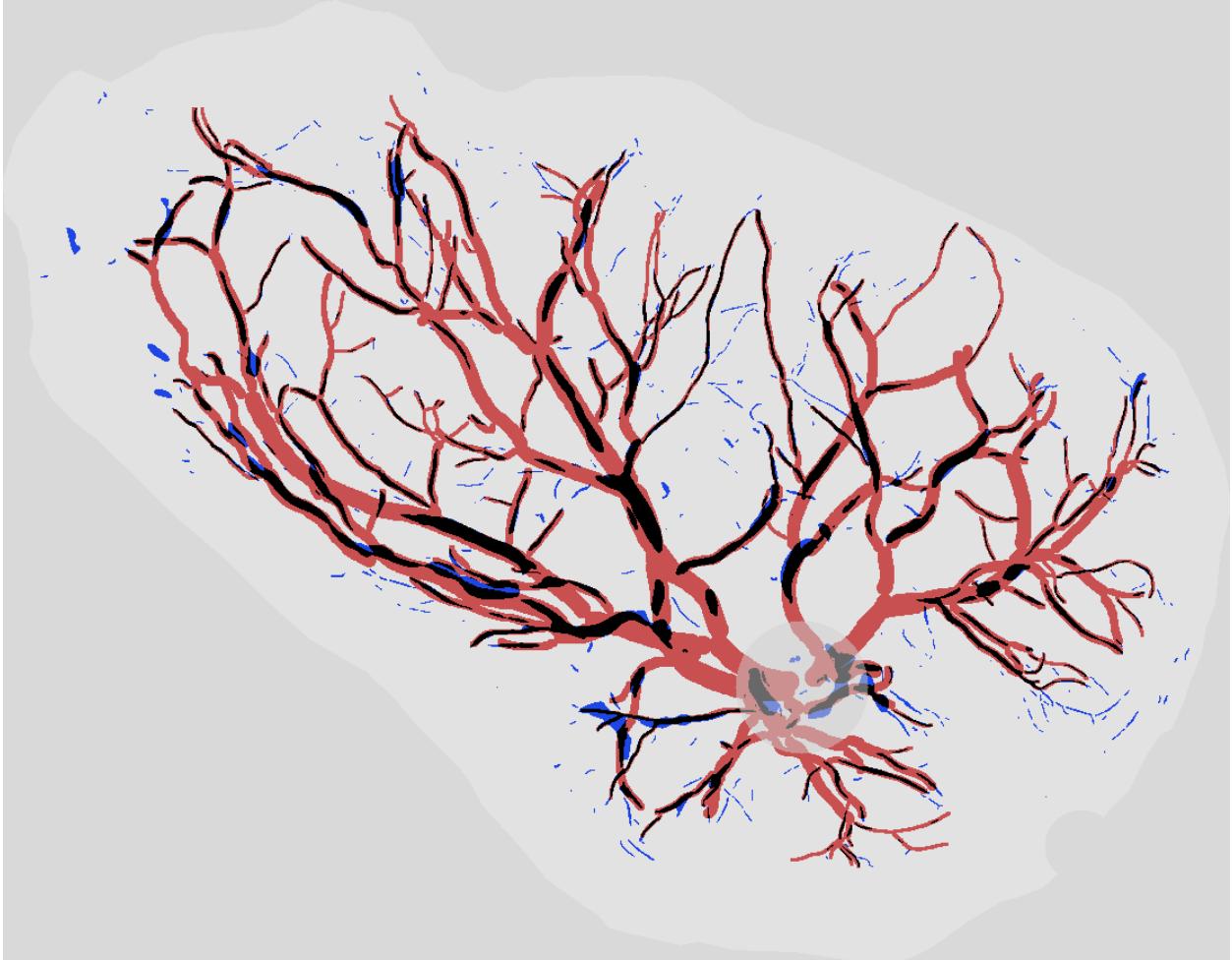


FIGURE 31: Sample confusion matrix

$$MCC = \frac{TP \times TN - FP \times FN}{\sqrt{(TP + FP)(TP + FN)(TN + FP)(TN + FN)}} \quad (10.2)$$

where precision is a ratio between 0 % and 100% and the MCC is a measure between -1 and 1. Precision (or positive predictive power) is of course a ratio between how many pixels were labeled correctly and all pixels labeled positive (correctly or incorrectly). This is a useful score for us—if we are using Frangi as a prefiltering for a more robust technique, we would not want to provide any wrong information or seeds to that algorithm. Precision therefore does an okay job of representing that scenario: we are not penalized for what we do not label as true, as long as our reports of true are correct.

Of course, we cannot rely on precision as our sole quantitative factor alone—we could simply return everything negative and receive a perfect score of 100% precision. Therefore we will gauge that measure with that of the MCC [29]. The main advantage of the MCC is that it is well balanced no matter what the size of the two classes are, and will only be high if the approximation scores well against both labels. A score of 1.0 means the approximation is 100% correct, a score of -1.0 means that everything is completely incorrect, and a score of 0 means that the test performs only as well as random guessing. In our analysis, we will consider both the MCC and precision of a particular segmentation simultaneously. We would like an MCC score as high as possible, but will contextually settle for a lower score as long as the approximation is still *precise*.

One final point about these measures is that we have decided to report their scores only within the placental plate, rather than the entire rectangular image. Since the area outside of plate is masked from consideration, those points will be true negatives no matter what, and we don't want this artificial padding to influence our score. That being said, we do currently concede one part right now: we will also mask an area around the umbilical cord insertion point, as the large amount of noise here will mean that our scores are artificially low. We would like to remove these areas, but for now we will

simply not score them.

Postprocessing Techniques

We display several four relatively immediate postprocessing techniques on the multiscale Frangi output to obtain an actual PCSVN extraction. Again we stress that the Frangi filter itself does not produce a segmentation, but instead could be used as a preprocessing step. In fact, Frangi in his original paper [12] refrained from any explicit analysis of the Frangi score apart from taking the maximum across all scales, as in ??.

Still, we wish to demonstrate some several immediate methods of postprocessing these samples in order to illustrate the usefulness of this optimized Frangi filter.

Method A: Fixed Threshold

In the fixed threshold method, we say that a pixel (x, y) of the image corresponds to a vessel if $V_{\max} > \alpha$. This α , as noted above, is unfortunately highly dependent on the image domain, and this merging method will tend to happily allow noise generated from scales that are too large or too small. . Another issue with this is the individual scales of the Frangi filter in the extreme cases are not known to scale—although Lindeberg introduced a normalization factor based on the scale to apply to the derivatives, we do not know of an optimal factor to use.

Unfortunately, even with our “rescaled” Frangi filter, this α cannot be picked without regard for the particular image domain. Equally problematic, we cannot guarantee that the Frangi filter will decay as our scale exceeds the the bounds where structure is expected to be found. Ideally we could create a filter that would do that.

Nonetheless, we wish to demonstrate the usefulness of the Frangi filter within our image domain towards the segmentation problem, and will therefore, like [2], consider a

thresholded \mathcal{V}_{\max} as a crude segmentation.

$$\mathcal{V}_{\Sigma\alpha}(x_0, y_0) = \begin{cases} 1 & \text{if } \mathcal{V}_{\max}(x, y) \geq \alpha \\ 0 & \text{else} \end{cases}, \quad , \alpha > 0 \text{ for } \alpha \text{ fixed.} \quad (10.3)$$

If we insist on such a performing such a thresholding, the “correct” choice of α unfortunately seems to depend on the image domain, so user intervention when dealing with the problem domain seems to be the best strategy (referred to in the code as **nz-percentile**). For lack of any better strategy, we could calculate a high percentile of the data and threshold there. Due to the large number of zeros outputted by the filter, we opt instead to take the q th percentile of only nonzero values of V_{Σ} .

A more sincere use of thresholding might be to select a very high threshold, and then use those as seeds for a further technique. We will discuss alternatives methods of aggregating results from our multiscale method, as well as optimal values for parameters and scales. As a final note, we admit that any future extensions of this work (as will be discussed in chapter 12) should not hold too much stock in this thresholded result, and analyzing the raw vesselness score eq. (5.1), or even the un-merged scale-wise scores, would be far more rewarding.

Method B: Percentile Based Merging

The idea behind percentile-based merging is beneficial for large multiscale methods. At each scale, we would like to assume that there is *some* curvilinear content that could be identified. With that in mind, we could simply accept from each scales scores in a very high percentile. We chose for our demonstration a fairly large percentile, 95, and furthermore boster this by requiring that any selected pixels be in the 95th percentile of nonzero and unmasked pixels—otherwise the average is artificially low due to the large background and pixels with zero Frangi score. The use of percentiles

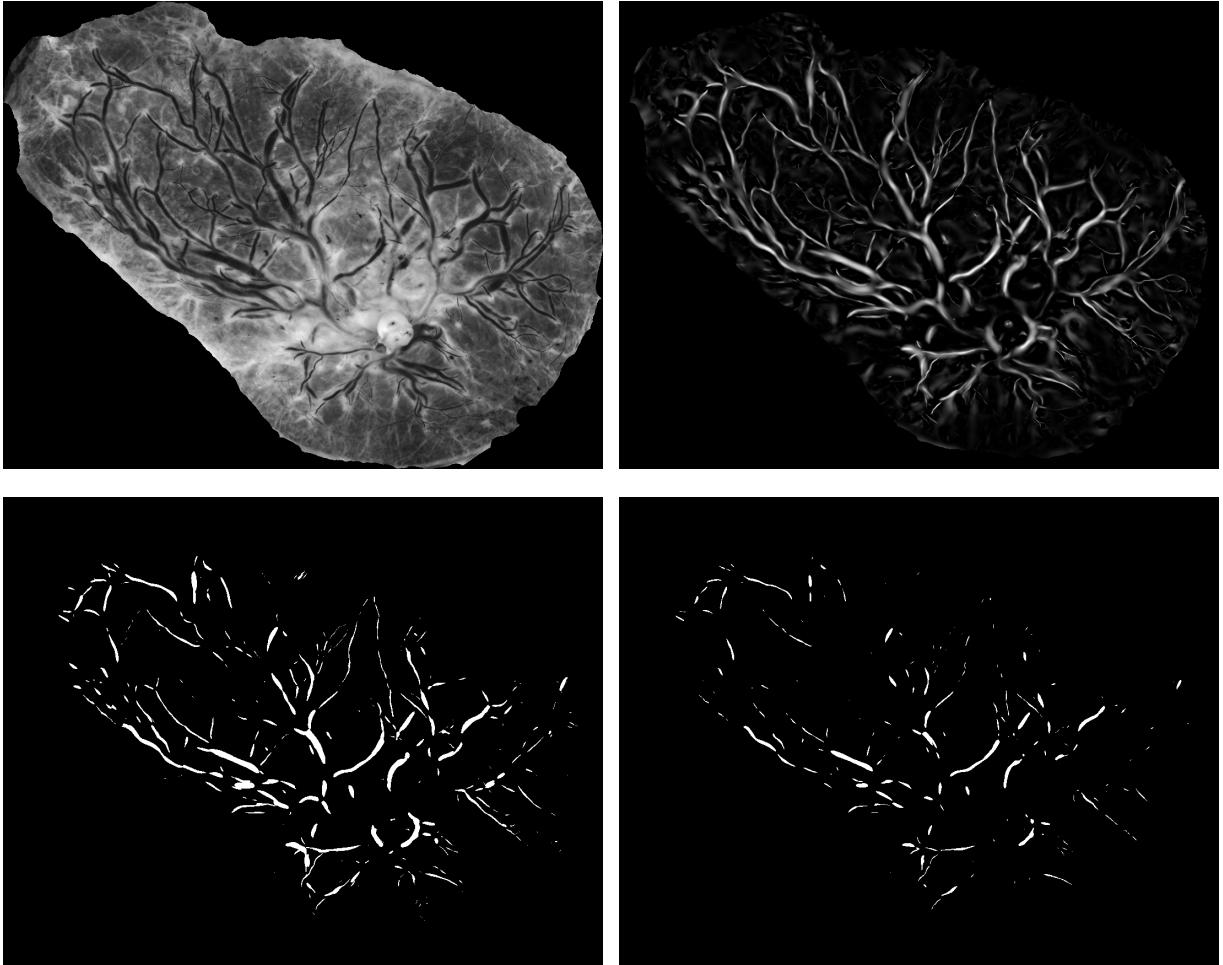


FIGURE 32: Nonzero-percentile thresholding of \mathcal{V}_{\max}

removes dependence of picking a particular threshold on the problem, while allowing the most prominent features to emerge at each scale, but of course it unfortunately treats all scales equally, so the success of the multiscale approach here is very dependent on choice of σ_{\min} and σ_{\max} .

We briefly demonstrate this in fig. 32 on a particularly well-behaved sample. The top left value image is the original (grayscale image), the top right is \mathcal{V}_{\max} , the bottom left is the 95th percentile of nonzero scores of each scale, and the bottom right is the 98th percentile of nonzero scores at each scale.

Method C: Scale-Based Random Walker

We observed that areas where Frangi scores are zero in well-behaved samples seem to neatly outline prominent vascular features. Following this idea, we employed a random walker segmentation [30] (which is implemented by `scikit-image`). Random walk segmentation comes about by solving a diffusion problem over a discrete array (in this case, the Frangi vesselness score itself) given starting markers. At each scale, we positively labeled pixels whose Frangi score was very high ($V_\sigma(x_0, y_0) > .4$), and negatively labeled pixels whose score was 0 (i.e. where the leading principal eigenvalue was positive). The result of this technique is demonstrated in ?? and the result (along with the original sample for comparison) is shown in fig. 34. In ??, the first column is the Frangi vesselness score at that scale, where black is a score of 0, to emphasize the difference between a score of zero and even a very small positive score, which appear in blue. The middle score are markers passed to the random walker—blue are seeds labelled with a “1” (where the Frangi vesselness score is 0), green is labeled “2” (where $V > .4$), and purple represents unknowns that will either assigned either label. In the last column, the result of the random walker is given—areas that have been added to the label “2” are shown in yellow. Although the result of random walker segmentation is technically a binary matrix, we still show the original seeds of label 2 in green for easier comparison. Similarly, the purple in the right column has actually been labeled “1” for non-vascular, but is left in its original color to emphasize what was assigned background. In fig. 34 we show the original image and the result of merging all positively marked pixels at each scale. Black means the pixel was unmatched, while increasing colors of blue (larger scales) to white (smaller scales) indicate the smallest scale from which a pixel was marked after the random walker technique. Though we shall set up the multiscale method slightly differently in chapter 9, we used a Frangi anisotropy coefficient of $\beta = 0.35$, and 12 scales logarithmically spaced from $\sigma_1 = 2^{-1.5}$ to $\sigma_{12} = 2^{3.5}$ to generate

these figures. There is a parameter for the random walker algorithm (unfortunately also called β) which serves as a diffusion penalization coefficient (larger values making diffusion over the image less likely). We used `scikit-image`'s default value of 130.

Method D: Scale Based Sieving

Our final approach seeks to include not only pixels at each scale that pass a high threshold, but also adjacent pixels at that scale that pass a lower threshold. We proceed as follows. At each scale, take a low threshold, then label each connected region. Then, iterate through each labeled region and add to the final approximation any labeled region that contains a pixel that passes a higher threshold.

Method E: Trough Filling

As we discussed in section 5.1, we can simultaneously calculate the Frangi filter for light and dark curvilinear structures without any added computation time. We have shown the signed result of the Frangi filter at different scales two examples in fig. 35 and fig. 36, we can simultaneously calculate for a dark background and a light background. Since the Frangi filter normally throws away any response where $\lambda_2 < 0$ (if dark curvilinear features are targeted) or $\lambda_2 > 0$ (if light curvilinear features are targeted), we lose no computation time at all (although we must store more results). After computing the multiscale result, we can easily separate these into a positive and a negative strain, which we will denote $\mathcal{V}_{\max}^{(+)}$ and $\mathcal{V}_{\max}^{(-)}$. Our $\mathcal{V}_{\max}^{(+)}$ is the same as our \mathcal{V}_{\max} before, and $\mathcal{V}_{\max}^{(-)}$ is the same result as if we had taken the Frangi filter while only looking for the opposite type (light/dark) curvilinear feature. Plotting \mathcal{V}_{\max} over a scale of $[-1, 1]$ demonstrates an interesting effect. Whereas the Frangi filter generally is not reliable in terms of accurately predicting widths, we *can* get a sense of the width by looking at where there is a relatively strong response of opposite sign.

That is, at the "foot" of every trough on either side, we can see a bordering curvilinear structure of opposite sign. We perform strict Frangi filtering and separate the

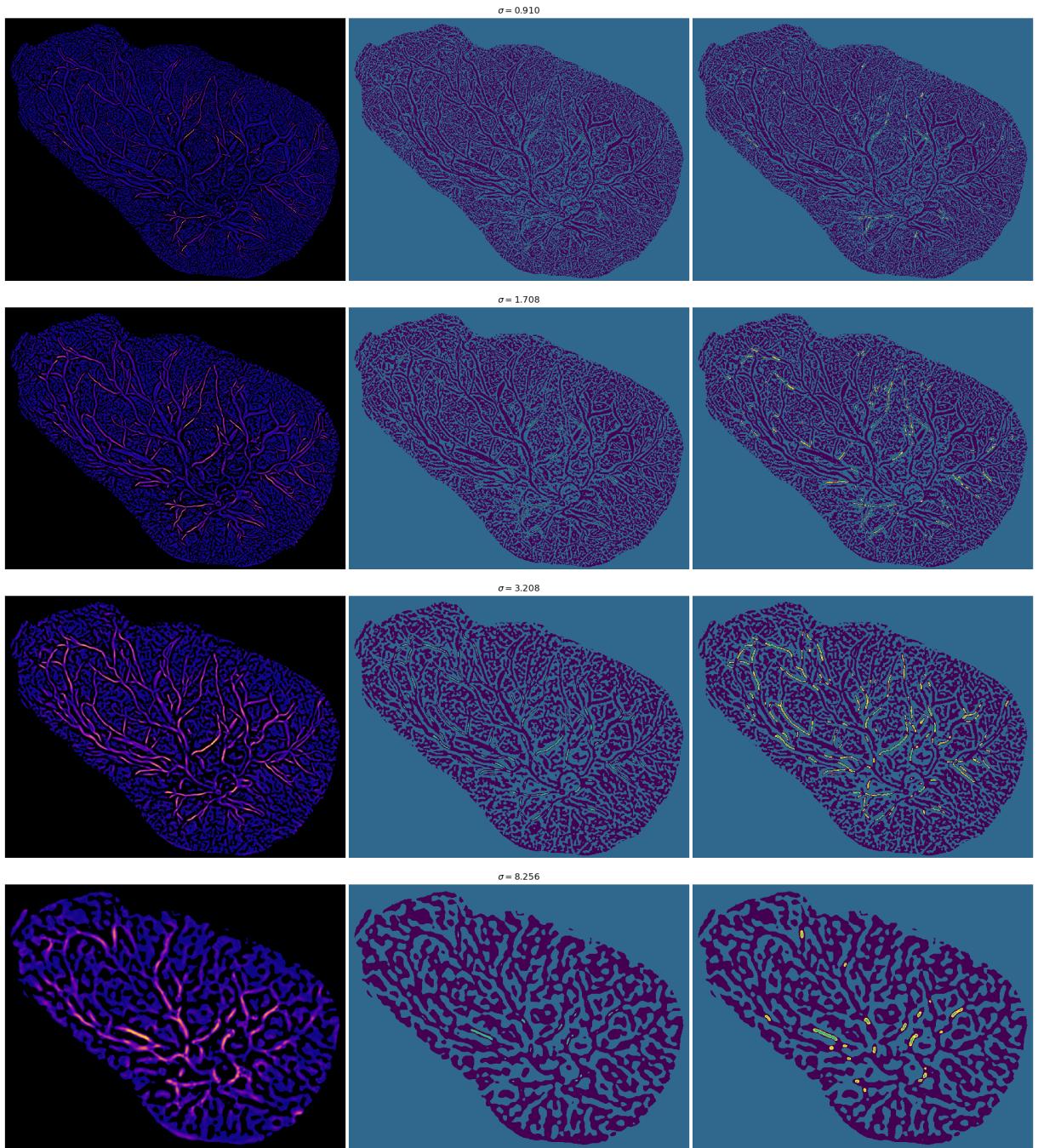


FIGURE 33: Scale-wise random walker segmentation (select scales)

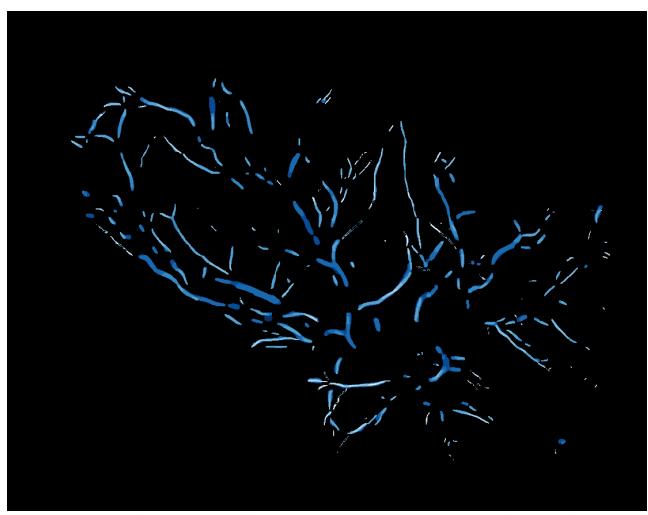


FIGURE 34: Random walker segmentation (result and sample)

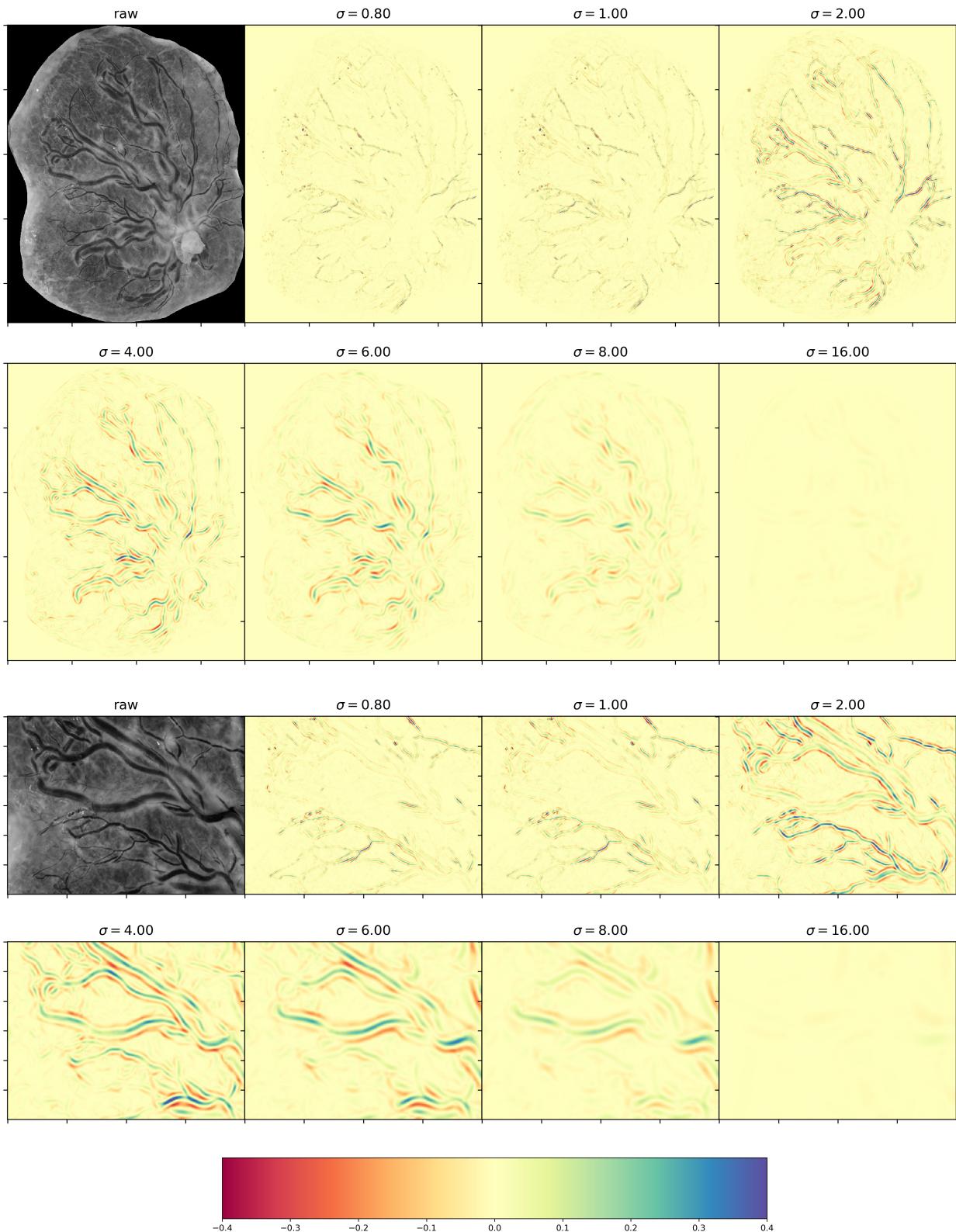


FIGURE 35: Signed Frangi output (plate and inset) (Example 1)

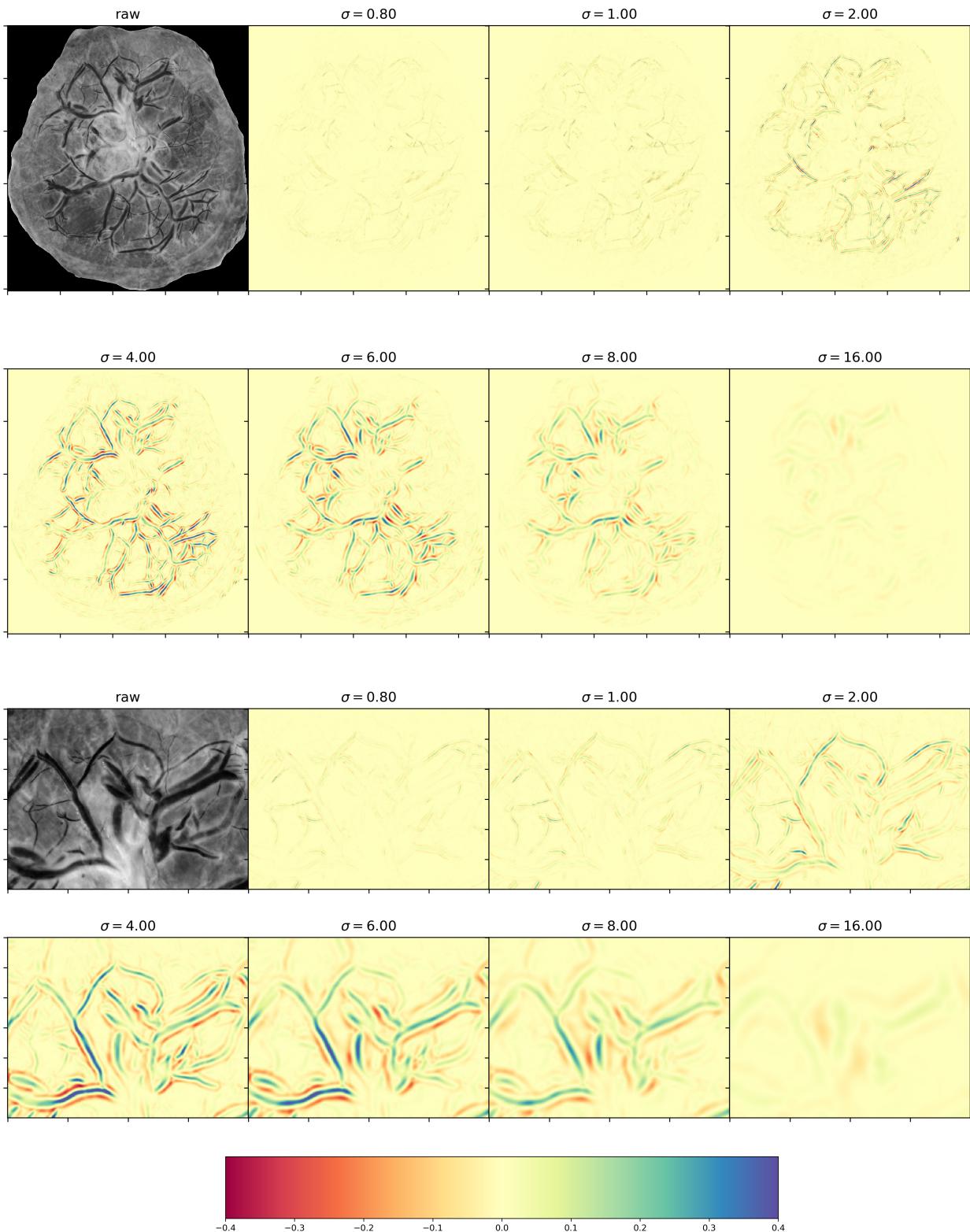


FIGURE 36: Signed Frangi output (plate and inset) (Example 1)

positive and negative components. We then perform a different threshold for each signed portion of the Frangi response—a strict one (say $\alpha^{(+)} > .4$) for the conventional \mathcal{V}_{\max} , and a much looser one for our opposite signed $\mathcal{V}_{\max}^{(-)} > \alpha^{(-)} = .05$. We also truncate the scales we consider for calculating $\mathcal{V}_{\max}^{(-)}$, say only the first 12 of 20.

We then perform a morphological thinning operation on our positive (or standard) Frangi response. We will refer to this thinned approximation as the “spine” and the (un-thinned) opposite signed component as the “margin.” For each pixel on the thinned spine, we iterate over disks of integer radius and dilate the pixel by a disk of that radius if that disk coincides with a margin point.

This allows us to extend the Frangi output from the point where it’s strongest all the way to the base of the curvilinear structure, providing a much better indication of the true width of the curvilinear structure.

CHAPTER 11

PRIMITIVE NETWORK COMPLETION

In this chapter we discuss the idea of network completion and demonstrate a relatively brute-force method of using a segmentation result to solve some of the network completion problem.

One of the biggest shortcomings of our demonstrated segmentation methods is that they frequently result in gaps in parts of the network. We demonstrate a way to rectify this problem in certain situations, and then discuss how to extend these arguments to fill larger, more uncertain gaps.

First, once we've produced a segmentation, we thin it down with [31] and look for endpoints of an otherwise connected point. Using a 3×3 structuring element, we iterate over each pixel and identify how many local neighbors it has. If a pixel has zero or one local neighbors, we identify it as an endpoint of the partial network. After identifying these endpoints, we assign each a label (i, j) depending on where the neighboring pixel is located, as according to fig. 37. We deem two endpoints potentially connectible only if they're not connected on the same side. That is, their labels (i, j) and (i', j') must have $i \neq i'$ or $j \neq j'$ (unless i or j is 1). For example, if an endpoint is connected to the partial network on its top side, any endpoint that connects to it cannot also be connected to a network on its top. If a pixel has no connections at all, with label $(1, 1)$, we do not restrict its connections at all. To save time (though we don't anticipate it will affect the result much), we also restrict pairs from being more than a set distance away (in this case, 100 pixels in Euclidean length).

After we limit the connections, we consider each pair of endpoints and draw a

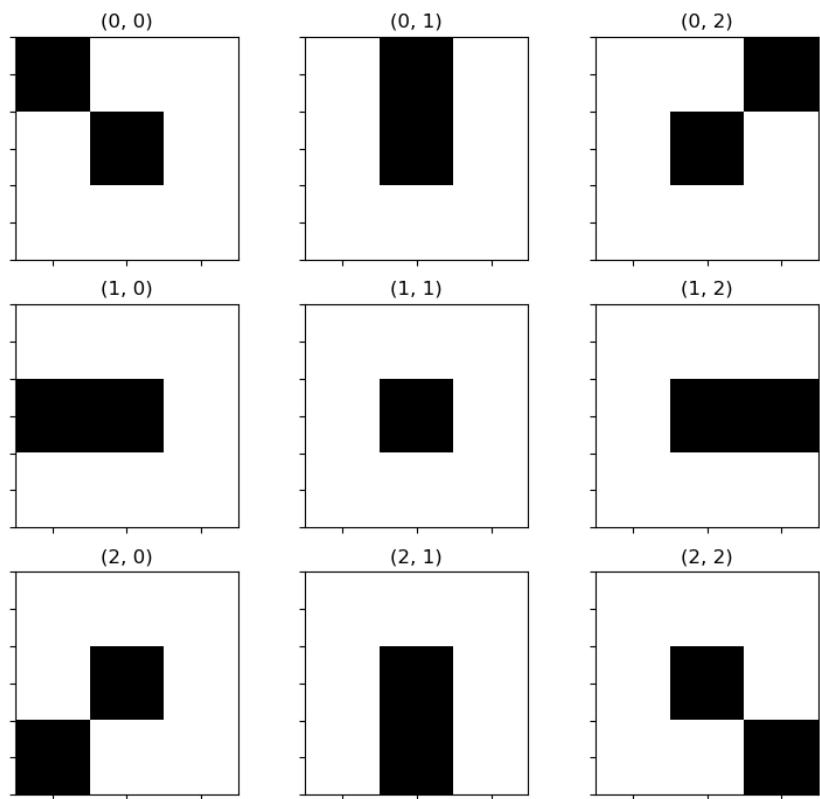


FIGURE 37: Endpoints labels based on adjacent neighbor location

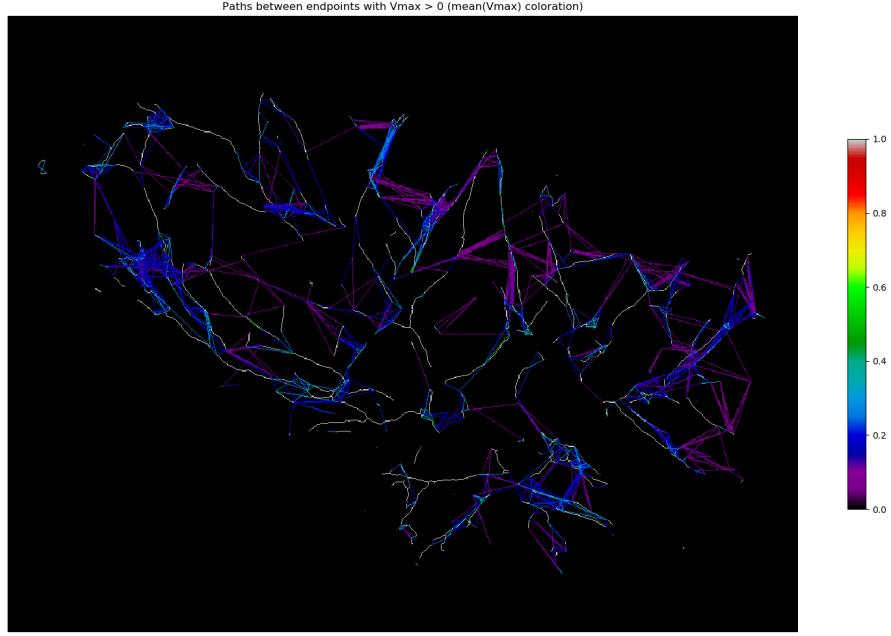


FIGURE 38: All lines between endpoints with nonzero \mathcal{V}_{\max}

straight line segment between the two. If that passes through a point where \mathcal{V}_{\max} is 0, we disallow that pair as well. We also disallow any line which crosses any part of the network which is known to exist. Finally, from the list of all remaining pairs of endpoints, we simply select the path along which the maximum mean value of \mathcal{V}_{\max} is achieved. fig. 38 shows non-violating paths between end-point pairs, and ?? shows a partially completed network (in yellow) overlaid on \mathcal{V}_{\max} .

We show the complete process for comparison on two different samples.

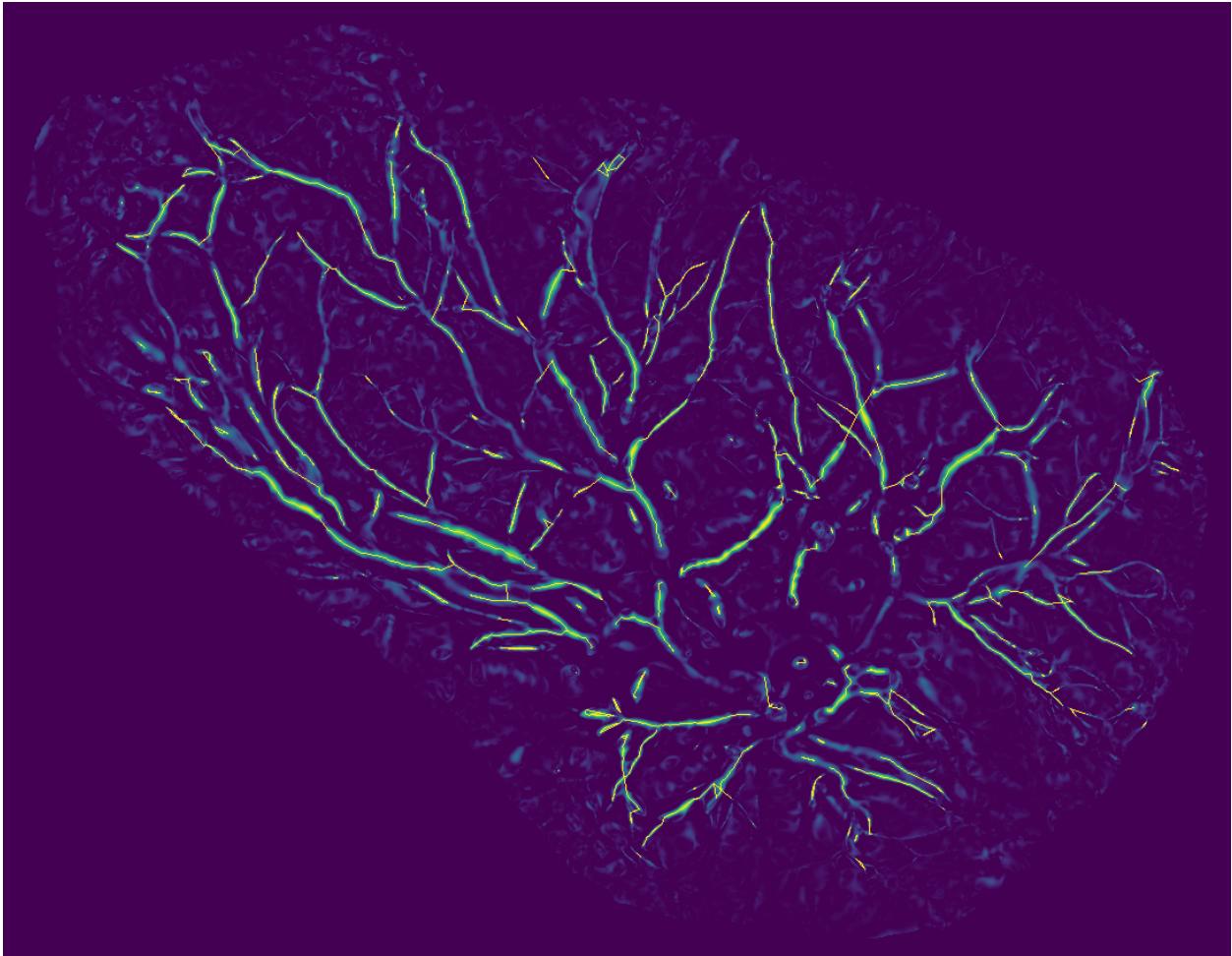


FIGURE 39: Partially completed network

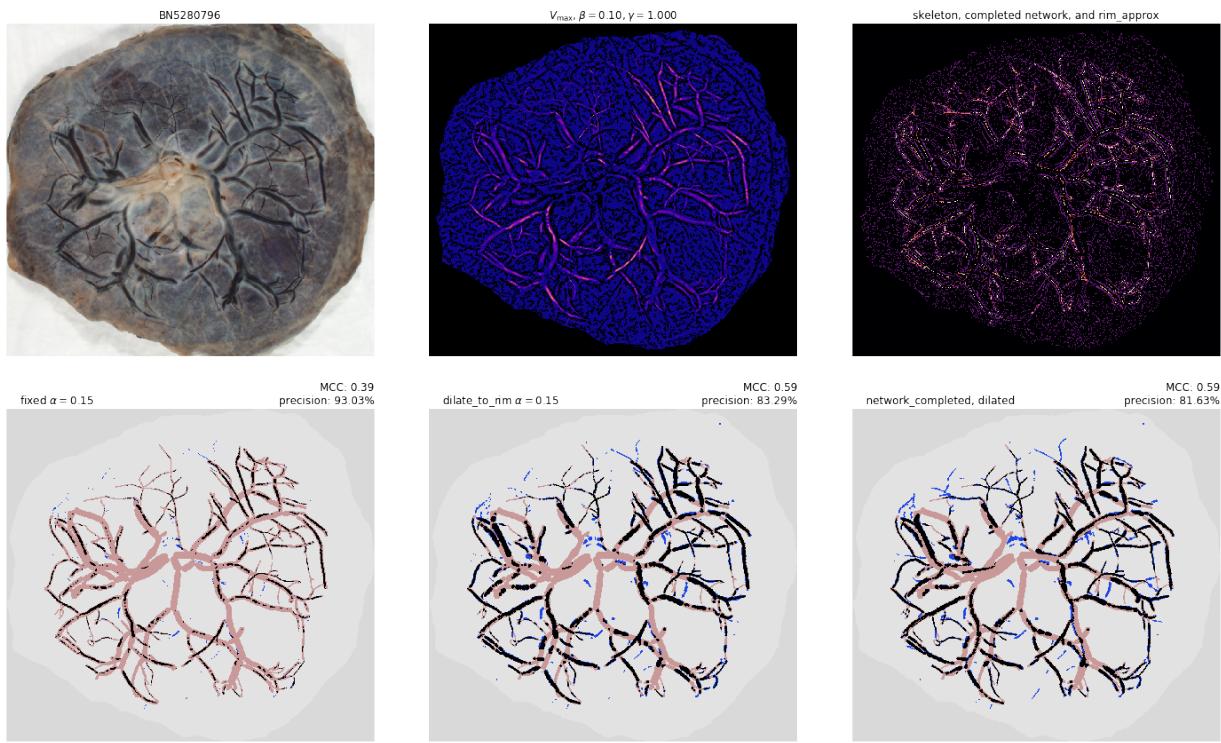


FIGURE 40: Trough Dilation and Network Completion (Example 1)

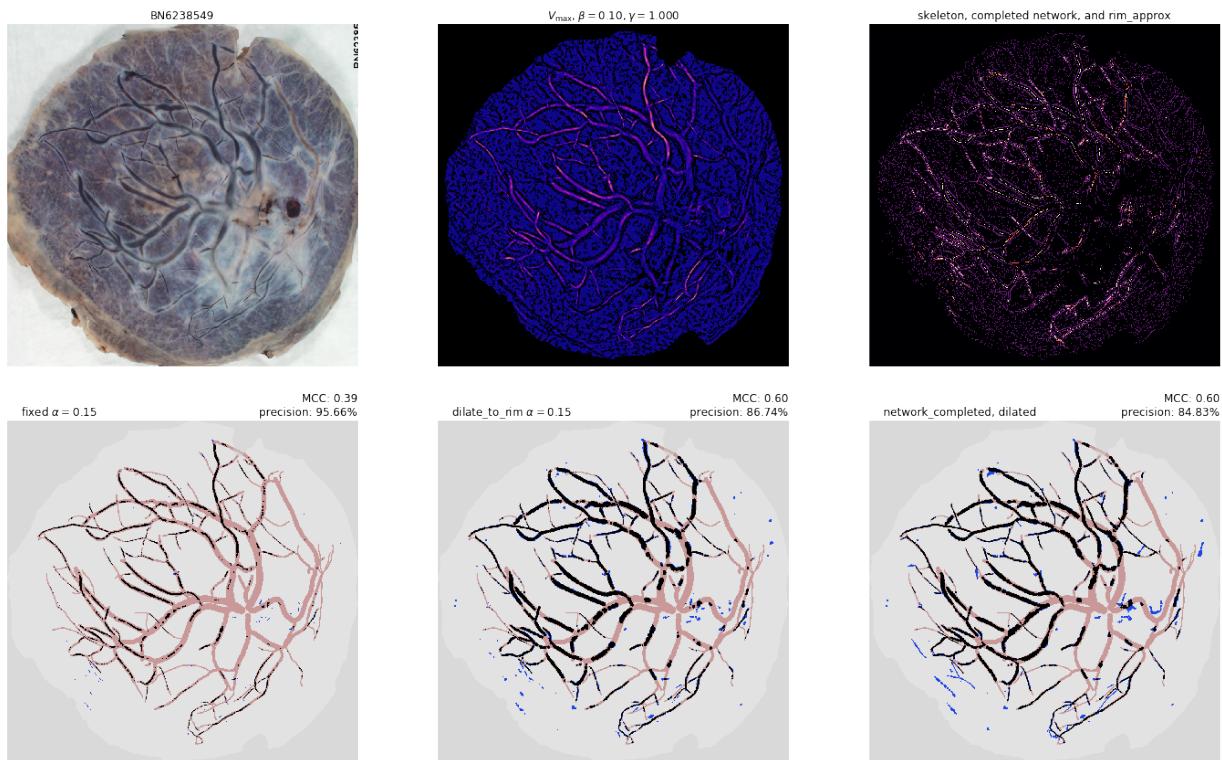


FIGURE 41: Trough Dilation and Network Completion (Example 2)

CHAPTER 12

CONCLUSION

We justified the use of differential geometry in 2D discrete image processing, and vastly improved upon the implementation of the Frangi filter. Our improved implementation allowed us to take more steps in our multiscale method and thus choose stricter parameters for Frangi scale. We used our multiscale Frangi vesselness measure to suggest several alternative approaches at merging the vesselness and compared their effectiveness as a precursor to segmentation and eventually network completion.

Future research directions

Our goal is to eventually solve the network connection problem.

- Perfect stump removal and watershedding to not rely on use of maxes/improve vesselness measure.
- Try something like [32] or use of principal curvatures.
- Implement the automatic scale selection and normalization of derivates as mentioned in Lindeberg [23] to relieve ourselves of our current dependency on manual selection of σ_{\min} and σ_{\max} .
- Use this as preprocessing for a Neural Network. (cite kara's work, katalinas work)
- Apply to more image domains (STARE, other placental domains).

APPENDICES

APPENDIX A
CODE LISTINGS

The following python scripts and modules were developed with the following packages:

- python 3.6
- numpy, version 1.12.0
- scipy, version 0.19.0
- scikit-image, version 0.13.0
- matplotlib, version 2.02

Earlier versions of these packages may be compatible but are not guaranteed to be so.

The scripts listed in this appendix are also hosted at github.com/wukm/pycake.

listings/add_margins.py

```
1 # -*- coding: utf-8 -*-
2 #!/usr/bin/env python3
3
4 from skimage.filters import sobel
5 from frangi import frangi_from_image
6 from plate_morphology import dilate_boundary
7 from skimage.morphology import remove_small_holes, remove_small_objects
8 from merging import nz_percentile
9
10 s = sobel(img)
11 s = dilate_boundary(s, mask=img.mask, radius=20)
12 finv = frangi_from_image(s, sigma=0.8, dark_bg=True)
13
14 finv_thresh = nz_percentile(finv, 80)
15
16 margins = remove_small_objects((finv > ft).filled(0), min_size=32)
17
18 margins_added = remove_small_holes(np.logical_or(margins, approx),
19                                     min_size=100, connectivity=2)
20
21 markers = np.zeros(img.shape, dtype=np.uint8)
22
23 markers[Fmax < .1] = 1
24 markers[margins_added] = 2
25
26 rw = random_walker(img, markers)
27 approx_rw = (rw==2)
28 confusion_rw = confusion(approx_rw, trace, bg_mask=ucip_mask)
29 mccs_rw = mccs(approx_rw, trace, bg_mask=ucip_mask)
30 pnc_rw = np.logical_and(skeltrace, rw2==2).sum() / skeltrace.sum()
```

listings/cut_demo.py

```
1 #!/usr/bin/env python3
2
3 import numpy as np
4 import matplotlib.pyplot as plt
5
6 from placenta import open_typefile, list_placentas, get_named_placenta
7 from plate_morphology import mask_cuts_simple, dilate_boundary
8
9 from skimage.color import gray2rgb
10 from skimage.morphology import thin, binary_dilation, disk, square
11 import numpy.ma as ma
12 import os.path
13
14 def l2_dist(p,q):
15     return int(np.round(np.sqrt((p[0]-q[0])**2 + (p[1]-q[1])**2)))
16
17 placentas = list_placentas('T-BN')
18 samples_with_cuts = list()
19
20 for filename in list_placentas('T-BN'):
21
22     # this one has two cuts, another one has two cuts as well
23     #if filename != "T-BN2459820.png":
24     #    continue
25
26     img = get_named_placenta(filename)
27     ucip = open_typefile(filename, 'ucip')
28
29     #C, has_cut = mask_cuts(img, ucip, return_success=True, in_place=False)
30
31     #if has_cut:
32
33         # dilcut = img.copy()
34
35         # print(filename, "has a cut!")
36         # samples_with_cuts.append(filename)
37
38         # B = np.all(ucip==(0,0,255), axis=-1)
39         # G = np.all(ucip==(0,255,0), axis=-1)
40
41         # cutmarks = np.nonzero(thin(B))
42         # perimeter = np.nonzero(G)
43
44         # #for array in the tuple that comes out of np.nonzero(thin(B))
45         # # or just one if it's just a single thing i guess?
46
47         # # the x, y points of the cutmarks are in columns
48         # cutinds = np.stack(cutmarks)
49
50         # for P in cutinds.T:
51
52             # consider larger and larger window sizes
53             # for W in [100,200,300]:
54             #     # consider all perimeter elements within these bounds
55
56             #     rmin, rmax = max(0, P[0]-W), min(img.shape[0], P[0]+W)
57             #     cmin, cmax = max(0, P[1]-W), min(img.shape[1], P[1]+W)
58             #     window = np.s_[rmin:rmax, cmin:cmax]
59
60             #     # perimeter indices within the window
61             #     pinds = [(x,y) for x, y in zip(*perimeter)
62             #             if x > rmin and x < rmax and y > cmin and y < cmax]
```

```

63     #
64     #         if pinds:
65     #             break
66     #     if pinds:
67
68     #         # max distance to boundary point in the window
69     #         # we really only need to keep the largest; deque?
70     #         dists = sorted([(pp, l2_dist(P, pp)) for pp in pinds],
71     #                         key=lambda t: t[1])
72     #         r = int(dists[-1][1]) + 1 # get largest radius but closest point
73     #         P = dists[0][0]
74     #         B = np.zeros_like(img.mask)
75
76     #         B[cutmarks] = True
77
78     #         # center a disk of found radius there
79     #         D = disk(r)
80     #         winx = max(P[0]-r,0), min(P[0]+r+1,B.shape[0])
81     #         winy = max(P[1]-r,0), min(P[1]+r+1,B.shape[1])
82     #         try:
83     #             B[winx[0]:winx[1], winy[0]:winy[1]] = D
84     #         except ValueError:
85     #             # they're out of bounds so it's a size mismatch. fix it
86     #             # by starting/ending D index with opposite sign of the initial
87     #             # p +/- radius that was out of bounds
88     #             # for example P[0]-r was -9 and everything else was fine
89     #             # so you just need to set left side to D[9:,:]
90     #             # but you should wrap this up in a function so the three times
91     #             # you do it here and the one time in ucip all gets the same
92     #             # code
93     #             pass
94     #         dilcut[B] = ma.masked
95
96     #     else:
97     #         # this is probably not going to happen, but just in case no
98     #         # nearby perimeter was found, just... give up
99     #         pass
100
101    #     rminv, rmaxv = max(0, rmin-W//2), min(img.shape[0], rmax+W//2)
102    #     cminv, cmaxv = max(0, cmin-W//2), min(img.shape[1], cmax+W//2)
103    #     view = np.s_[rminv:rmaxv, cminv:cmaxv]
104    #     montage = np.hstack((gray2rgb(img.filled(0)[view]),
105    #                           ucip[view],
106    #                           gray2rgb(C.filled(0)[view]),
107    #                           gray2rgb(dilcut.filled(0)[view])))
108    #     filestub, _ = os.path.splitext(filename)
109    #     plt.imsave(f'demo_output/cut_demo/{filestub}_cutopts.png', montage)
110    #     #plt.imshow(montage)
111    #     plt.show()
112    #     plt.close()
113    mimg, success = mask_cuts_simple(img, ucip, return_success=True)
114    if success:
115        montage = np.hstack((img.filled(0),
116                             mimg.filled(0)))
117        plt.imshow(montage)
118        plt.show()
119        plt.close()
120    print("*"*80)
121    print(f"there were {len(placentas)} total samples",
122          f"and {len(samples_with_cuts)} of them had cuts")

```

listings/diffgeo.py

```

1 #!/usr/bin/env python3
2
3 import numpy as np
4 import numpy.ma as ma
5
6 from skimage.feature import hessian_matrix, hessian_matrix_eigvals
7 from numpy.linalg import eig
8
9
10 def principal_curvatures(img, sigma=1.0, H=None):
11     """Calculate the approximated principal curvatures of an image
12
13     Return the (approximated) principal curvatures  $\{\kappa_1, \kappa_2\}$  of an image,
14     that is, the eigenvalues of the Hessian at each point  $(x,y)$ . The output
15     is arranged such that  $|\kappa_1| \leq |\kappa_2|$ . Note that the Hessian of the image,
16     if not provided, is computed using skimage.feature.hessian_matrix, which
17     can be very slow for large sigmas.
18
19 Parameters
20 -----
21 img: array or ma.MaskedArray
22
23     An ndarray representing a 2D or multichannel image. If the image is
24     multichannel (e.g. RGB), then each channel will be processed
25     individually. Additionally, the input image may be a masked array-- in
26     which case the output will preserve this mask identically.
27
28 sigma: float, optional
29     Standard deviation of the Gaussian (used to calculate the hessian
30     matrix).
31 H: list of array, optional
32     The hessian itself ( $H_{xx}, H_{xy}, H_{yy}$ ) whose eigenvalues will be calculated.
33     Use this option if you're going to calculate the Hessian using faster
34     means, e.g. via FFT.
35
36 Returns
37 -----
38 (K1, K2): tuple of arrays
39     K1, K2 each are the exact dimension of the input image, ordered in
40     magnitude such that  $|\kappa_1| \leq |\kappa_2|$  in all locations.
41
42 Examples
43 -----
44 >>> K1, K2 = principal_curvatures(img)
45 >>> K1.shape == img.shape
46 True
47 >>> (K1 <= K2).all()
48 True
49 >>> K1.mask == img.mask
50 True
51 """
52
53 # determine if multichannel
54 multichannel = (img.ndim == 3)
55
56 if not multichannel:
57     # add a trivial dimension
58     img = img[:, :, np.newaxis]
59
60 K1 = np.zeros_like(img, dtype='float64')
61 K2 = np.zeros_like(img, dtype='float64')
62
63 for ic in range(img.shape[2]):
```

```

64     channel = img[:, :, ic]
65
66     # returns the tuple (Hxx, Hxy, Hyy)
67     if H is None:
68         H = hessian_matrix(channel, sigma=sigma)
69
70     # returns tuple (l1, l2) where l1 >= l2 but this *includes sign*
71     L = hessian_matrix_eigvals(H)
72     L = reorder_eigs(L)
73
74     # Make K2 larger in magnitude, as consistent with Frangi paper
75     K1[:, :, ic] = L[0, :, :]
76     K2[:, :, ic] = L[1, :, :]
77
78 try:
79     mask = img.mask # get mask to add to each if input was a masked array
80
81 except AttributeError:
82     pass # there's no mask, so do nothing
83
84 else:
85     K1 = ma.masked_array(K1, mask=mask)
86     K2 = ma.masked_array(K2, mask=mask)
87
88 # now undo the trivial dimension
89 if not multichannel:
90     K1 = np.squeeze(K1)
91     K2 = np.squeeze(K2)
92
93 return K1, K2
94
95
96
97 def reorder_eigs(L):
98     """reorder eigenvalues by decreasing magnitude.
99
100    Eigenvalues are outputted from hessian_matrix_eigvals so that L1 >= L2.
101    This reorders this so that |L1| >= |L2| instead (where L1,L2=L)
102    Parameters
103    -----
104    L: ndarray or iterable of ndarrays
105        As outputted by, say, hessian_matrix_eigs. If a single ndarray, it
106        should be the shape (N, *img.shape) where there are N eigenvalues to
107        reorder. You may also input a tuple like (L1,L2).
108    Returns
109    -----
110    eigs: ndarray
111        The eigenvalues in decreasing order of magnitude; that is
112        eigs[i,j,k] is the ith-largest eigenvalue at position (j, k).
113        Each of these is the same shape the original inputs, but
114        np.abs(L1r) >= np.abs(L2r) will be true. See warning below.
115
116
117 Warnings / Notes
118 -----
119 Please note the order! Outputs are given in *decreasing* magnitude. This is
120 done to align with the behavior of skimage.feature.hessian_matrix_eigvals,
121 but if you want to label them according to the Frangi filter (where k2
122 denotes the *larger* magnitude eigenvalue, you should reverse the labels:
123
124     >>>k2, k1 = reorder_eigs(L) # k2, k1 as frangi labeled them
125     >>>np.all(np.abs(k2) >= np.abs(k1))
126     True
127

```

```

128
129 It doesn't actually matter the order in which inputs are inputted (they
130 will be sorted the same regardless).
131
132 Example
133 -----
134 >>>K1,K2 = hessian_matrix_eigvals(H)
135 >>>(K1 >= K2).all()
136 True
137 >>>(np.abs(K1) <= np.abs(K2)).all()
138 False
139 >>>K1r, K2r = reorder_eigs(K1,K2)
140 >>>(K1r <= K2r).all()
141 False
142 >>>(np.abs(K1r) <= np.abs(K2r)).all()
143 True
144
145 TODO
146 -----
147 Support out= keyword
148 """
149 # this will do nothing if L is already an array but will make it an array
150 # if it's a tuple/list/iterable
151 L = np.stack(L)
152 mag = np.argsort(np.abs(L), axis=0)
153
154 # now L2 is larger in absolute value, as consistent with Frangi paper
155 return np.take_along_axis(L, mag, axis=0)
156
157
158 def principal_directions(img, sigma, H=None, mask=None):
159     """Calculate principal directions of
160     will ignore calculation of principal directions of masked areas
161
162     mask should be positive where the PD's should *NOT* be calculated
163     this function actually returns the theta corresponding to
164     leading and trailing principal directions, i.e. angle w / x axis
165     """
166
167     if H is None:
168         H = hessian_matrix(img, sigma)
169
170     Hxx, Hxy, Hyy = H
171
172
173     # determine if there was a supplied mask or use images if it exists
174     if mask is None:
175         try:
176             mask = img.mask
177         except AttributeError:
178             masked = False
179         else:
180             masked = True
181     else:
182         masked = True
183
184     dims = img.shape
185
186     # where to store
187     trailing_thetas = np.zeros_like(img, dtype='float64')
188     leading_thetas = np.zeros_like(img, dtype='float64')
189
190     # maybe implement a small angle correction
191     for i, (xx, xy, yy) in enumerate(np.nditer([Hxx, Hxy, Hyy])):

```

```

192
193     # grab the (x,y) coordinate of the hxx, hxy, hyy you're using
194     subs = np.unravel_index(i, dims)
195
196     # ignore masked areas (if masked array)
197     if masked and mask[sub]:
198         continue
199
200     h = np.array([[xx, xy], [xy, yy]]) # per-pixel hessian
201     l, v = eig(h) # eigenvectors as columns
202
203     # reorder eigenvectors by (increasing) magnitude of eigenvalues
204     v = v[:, np.argsort(np.abs(l))]
205
206     # angle between each eigenvector and positive x-axis
207     # arccos of first element (dot product with (1,0) and eigvec is already
208     # normalized)
209     trailing_thetas[subs] = np.arccos(v[0, 0]) # first component of each
210     leading_thetas[subs] = np.arccos(v[0, 1]) # first component of each
211
212     if masked:
213         leading_thetas = ma.masked_array(leading_thetas, mask)
214         trailing_thetas = ma.masked_array(trailing_thetas, mask)
215
216     return trailing_thetas, leading_thetas
217
218
219 if __name__ == "__main__":
220     pass
221
222
223     #from get_base import get_preprocessed
224     #import matplotlib.pyplot as plt
225     #from functools import partial
226     #from fpd import get_targets
227     #b = partial(plt.imshow, cmap=plt.cm.Blues)
228     #sp = partial(plt.imshow, cmap=plt.cm.spectral)
229     #s = plt.show
230
231     #import time
232
233     #img = get_preprocessed(mode='G')
234
235     #for sigma in [0.5, 1, 2, 3, 5, 10]:
236
237     #    print('-'*80)
238     #    print('σ=', sigma)
239     #    print('calculating hessian H')
240
241     #    tic = time.time()
242     #    H = hessian_matrix(img, sigma=sigma)
243
244     #    toc = time.time()
245     #    print('time elapsed: ', toc - tic)
246     #    tic = time.time()
247     #    print('calculating hessian via FFT (F)')
248     #    h = fft_hessian(img, sigma)
249
250     #    toc = time.time()
251     #    print('time elapsed: ', toc - tic)
252     #    tic = time.time()
253     #    print('calculating principal curvatures for σ={}'.format(sigma))
254     #    K1, K2 = principal_curvatures(img, sigma=sigma, H=H)
255     #    toc = time.time()

```

```

256     #     print('time elapsed: ', toc - tic)
257     #     tic = time.time()
258     #     print('calculating principal curvatures for σ={}'.format(sigma))
259     #     k1,k2 = principal_curvatures(img, sigma=sigma, H=h)
260
261     #     toc = time.time()
262     #     print('time elapsed: ', toc - tic)
263     #     tic = time.time()
264
265     ######
266
267     #     print('calculating targets for σ={}'.format(sigma))
268     #     T = get_targets(K1,K2, threshold=False)
269
270     #     toc = time.time()
271     #     print('time elapsed: ', toc - tic)
272     #     tic = time.time()
273
274     #     print('calculating targets for σ={}' (fast).format(sigma))
275     #     t = get_targets(k1,k2, threshold=False)
276
277     #     toc = time.time()
278     #     print('time elapsed: ', toc - tic)
279
280     ######
281
282     #     print('extending masks')
283
284     #     # extend mask over nontargets items
285     #     img1 = ma.masked_where( T < T.mean(), img)
286     #     img2 = ma.masked_where( t < t.mean(), img)
287
288     #     tic = time.time()
289     #     print('calculating principal directions for σ={}'.format(sigma))
290     #     T1,T2 = principal_directions(img1, sigma=sigma, H=H)
291     #     toc = time.time()
292     #     print('time elapsed: ', toc - tic)
293     #     tic = time.time()
294
295     #     print('calculating principal directions for σ={}' (fast).format(sigma))
296     #     t1,t2 = principal_directions(img2, sigma=sigma, H=h)
297     #     toc = time.time()
298     #     print('time elapsed: ', toc - tic)

```

listings/extract_NCS_pcsvn.py

```

1 #!/usr/bin/env python3
2
3 """
4 This is the main program. It approximates the PCCSVN of a list of samples.
5 It does not do network completion.
6 """
7
8
9 from placenta import (get_named_placenta, cropped_args, cropped_view,
10                      list_placentas, list_by_quality, open_typefile,
11                      open_tracefile, add_ucip_to_mask, measure_ncs_markings)
12
13 from merging import nz_percentile, apply_threshold, sieve_scales, view_slices
14
15 from scoring import (compare_trace, rgb_to_widths, merge_widths_from_traces,
16                      filter_widths, mcc, confusion, skeletonize_trace)
17

```

```

18 from pcsvn import extract_pcsvn, scale_label_figure, get_outname_lambda
19 from preprocessing import inpaint_hybrid
20
21 import numpy as np
22 import numpy.ma as ma
23
24 import matplotlib.pyplot as plt
25
26 import os.path
27 import os
28 import json
29 import datetime
30 import pandas
31
32 # for some post_processing, this needs to be moved elsewhere
33 from skimage.filters import sobel
34 from frangi import frangi_from_image
35 from plate_morphology import dilate_boundary, mask_cuts_simple
36 from skimage.morphology import remove_small_holes, remove_small_objects
37 from skimage.segmentation import random_walker
38 from postprocessing import random_walk_fill, random_walk_scalewise
39
40
41 # INITIALIZE SAMPLES -----
42 #     There are several ways to initialize samples. Uncomment one.
43
44 # load all 201 samples
45 # placentas = list_placentas('T-BN')
46 # load placentas from a certain quality category 0=good, 1=okay, 2=fair, 3=poor
47
48 #placentas = list_by_quality(2)
49 #placentas.extend(list_by_quality(3))
50
51 placentas = list_by_quality(0, N=1)
52 # load from a file (sample names are keys of the json file)
53 # placentas = list_by_quality(json_file='manual_batch.json')
54
55 # for a single named sample, use a 1 element list.
56 # placentas = ['T-BN0204423.png']
57
58 #placentas = ['barium1.png',]
59 # RUNTIME OPTIONS -----
60 #     Where to save and whether or not to use old targets.
61
62 MAKE_NPZ_FILES = False # pickle frangi targets if you can
63 USE_NPZ_FILES = False # use old npz files if you can
64 NPZ_DIR = 'output/181204-test' # where to look for npz files
65 OUTPUT_DIR = 'output/181204-test' # where to save outputs
66
67 # add in a meta switch for verbosity (or levels)
68 #VERBOSE = False
69
70 # FRANGI / EXTRACT_PC SVN OPTIONS -----
71
72 # Find bright curvilinear structure against a dark background -> True
73 # Find dark curvilinear structure against a bright background -> False
74 # DARK_BG -> ignore and return signed Frangi scores
75 DARK_BG = False
76
77 # Along with the above, this will return "opposite" signed frangi scores.
78 # if this is True, then DARK_BG controls the "polarity" of the filter.
79 # See frangi.get_frangi_targets for details.
80 SIGNED_FRANGI = False
81

```

```

82 # Do not calculate hessian scores close to the boundary (this is important
83 # mainly in terms of ensuring that the hessian is very large on the edge of
84 # the plate (which would influence gamma calculation)
85 DILATE_PER_SCALE = True
86
87 # Attempt to remove glare from sample (some are OK, some are bad)
88 FLATTEN_MODE = 'L' # 'G' or 'L',
89 REMOVE_GLARE = True
90 REMOVE_CUTS = True
91
92 # Which scales to use
93 SCALE_RANGE = (-1.5, 3.5); SCALE_TYPE = 'logarithmic'
94 #SCALE_RANGE = (.2, 12); SCALE_TYPE = 'linear'
95 N_SCALES = 20
96
97 # use this if you want to use a custom argument (comment out the above)
98 SCALES = None
99 #SCALE_RANGE = None, SCALE_TYPE == 'custom'
100
101
102 # Explicit Frangi Parameters (pass a scalar, array as long as scales)
103 BETAS = 0.35
104 GAMMAS = 0.5
105 CS = None # pass scalar, array, or None
106 ALPHAS = None # set custom alphas or calculate later
107 FIXED_ALPHA = .4
108
109 RESCALE_FRANGI = True
110 GRADIENT_FILTER = False
111
112
113 # Scoring Decisions (don't need to touch these)
114 UCIPI_RADIUS = 60 # area around the umbilical cord insertion point to ignore
115 INV_SIGMA = 0.8
116 # some other initializations, don't mind me
117
118
119
120
121 # CODE BEGINS HERE -----
122
123 if SCALES is None:
124     if SCALE_TYPE == 'linear':
125         scales = np.linspace(*SCALE_RANGE, num=N_SCALES)
126     elif SCALE_TYPE == 'logarithmic':
127         scales = np.logspace(*SCALE_RANGE, num=N_SCALES, base=2)
128 else:
129     scales = SCALES
130     SCALE_TYPE = 'custom' # this and the next three lines are just for logging
131     N_SCALES = len(SCALES)
132     SCALES = (min(SCALES), max(SCALES))
133
134 mccs = dict() # empty dict to store MCC's of each sample
135 pncs = dict() # empty dict to store percent network covered for each sample
136 precisions = dict()
137
138 n_samples = len(placentas)
139
140 if not os.path.exists(OUTPUT_DIR):
141     os.makedirs(OUTPUT_DIR)
142
143 print(n_samples, "samples total!")
144
145 for i, filename in enumerate(placentas):

```

```

146
147 print('*'*80)
148 print(f'extracting PCSVN of {filename}\t({i} of {n_samples})')
149
150 # --- Setup, Preprocessing, Frangi Filter (it's mixed up) -----
151
152 raw_img = get_named_placenta(filename, mode=FLATTEN_MODE)
153
154 ucip = open_typefile(filename, 'ucip')
155
156 if REMOVE_CUTS:
157     #img, has_cut = mask_cuts_simple(raw_img, ucip, return_success=True)
158     #img.data[img.mask] = 0 # actually zero out that area
159     print("removing cuts doesn't do anything anymore")
160     pass
161 else:
162     img = raw_img.copy()
163
164 if REMOVE_GLARE:
165     img = inpaint_hybrid(img)
166
167
168 if USE_NPZ_FILES:
169     # find the first npz file with the sample name in it in the
170     # specified directory.
171     stub = filename.rstrip('.png')
172     for f in os.scandir(NPZ_DIR):
173         if f.name.endswith('npz') and f.name.startswith(stub):
174             npz_filename = os.path.join(NPZ_DIR, f.name)
175             print(f'using the npz file {npz_filename}')
176             break # we'll just use the first one we can find.
177     else:
178         print(f'no npz file found for {filename}.')
179     npz_filename = None
180 else:
181     npz_filename = None
182
183 # set a lambda function to make output file names
184 outname = get_outname_lambda(filename, output_dir=OUTPUT_DIR)
185
186 if npz_filename is not None:
187
188     F = np.load(npz_filename)['F']
189
190     # in case preprocessing happens inside extract_pcsvn, do it out here
191
192     print('successfully loaded the frangi targets!')
193
194 else:
195     print('finding multiscale frangi targets')
196
197     # F is an array of frangi scores of shape (*img.shape, N_SCALES)
198     F, jfile = extract_pcsvn(img, filename, dark_bg=DARK_BG, beta=BETAS,
199                               scales=scales, gamma=GAMMAS, c=CS,
200                               kernel='discrete', dilate_per_scale=True,
201                               verbose=False, signed_frangi=SIGNED_FRANGI,
202                               generate_json=True, output_dir=OUTPUT_DIR,
203                               rescale_frangi=RESCALE_FRANGI,
204                               gradient_filter=GRADIENT_FILTER)
205
206 if MAKE_NPZ_FILES:
207     npzfile = ".".join((outname("F")).rsplit('.', maxsplit=1)[0], 'npz')
208
209     print("saving frangi targets to ", npzfile)

```

```

210     np.savez_compressed(npzfile, F=F)
211
212 # --- Merging & Postprocessing -----
213
214 # This is the maximum frangi response over all scales at each location
215 Fmax = F.max(axis=-1)
216
217 print("...making outputs")
218
219 if ALPHAS is None:
220     print("thresholding ALPHAS with top 5% scores at each scale")
221     ALPHAS = np.array([nz_percentile(F[..., k], 95.0)
222                         for k in range(N_SCALES)])
223
224 # the maximum value of the entire image at each scale
225 scale_maxes = np.array([F[..., i].max() for i in range(F.shape[-1])])
226
227 table = pandas.DataFrame(np.dstack((scales, ALPHAS, scale_maxes)).squeeze(),
228                           columns=('σ', 'α_p', 'max(F_σ)'))
229
230 print(table)
231 # threshold the responses at each of these values and get labels of max
232 approx, labs = apply_threshold(F, ALPHAS, return_labels=True)
233
234 # --- Scoring and Outputs -----
235
236 # get the main (boolean) tracefile and the RGB tracefiles
237 trace = open_tracefile(filename, as_binary=True)
238 A_trace = open_typefile(filename, 'arteries')
239 if A_trace is None:
240     # there are no special trace files for this sample
241     skeltrace = skeletonize_trace(trace)
242 else:
243     V_trace = open_typefile(filename, 'veins')
244     skeltrace = skeletonize_trace(A_trace, V_trace)
245
246     # get a matrix of pixel widths in the trace
247     widths = merge_widths_from_traces(A_trace, V_trace, strategy='arteries')
248
249 # find cord insertion point and resolution of the image
250 ucip_midpoint, resolution = measure_ncs_markings(ucip)
251 # if verbose:
252 #     print(f"The umbilical cord insertion point is at {ucip_midpoint}")
253 #     print(f"The resolution of the image is {resolution} pixels per cm.")
254
255 if ucip_midpoint is None:
256     ucip_mask = img.mask
257 # mask anywhere close to the UCIP
258 else:
259     ucip_mask = add_ucip_to_mask(ucip_midpoint,
260                                   radius=int(UCIP_RADIUS), mask=img.mask)
261
262 # The following are examples of things you can do:
263
264 # matrix of widths of traced image
265 # min_widths = merge_widths_from_traces(A_trace, V_trace,
266 #                                         strategy='minimum')
267
268 # trace ignoring largest vessels (19 pixels wide)
269 # trace_smaller_only = filter_widths(min_widths, min_width=3, max_width=17)
270 # trace_smaller_only != 0
271
272 # use only some scales
273 #approx_L0, labs_L0 = apply_threshold(F[:, :, LO_offset:], ALPHAS[LO_offset:])

```

```

274 approx_FA, labs_FA = apply_threshold(F, FIXED_ALPHA)
275
276 # fix labels to incorporate offset
277 #labs_L0 = (labs_L0 != 0)*(labs_L0 + LO_offset)
278
279 # confusion matrix against default trace
280 confuse = confusion(approx, trace, bg_mask=ucip_mask)
281 #confuse_L0 = confusion(approx_L0, trace, bg_mask=ucip_mask)
282 confuse_FA = confusion(approx_FA, trace, bg_mask=ucip_mask)
283
284 m_score, counts = mcc(approx, trace, ucip_mask, return_counts=True)
285 m_score_FA, counts_FA = mcc(approx_FA, trace, ucip_mask,
286                             return_counts=True)
287
288 # this all just verifies that the 4 categories were added up
289 # correctly and match the total number of pixels in the reported
290 # placental plate.
291 TP, TN, FP, FN = counts # return these for more analysis?
292
293 total = np.sum(~ucip_mask)
294 #print(f'TP: {TP}\t TN: {TN}\nFP: {FP}\tFN: {FN}')
295 # just a sanity check
296 #print(f'TP+TN+FP+FN={TP+TN+FP+FN}\ttotal pixels={total}')
297
298 #approx_rw, markers, margins_added = random_walk_fill(img, Fmax, .3, .01,
299 #                                                    DARK_BG)
300
301 approx_rw, labs_rw = random_walk_scalewise(F, .4, return_labels=True)
302
303 confuse_rw = confusion(approx_rw, trace, bg_mask=ucip_mask)
304 m_score_rw, counts_rw = mcc(approx_rw, trace, ucip_mask,
305                             return_counts=True)
306 pnc_rw = (skeltrace & approx_rw).sum() / skeltrace.sum()
307
308
309 # --- Generating Visual Outputs-----
310
311 SCALE_CMAP = ('plasma', (1,1,1,1))
312
313 crop = cropped_args(img) # these indices crop out the mask significantly
314
315 fmax_colors = plt.cm.plasma
316 fmax_colors.set_bad('k', 1)
317 # save the raw, unaltered image
318 plt.imsave(outname('0_raw'), raw_img[crop].filled(0), cmap=plt.cm.gray)
319
320 # save the preprocessed image
321 plt.imsave(outname('1_img'), img[crop].filled(0), cmap=plt.cm.gray)
322
323 # save the maximum frangi output over all scales
324 plt.imsave(outname('2_fmax'), ma.masked_where(Fmax==0,Fmax)[crop], vmin=0,
325             vmax=1.0, cmap=fmax_colors)
326
327 # only save the colorbar the first time
328 save_colorbar = (i==0)
329 scale_label_figure(labs, scales, crop=crop,
330                     savefilename=outname('3_labeled'), image_only=True,
331                     save_colorbar_separate=save_colorbar,
332                     basecolor=SCALE_CMAP[1], base_cmap=SCALE_CMAP[0],
333                     output_dir=OUTPUT_DIR)
334
335 plt.imsave(outname('4_confusion'), confuse[crop])
336
337

```

```

338 scale_label_figure(labs_rw, scales, crop=crop,
339                     savefilename=outname('A_labeled_rw'), image_only=True,
340                     save_colorbar_separate=save_colorbar,
341                     basecolor=SCALE_CMAP[1], base_cmap=SCALE_CMAP[0],
342                     output_dir=OUTPUT_DIR)
343
344
345 plt.imsave(outname('7_confusion_FA'), confuse_FA[crop])
346 plt.imsave(outname('B_confusion_rw'), confuse_rw[crop])
347 #plt.imsave(outname('A_markers_rw'), markers[crop])
348 #plt.imsave(outname('9_margin_for_rw'), confuse_margins[crop])
349 percent_covered = (skeltrace & approx).sum() / skeltrace.sum()
350 percent_covered_FA = (skeltrace & approx_FA).sum() / skeltrace.sum()
351
352
353 st_colors = {
354     'TN': (79, 79, 79), # true negative# 'f7f7f7'
355     'TP': (0, 0, 0), # true positive # '000000'
356     'FN': (201, 53, 108), # false negative # 'f1a340' orange
357     'FP': (92, 92, 92), # false positive
358     'mask': (247, 200, 200) # mask color (not used in MCC calculation)
359 }
360
361
362 plt.imsave(outname('5_coverage'), confusion(approx, skeltrace,
363                                              colordict=st_colors)[crop])
364 plt.imsave(outname('8_coverage_FA'), confusion(approx_FA, skeltrace,
365                                              colordict=st_colors)[crop])
366 plt.imsave(outname('C_coverage_rw'), confusion(approx_rw, skeltrace,
367                                              colordict=st_colors)[crop])
368
369 # make the graph that shows what scale the max was pulled from
370
371 scale_label_figure(labs_FA, scales, crop=crop,
372                     savefilename=outname('6_labeled_FA'), image_only=True,
373                     basecolor=SCALE_CMAP[1], base_cmap=SCALE_CMAP[0],
374                     save_colorbar_separate=False, output_dir=OUTPUT_DIR)
375
376 V = np.transpose(F, axes=(2, 0, 1))
377
378 #view_slices(F[crop], axis=-1, scales=scales)
379
380 print('starting to sieve')
381 sieved = sieve_scales(V, 98, 95)
382
383 approx_S, labs_S = (sieved != 0), sieved
384 confuse_S = confusion(approx_S, trace, bg_mask=ucip_mask)
385
386 scale_label_figure(labs_S, scales, crop=crop,
387                     savefilename=outname('D_labeled_S'), image_only=True,
388                     basecolor=SCALE_CMAP[1], base_cmap=SCALE_CMAP[0],
389                     save_colorbar_separate=False, output_dir=OUTPUT_DIR)
390
391 plt.imsave(outname('E_confusion_S'), confuse_S[crop])
392
393 m_score_S, counts_S = mcc(approx_S, trace, ucip_mask, return_counts=True)
394 pnc_S = (skeltrace & approx_S).sum() / skeltrace.sum()
395
396 mccs[filename] = (m_score, m_score_FA, m_score_rw, m_score_S )
397 pncs[filename] = (percent_covered, percent_covered_FA, pnc_rw, pnc_S)
398
399
400 print('percentage of skeltrace covered:(percentile filtering)',
401       f'{percent_covered:.2%}')

```

```

402 print('percentage of skeltrace covered (fixed alpha):',
403       f'{percent_covered_FA:.2%}')
404 print('percentage of skeltrace covered (random_walker):',
405       f'{pnc_rw:.2%}')
406 print('percentage of skeltrace covered (sieving):',
407       f'{pnc_S:.2%}')

408 print(f'mcc score of {m_score:.3} for percentile filtering')
409 print(f'mcc score of {m_score_FA:.3} with fixed alpha {FIXED_ALPHA}')
410 print(f'mcc score of {m_score_rw:.3} after random walker')
411 print(f'mcc score of {m_score_S:.3} after sieving')

412
413
414 precision_score = lambda t: int(t[0]) / int(t[0] + t[2])
415
416 precision = precision_score(counts)
417 precision_FA = precision_score(counts_FA)
418 precision_rw = precision_score(counts_rw)
419 precision_S = precision_score(counts_S)
420
421 precisions[filename] = (precision, precision_FA, precision_rw, precision_S)
422
423 print(f'precision of {precision:.3} for percentile filtering')
424 print(f'precision of {precision_FA:.3} for fixed alpha')
425 print(f'precision of {precision_rw:.3} for random walker')
426 print(f'precision of {precision_S:.3} for sieving')

427 scoretable = pandas.DataFrame(np.vstack((mccs[filename], pncts[filename],
428                                         precisions[filename])),
429                                 columns=('PF', 'FA', 'RW', 'PS'),
430                                 index=('MCC', 'skel coverage', 'precision'))
431
432 print(scoretable)
433 print('\n\n')
434 print(scoretable.to_latex())

435
436
437
438     # THIS IS ALL A HORRIBLE MESS. FIX IT
439     # why don't you just return the dict instead
440     with open(jfile, 'r') as f:
441         slog = json.load(f)

442 c2d = lambda t: dict(zip(('TP', 'TN', 'FP', 'FN'), [int(c) for c in t]))

443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461 # Post-run Meta-Output and Logging -----
462
463 timestamp = datetime.datetime.now()
464 timestamp = timestamp.strftime("%y%m%d_%H%M")
465

```

```

466 mccfile = os.path.join(OUTPUT_DIR, f"runlog_{timestring}.json")
467
468 runlog = {
469     'time': timestring,
470     'DARK_BG': DARK_BG,
471     'DILATE_PER_SCALE': DILATE_PER_SCALE,
472     'SCALE_RANGE': SCALE_RANGE,
473     'SCALE_TYPE': SCALE_TYPE,
474     'N_SCALES': N_SCALES,
475     'scales': list(scales),
476     'ALPHAS': list(ALPHAS),
477     'BETAS': None,
478     'use_npz_files': False,
479     'remove_glare': REMOVE_GLARE,
480     'files': list(placentas),
481     'MCCS': mccs,
482     'PNC': pncts,
483     'precisions': precisions
484 }
485
486 # save to a json file
487 with open(mccfile, 'w') as f:
488     json.dump(runlog, f, indent=True)

```

listings/frangi_graphing.py

```

1 import matplotlib as mpl
2 from mpl_toolkits.mplot3d import Axes3D
3 import matplotlib.pyplot as plt
4 import numpy as np
5 from numpy import exp
6 from skimage.io import imread
7 from skimage.util import montage
8 from itertools import product
9
10 def s(x, gamma):
11     """normalized structureness factor.
12     x is the ratio of the input to the maximum possible structureness factor
13     (smax) at that scale (which would cancel out with the c in the denominator)
14     """
15     return (1 - exp(-x**2 / (2*gamma**2))) / (1 - exp(-1/(2*gamma**2)))
16
17 def r(y, beta):
18     """normalized anisotropy factor
19     y is the ratio |k1 / k2|, so y=0 corresponds to perfectly isotropic
20     and y->1 corresponds to highly anisotropic
21     """
22     return np.exp(-y**2 / (2*beta**2))
23
24 #plt.rc('text', usetex=True)
25 #plt.rc('font', family='serif')
26
27
28 dom = np.linspace(0, 1)
29 plt.close('all')
30
31 # show dependence of structureness factor on its parameter
32 for gamma in [0.1, 0.25, 0.35, 0.5, 0.9, 1, 2, 10, 1000]:
33     plt.plot(dom, s(dom, gamma), label=r'$\gamma$ = ' + format(gamma))
34
35
36

```

```

37 plt.ylabel(r' $\left(1 - \exp\left\{\frac{-S}{2(\gamma S_{max})^2}\right\}\right)$ ' ,  

38         fontsize=14)  

39 plt.xlabel(r' $(S/S_{max})$ ' , fontsize=14)  

40 plt.title(r'Dependence of Structureness Factor on Parameter  $\gamma = (c/S_{max})$ ' )  

41 plt.legend()  

42  

43 #plt.show()  

44 plt.close('all')  

45  

46 for beta in [0.1, 0.25, 0.35, 0.5, 0.9, 1, 2, 10, 1000]:  

47     plt.plot(dom, r(dom, beta), label=r' $\beta = .format(beta))$ ' )  

48  

49 plt.ylabel(r' $\exp\left\{\frac{-A}{2\beta^2}\right\}$ ' ,  

50         fontsize=14)  

51 plt.xlabel(r' $A = |\lambda_1/\lambda_2|$ ' , fontsize=14)  

52 plt.title(r'Dependence of Anisotropy Factor on Parameter  $\beta$ ' )  

53 plt.legend()  

54  

55 #plt.show()  

56 plt.close('all')  

57  

58 prange = [0.1, 0.25, 0.5, 0.9, 1, 1.5]  

59  

60 for n, (beta, gamma) in enumerate(product(prange, prange)):  

61     fig = plt.figure(figsize=(8,5))  

62     ax = fig.gca(projection='3d')  

63     X, Y = np.meshgrid(dom, dom)  

64  

65     Z = r(X,beta)*s(Y,gamma)  

66  

67     surf = ax.plot_surface(X,Y,Z, cmap='coolwarm', linewidth=0)  

68  

69     ax.set_xlabel(r' $|\lambda_1/\lambda_2|$ ' )  

70     ax.set_ylabel(r' $(S/S_{max})$ ' )  

71  

72     ax.set_title(r'Rescaled Frangi filter, "  

73                 r" $\beta = , \gamma = .format(beta, gamma))$ " )  

74  

75     #fig.colorbar(surf, shrink=0.5, aspect=5)  

76     fig.tight_layout()  

77  

78     plt.savefig(f'demo_output/frangi3d/{n}.png', dpi=300)  

79  

80     plt.close()  

81  

82 imgs = [imread(f'demo_output/frangi3d/{n}.png') for n in range(36*1)]  

83 imgs = np.stack(imgs)  

84  

85 for n in range(6):  

86     plt.imsave(f'demo_output/frangi3d/frangi3dpart{n}.png',  

87                 montage(imgs[(n*6):((n+1)*6)], multichannel=True,  

88                 grid_shape=(3,2)))

```

listings/frangi.py

```

1 import numpy as np
2 import numpy.ma
3 from hfft import fft_hessian, fft_gradient
4 from diffgeo import principal_curvatures
5 from plate_morphology import dilate_boundary

```

```

6 from merging import nz_percentile
7
8 def frangi_from_image(img, sigma, beta=0.5, gamma=0.5, c=None, dark_bg=True,
9                      dilation_radius=None, kernel=None, signed_frangi=False,
10                     return_debug_info=False, verbose=False,
11                     rescale_frangi=False, gradient_filter=False):
12     """Calculate the (uniscale) Frangi vesselness measure on a grayscale image
13
14     Parameters
15     -----
16     img: ndarray or ma.MaskedArray
17         a one-channel image. If this is a masked array (preferred), ignore the
18         masked regions of the image
19     sigma: float
20         Standard deviation of the gaussian, used to calculate derivatives.
21     beta: float, optional
22         The anisotropy parameter of the Frangi filter (default is 0.5)
23     gamma: float, optional
24         Scaling factor for the structureness parameter of the Frangi
25         filter. The structureness parameter will be set to gamma * maximum
26         of the hessian norm. (Default is 0.5)
27     c: float or None, optional
28         The strutureness parameter of the Frangi filter. If this is set then
29         gamma is ignored. (Default is None).
30     dilation_radius: int or None
31         If dilation radius is supplied, then areas within that amount of pixels
32         will not be calculated. This is preferable in certain contexts,
33         especially when there is a dark background and dark_bg=True. This is
34         especially recommended for small sigmas and when gamma is not provided.
35         None to forgo this procedure (default). A mask must be supplied for
36         this to make sense.
37     dark_bg: boolean or None
38         if True, then frangi will select only for bright curvilinear
39         features; if False, then Frangi will select only for dark
40         curvilinear structures. if None instead of a bool, then curvilinear
41         structures of either type will be reported.
42     signed_frangi: bool, optional
43         if signed is True, the result will be the same as if dark_bg is set
44         to None, except that the sign will change to match the desired
45         features. See example below.
46     return_debug_info: bool, optional
47         will return a large dict consisting of several large matrices,
48         calculated hessian, etc.
49
50     scale_dict = {'sigma': sigma,
51                  'beta': beta,
52                  'gamma': gamma,
53                  'c': c,
54                  'H': hesh,
55                  'F': targets,
56                  'k1': k1,
57                  'k2': k2,
58                  'border_radius': dilation_radius
59 }
60
61     Returns
62     -----
63     ...
64
65     Notes
66     -----
67     Although default is 0.5, this means that the structureness factor of the
68     Frangi score will only be 0.86 at its maximum. Larger values of gamma
69     will only dampen the frangi filter more. Smaller values toward 0 will
    result in a "looser" filter. For example, if gamma = .25, then the

```

```

70 maximum score is (1-exp{-8}) around .999 (it may be desirable that the
71 franginess score should be able to achieve a score of 1).
72
73 This function will accept 0 an input, and the structureness factor will
74 be set to 1 everywhere (the limiting case as gamma -> 0)
75
76 Frangi structureness factor is (1 - exp((-S**2)/(2*c**2)))
77 """
78 hesh = fft_hessian(img, sigma, kernel=kernel) # the triple (Hxx,Hxy,Hyy)
79 # calculate principal curvatures with |k1| <= |k2|
80
81
82 k1, k2 = principal_curvatures(img, sigma, H=hesh)
83
84 if dilation_radius is not None:
85     # pass None to just get the mask back
86     collar = dilate_boundary(None, radius=dilation_radius, mask=img.mask)
87
88     # get rid of "bad" K values before you calculate gamma and Frangi
89     k1[collar] = 0
90     k2[collar] = 0
91     hesh[0][collar] = 0
92     hesh[1][collar] = 0
93     hesh[2][collar] = 0
94 else:
95     collar = img.mask.copy()
96
97
98 # no need to set gamma or c anymore. will be set inside get_frangi_targets
99 #if c is None:
100 #    Frangi suggested 'half the max Hessian norm' as an empirical
101 #    half the max spectral radius is easier to calculate so do that
102 #    shouldn't be affected by mask data but should make sure the
103 #    mask is *well* far away from perimeter
104 #    we actually calculate half of max hessian norm
105 #    using frob norm = sqrt(trace(AA^T))
106 #    alternatively you could use gamma = .5 * np.abs(k2).max()
107 #hnorm = hessian_norm(hesh, mask=collar)
108 #print(f'\sigma={sigma:2f}')
109 #gamma0 = .5*hessian_norm(hesh).max()
110 #print(f'\t\gamma0={gamma0:.5f} = frob-norm \gamma pre-dilation')
111
112 #gamma1 = .5*hessian_norm(hesh, mask=collar).max()
113 #print(f'\t\gamma1={gamma1:.5f} = frob-norm \gamma post-collar dilation {dilation_radius}')
114 #l2gamma = .5*np.max(np.abs(k2))
115 #print(f'\t\gamma2={l2gamma:.5f} = from L2-norm \gamma (K2 with collar)')
116
117 #hdilation = int(max(np.ceil(sigma),10))
118 #hcollar = dilate_boundary(None, radius=hdilation, mask=img.mask)
119 #gamma = .5 * max_hessian_norm(hesh, mask=hcollar)
120
121 #print(f'\t\gamma3={gamma:.5f} = \gamma post-hdilation (radius {hdilation}) (old \gamma)')
122
123 #print('changing \gamma to L2-norm with collar')
124 #gamma = max(gamma1, l2gamma, gamma, gamma0)
125
126 # wish this scaled a little better
127
128 # a very large gamma here will make the Frangi score zero
129 # a very small gamma means that we are artificially inflating the
130 # structureness measure
131 #import matplotlib.pyplot as plt
132 #plt.imshow(hnorm*(~collar))

```

```

134 #plt.show()
135 #print(hnorm[~collar].min(), hnorm[~collar].max())
136 #if hnorm[~collar].max() < 0.1:
137 #    print(f'max hessian norm is very small at this scale ({sigma},{hnorm[~collar].max})
138 #          you should maybe skip this scale')
139 #elif hnorm[~collar].min() < 0.001:
140 #    # only trigger if the first one didn't
141 #    print(f'min hessian norm is very small at this scale ({sigma}, {hnorm[~collar].min})
142 #          be carefully of artificially inflated scores')
143 #S = np.sqrt(k1**2 + k2**2)
144 #import matplotlib.pyplot as plt
145 #plt.imshow(S)
146 #plt.show()
147 #plt.close()
148 #print('max hessian norm (Frob): ', hnorm.max())
149 #print('max structurenness: ', S.max())
150 #c = gamma*S.max()
151
152 if verbose:
153     print(f'finding Frangi targets with β={beta} and γ={c:.2}')
154
155 targets = get_frangi_targets(k1, k2, beta=beta, gamma=gamma, c=c,
156                             dark_bg=dark_bg, signed=signed_frangi,
157                             rescale_frangi=rescale_frangi)
158
159 if gradient_filter:
160     # obviously you could compute this at the same time as the hessian :/
161
162     g = fft_gradient(img, sigma)
163     g = dilate_boundary(g, radius=20, mask=img.mask)
164
165     # you could technically pass a function to switch between these
166     # behaviors
167     low_g = (g < nz_percentile(g, 50)).filled(0)
168
169     targets[~low_g] = 0
170
171 if not return_debug_info:
172     return targets
173 else:
174
175     # for logging we have to recalculate this
176     if c is not None:
177         c = gamma * max(np.sqrt(k1**2 + k2**2))
178
179     scale_dict = {'sigma': sigma,
180                 'beta': beta,
181                 'gamma': gamma,
182                 'c': c,
183                 'H': hesh,
184                 'F': targets,
185                 'k1': k1,
186                 'k2': k2,
187                 'border_radius': dilation_radius
188                 }
189
190     return targets, scale_dict
191
192 def get_frangi_targets(K1, K2, beta=0.5, gamma=0.5, c=None,
193                         dark_bg=True, signed=False, rescale_frangi=False):
194     """Calculate the Frangi vesselness measure from eigenvalues.
195
196     Parameters

```

```

198 -----
199     K1, K2 : ndarray (each)
200         each is an ndarray of eigenvalues (approximated principal
201         curvatures) for some image.
202     beta: float
203         the anisotropy parameter (default is 0.5)
204     gamma: float or None
205         Scaling factor for the the structureness parameter. The structureness
206         parameter c will be set to gamma times the maximum of the Hessian
207         norm, sqrt(K1**2 + K2**2). Default is 0.5
208     c: float or None
209         The frangi structureness parameter. If this is set, gamma above will
210         be ignored.
211     dark_bg: boolean or None
212         if True, then frangi will select only for bright curvilinear
213         features; if False, then Frangi will select only for dark
214         curvilinear structures. if None instead of a bool, then curvilinear
215         structures of either type will be reported.
216     signed: boolean
217         if signed is True, the result will be the same as if dark_bg is set
218         to None, except that the sign will change to match the desired
219         features. See example below.
220
221 Returns
222 -----
223     F: ndarray, same shape as K1
224         the Frangi vesselness measure.
225
226 Notes
227 -----
228 If beta or gamma are set to 0, then the frangi anisotropy factor will be
229 set to 0 or 1 everywhere (which is the limiting case as beta->0 or
230 gamma->0) You can set beta = 'inf' or np.inf to set anisotropy factor to 1.
231
232 Examples
233 -----
234 >>>f1 = get_frangi_targets(K1,K2, dark_bg=True, signed=True)
235 >>>f2 = get_frangi_targets(K1,K2, dark_bg=False, signed=True)
236 >>>np.all(f1 == -f2)
237 True
238
239 >>> F = get_frangi_targets(K1,K2, gamma=0.5)
240 >>> Falt = get_frangi_targets(K1,K2, c=0.5*np.sqrt(K1**2 + K2**2))
241 >>> np.all(F == Falt)
242 True
243 """
244
245 A = anisotropy(K1, K2, beta=beta)
246 S = structureness(K1, K2, gamma=gamma, c=c)
247
248 anisotropy_factor = np.exp(-A)
249 structureness_factor = (1 - np.exp(-S))
250
251 F = anisotropy_factor * structureness_factor
252
253 if rescale_frangi:
254     if c is not None:
255         # more like will not
256         print('c was set to an arbitrary value. cannot rescale')
257     else:
258         max_theoretical = (1 - np.exp(-1/(2*gamma**2)))
259         F = F / max_theoretical
260
261 # now just filter/ change sign as appropriate.

```

```

262     if not signed:
263         # calculate the regular frangi filter
264         if dark_bg is None:
265             #keep F the way it is
266             pass
267         elif dark_bg:
268             # zero responses from positive curvatures
269             F = (K2 < 0)*F
270         else:
271             # zero responses from negative curvatures
272             F = (K2 > 0)*F
273     else:
274         if dark_bg is None:
275             # output is already signed
276             pass
277         elif dark_bg:
278             # positive curvature spots will be made negative
279             F[K2 > 0] = -1 * F[K2 > 0]
280         else:
281             # negative curvature spots will be made positive
282             F[K2 < 0] = -1 * F[K2 < 0]
283
284     # finally, reapply the mask if the inputs came with one
285     if numpy.ma.is_masked(K1):
286         F = numpy.ma.masked_array(F, mask=K1.mask)
287
288     return F
289
290
291 def hessian_norm(hesh, mask=None):
292     """Calculate Frobenius norm of Hessian.
293
294     Calculates the maximal value (over all pixels of the image) of the
295     Frobenius norm of the Hessian. This should be the same as the square root
296     of unscaled structureness.
297
298     Parameters
299     -----
300     hesh: a tuple of ndarrays
301         The tuple hxx,hxy,hyy which are all the same shape. The hessian at
302         the point (m,n) is then [[hxx[m,n], hxy[m,n]],
303         [hxy[m,n], hyy[m,n]]]
304
305     Returns
306     -----
307     float
308     """
309
310     hxx, hxy, hyy = hesh
311
312     # frob norm is just sqrt(trace(AA^T)) which is easy for a 2x2
313     hnorm = (hxx**2 + 2*hxy**2 + hyy**2)
314
315     if mask is not None:
316         hnorm[mask] = 0
317
318     hnorm = np.sqrt(hnorm)
319     return hnorm
320
321
322 def anisotropy(K1,K2, beta=0.5):
323     """Convenience function for the exponential argument in the Frangi
324     anisotropy factor.
325

```

```

326 According to Frangi (1998) this is technically  $(A^{**2}) / (2*\beta^{**2})$ 
327 unless beta is None, in which case just  $A^{**2}$  is returned
328
329 The frangi vesselness factor is formally  $(\exp(-R))$ 
330 where R is what's returned by this function
331 """
332
333 A = (K1 / K2) ** 2
334 #print(f'inside anisotropy, \beta={beta}')
335 if beta == 0:
336     return np.zeros_like(A) # the limiting case as beta -> 0
337
338 elif beta == 'inf' or np.isinf(beta):
339     return np.ones_like(A) # the limiting case as beta -> inf
340
341 elif beta is None:
342     return A # just return the  $A^{**2}$  part (why though)
343 else:
344     return A / (2*beta**2)
345
346
347 def structureness(K1, K2, gamma=0.5, c=None):
348     """Convenience function for Structureness measure.
349     According to Frangi (1998) this is technically  $S^{**2}$ 
350     """
351     S = K1**2 + K2**2
352
353     # if c is not provided, calculate it
354     if c is None:
355         c = gamma * np.sqrt(S).max() # the max Frob norm of the Hessian
356
357     #print(f'inside structureness, \gamma={gamma}, c={c}')
358
359     if c == 0:
360         return np.zeros_like(S)
361
362     elif c == 'inf' or np.isinf(c):
363         return np.ones_like(S)
364
365     elif c is None:
366         return S
367
368     else:
369         return S / (2*c**2)
370

```

listings/gradient_filter_demo.py

```

1 #!/usr/bin/env python3
2
3 import numpy as np
4 import matplotlib.pyplot as plt
5 from skimage.util import img_as_float
6 from skimage.io import imread
7 from placenta import get_named_placenta, list_by_quality, cropped_args,
8     img_as_float
9
10 from frangi import frangi_from_image
11 from hfft import fft_gradient, fft_hessian, fft_gaussian
12 from merging import nz_percentile
13 from plate_morphology import dilate_boundary
14 import os.path, os

```

```

15
16 MAKE_OUTPUTS = False
17 OUTPUT_DIR = 'demo_output/gradient_filter_demo'
18
19 BETA = .5
20
21 if not os.path.exists(OUTPUT_DIR):
22     os.makedirs(OUTPUT_DIR)
23
24 filename = list_by_quality(N=1)[0]
25 img = get_named_placenta(filename)
26 crop = cropped_args(img)
27
28 F0 = list()
29 F1 = list()
30
31 scales = np.logspace(-1, 3, num=12, base=2)
32
33 for n, sigma in enumerate(scales):
34
35     f0 = frangi_from_image(img, sigma, beta=BETA, dark_bg=False,
36                            dilation_radius=20, gradient_filter=False)
37
38     f1 = frangi_from_image(img, sigma, beta=BETA, dark_bg=False,
39                            dilation_radius=20, gradient_filter=True)
40
41     # simulate g
42     #g = fft_gradient(img, sigma)
43     #g = dilate_boundary(g, radius=20, mask=img.mask)
44     #g = g < nz_percentile(g, 50)
45     #g_filter = (~g).filled(0)
46
47 if MAKE_OUTPUTS:
48     fig, ax = plt.subplots(ncols=2, nrows=1, figsize=(10,4))
49
50     ax[0].imshow(f0.filled(0)[crop], vmin=0, vmax=1, cmap='nipy_spectral')
51     ax[0].axis('off')
52     ax[0].set_title(f'Standard Frangi  $\sigma={\text{sigma}}:2f$ ', fontsize=10)
53
54     ax[1].imshow(f1.filled(0)[crop], vmin=0, vmax=1, cmap='nipy_spectral')
55     ax[1].axis('off')
56     ax[1].set_title(f'w/ gradient filter', fontsize=10)
57
58     #ax[2].imshow(g_filter[crop].T, cmap='nipy_spectral')
59     #ax[2].axis('off')
60     #ax[2].set_title(f'Gradient filter  $\sigma={\text{sigma}}:2f$ ')
61
62     #plt.show()
63     plt.tight_layout()
64     plt.savefig(os.path.join(OUTPUT_DIR, f'gf_scale_{n:0{2}}.png'))
65     plt.close('all')
66
67 F0.append(f0)
68 F1.append(f1)
69
70 F0 = np.stack(F0)
71 F1 = np.stack(F1)
72
73
74 if MAKE_OUTPUTS:
75     fig, ax = plt.subplots(ncols=2, nrows=1, figsize=(10,4))
76
77     ax[0].imshow(F0.max(axis=0).filled(0)[crop], vmin=0, vmax=1,
78                  cmap='nipy_spectral')

```

```

79 ax[0].axis('off')
80 ax[0].set_title(f'Standard Frangi F_max', fontsize=10)
81
82 ax[1].imshow(F1.max(axis=0).filled(0)[crop], vmin=0, vmax=1,
83                 cmap='nipy_spectral')
84 ax[1].axis('off')
85 ax[1].set_title(f'w/ gradient filter', fontsize=10)
86
87 plt.tight_layout()
88 #plt.show()
89 plt.savefig(os.path.join(OUTPUT_DIR, f'gf_Fmax.png'))
90 plt.close('all')

```

listings/hfft_accuracy.py

```

1 #!/usr/bin/env python3
2 """
3 here you want to show the accuracy of hfft.py
4 BOILERPLATE
5
6 show that gaussian blur of hfft is accurate, except potentially around the
7 boundary proportional to sigma.
8 or if they're off by a scaling factor, show that the derivates
9 (taken the same way) are proportional.
10
11 pseudocode
12
13 A = gaussian_blur(image, sigma, method='conventional')
14 B = gaussian_blur(image, sigma, method='fourier')
15
16 zero_order_accurate = isclose(A, B, tol)
17
18 J_A = get_jacobian(A)
19 J_B = get_jacobian(B)
20
21 first_order_accurate = isclose(J_A, J_B, tol)
22
23 A_eroded = zero_around_plate(A, sigma)
24 B_eroded = zero_around_plate(B, sigma)
25
26 J_A_eroded = zero_around_plate(J_A, sigma)
27 J_B_eroded = zero_around_plate(J_B, sigma)
28
29 zero_order_accurate_no_boundary = isclose(A_eroded, B_eroded, tol)
30 first_order_accurate = isclose(J_A_eroded, J_B_eroded, tol)
31
32 """
33
34 from placenta import get_named_placenta, cropped_args
35
36 from itertools import combinations_with_replacement
37 from skimage.exposure import rescale_intensity
38
39 from hfft import fft_hessian, fft_gaussian, fft_dgk
40 from scipy.ndimage import gaussian_filter
41 import matplotlib.pyplot as plt
42 from placenta import show_mask, list_by_quality
43
44 from scoring import mean_squared_error
45 from itertools import combinations

```

```

49 import numpy as np
50 from scipy.ndimage import laplace
51 import numpy.ma as ma
52
53 from skimage.segmentation import find_boundaries
54 from skimage.morphology import disk, binary_dilation
55
56 from plate_morphology import dilate_boundary
57
58 from diffgeo import principal_curvatures
59 from frangi import structureness, anisotropy, get_frangi_targets
60
61 from skimage.util import img_as_float
62
63 def plot_image_slices(arrs, fixed_axis=0, fixed_index=None, labels=None,
64                      formats=None, title=None):
65     """
66     arrs needs to be the same shape and dimension
67     could pass it to np.stack and check for a value error?
68
69     """
70     fig, ax = plt.subplots(figsize=(12,2))
71     # hopefully the fixed axis is 0 or 1. this gets the other one
72     it_axis = 1 if fixed_axis==0 else 0
73
74     # if it's a tuple, make it an array, etc. etc.
75     arrs = np.stack(arrs)
76
77     # make sure we can iterate over it if there's just as single image
78     if arrs.ndim < 3:
79         arrs = np.expand_dims(arrs,0)
80
81     if labels is None:
82         labels = [None for a in arrs]
83     if formats is None:
84         formats = ['' for a in arrs]
85
86     if fixed_index is None:
87         # find halfway point of the appropriate dimension from the first array
88         fixed_index = arrs[0].shape[fixed_axis] // 2
89
90     for a, lab, fmt in zip(arrs, labels, formats):
91         ax.plot(np.arange(a.shape[it_axis]),
92                 np.moveaxis(a, fixed_axis, 0)[fixed_index, :],
93                 fmt, label=lab)
94
95     if title is not None:
96         ax.set_title(title)
97
98     # can this be at least a little object-oriented? :(
99     fig.legend()
100
101 def multiway_comparison(arrs, scorefunc):
102
103     scores = np.zeros((len(arrs), len(arrs)))
104
105     for j in range(len(arrs)):
106         for k in range(j+1, len(arrs)):
107             scores[j,k] = scorefunc(arrs[j], arrs[k])
108
109     return scores
110
111 filename = list_by_quality(0)[5]
112

```

```

113 img = get_named_placenta(filename)
114 # so that scipy.ndimage.gaussian_filter doesn't use uint8 precision (jesus)
115 img = ma.masked_array(img_as_float(img), mask=img.mask)
116
117 test_sigmas = [.3, .6, 1.0, 5.0, 15, 30, 60, 90]
118
119 for sigma in test_sigmas:
120     print("*"*80, '\n\n', f"\sigma={sigma}")
121     #print('applying standard gauss blur')
122
123     # this is exactly how it's passed to skimage.feature.hessian_matrix...
124     A = gaussian_filter(img.filled(0), sigma, mode='constant', cval=0)
125
126     #print('applying fft gauss blur')
127     B = fft_gaussian(img, sigma, kernel='sampled')
128     C = fft_gaussian(img, sigma, kernel='discrete')
129
130     #print('calculating first derivatives')
131     # zero the masks before calculating derivates if they're masked
132     Agrad = np.gradient(A)
133     Bgrad = np.gradient(B)
134     Cgrad = np.gradient(C)
135
136
137 axes = range(img.ndim)
138
139 #print('calculating second derivatives')
140 # this is the same way it's done in skimage.feature.hessian_matrix...
141 H_A = [np.gradient(Agrad[ax0], axis=ax1)
142         for ax0, ax1 in combinations_with_replacement(axes, 2)]
143 H_B = [np.gradient(Bgrad[ax0], axis=ax1)
144         for ax0, ax1 in combinations_with_replacement(axes, 2)]
145 H_C = [np.gradient(Cgrad[ax0], axis=ax1)
146         for ax0, ax1 in combinations_with_replacement(axes, 2)]
147
148 #print('calculating eigenvalues of hessian')
149 ak1, ak2 = principal_curvatures(img, sigma=sigma, H=H_A)
150 bk1, bk2 = principal_curvatures(img, sigma=sigma, H=H_B)
151 ck1, ck2 = principal_curvatures(img, sigma=sigma, H=H_C)
152
153
154 #RA = anisotropy(ak1,ak2)
155 #RB = anisotropy(bk1,bk2)
156 #RC = anisotropy(ck1,ck2)
157
158 #SA = structureness(ak1, ak2)
159 #SB = structureness(bk1, bk2)
160 #SC = structureness(ck1, ck2)
161
162 ## ugh, apply masks here. too large to be conservative?
163 ## otherwise structureness only shows up for small sizes
164 new_mask = dilate_boundary(None, radius=int(3*sigma), mask=img.mask)
165
166
167 crop = cropped_args(img)
168
169 A = A[crop]
170 B = B[crop]
171 C = C[crop]
172
173
174 ak1 = ma.masked_array(ak1,new_mask)[crop]
175 ak2 = ma.masked_array(ak2,new_mask)[crop]
176 bk1 = ma.masked_array(bk1,new_mask)[crop]

```

```

177 bk2 = ma.masked_array(bk2,new_mask)[crop]
178 ck1 = ma.masked_array(ck1,new_mask)[crop]
179 ck2 = ma.masked_array(ck2,new_mask)[crop]
180
181 FA = get_frangi_targets(ak1,ak2, dark_bg=False).filled(0)
182 FB = get_frangi_targets(bk1,bk2, dark_bg=False).filled(0)
183 FC = get_frangi_targets(ck1,ck2, dark_bg=False).filled(0)
184
185
186 # the following shows a random vertical slice of A & B (when scaled)
187 labels = ('scipy.ndimage.gaussian_filter', 'fft_gaussian', 'fft_dgk')
188 formats = ('g:', 'k', 'b-.')
189 plot_image_slices((A,B,C), labels=labels, formats=formats,
190                     title=r'gaussian convolution  $\sigma = \text{.format}(\sigma)$ ')
191 plt.tight_layout()
192 plt.savefig('Gslice_sigma={:d}.png'.format(int(sigma*10)), dpi=300)
193 plot_image_slices((FA,FB,FC), labels=labels, formats=formats,
194                     title=r'Frangi filter response  $\sigma = \text{.format}(\sigma)$ ')
195 plt.tight_layout()
196 plt.savefig('Fslice_sigma={:d}.png'.format(int(sigma*10)), dpi=300)
197 #plt.show()
198
199 print('comparing gaussians (mean squared error)')
200 print(multiway_comparison((A,B,C), mean_squared_error))
201 print('comparing frangi response (mean squared error)')
202 print(multiway_comparison((FA,FB,FC), mean_squared_error))

```

listings/hfft_demo.py

```

1 #!/usr/bin/env python3
2
3 import numpy as np
4 from skimage.data import camera
5 from skimage.io import imread
6 from skimage.util import img_as_float
7
8 import matplotlib.pyplot as plt
9 from hfft import fft_gaussian, fft_hessian, fft_dgk
10 from scipy.ndimage import gaussian_filter
11
12 from scipy.linalg import norm
13 import timeit
14
15 #img = camera() / 255.
16 img = imread('samples/barium1.png', as_grey=True) / 255.
17 mask = imread('samples/barium1.mask.png', as_grey=True)
18
19 img = img_as_float(img)
20
21 # compare computation speed over sigmas
22
23 # N logarithmically spaced scales between 1 and 2^m
24 N = 32
25 m = 8
26 sigmas = np.logspace(0,m, num=N, base=2)
27
28 fft_results = list()
29 std_results = list()
30
31 for sigma in sigmas:
32     # test statements to compare (fft-based gaussian vs convolution-based)
33     fft_test_statement = "fft_gaussian(img,{},kernel='discrete')".format(sigma)

```

```

34 std_test_statement = "gaussian_filter(img, {})".format(sigma)
35 # run each statement 1 times (with 2 runs in each trial)
36 # returns/appends the average of 3 runs
37 fft_results.append(timeit.timeit(fft_test_statement,
38                             number=1, globals=globals()))
39 std_results.append(timeit.timeit(std_test_statement,
40                             number=1, globals=globals()))
41
42 # now actually evaluate both to compare
43 f = eval(fft_test_statement)
44 s = eval(std_test_statement)
45
46 # normalize each matrix by frobenius norm and take difference
47 # ideally should try to zero out the "mask" area
48 diff = np.abs(f / norm(f) - s / norm(s))
49 raw_diff = np.abs(f - s)
50 # don't care if it's the background
51 diff[mask==1] = 0
52 raw_diff[mask==1] = 0
53
54 # should format this stuff better into a legible table
55 print(sigma, diff.max(), raw_diff.max())
56
57 lines = plt.plot(sigmas, fft_results, 'go', sigmas, std_results, 'bo')
58 plt.xlabel('sigma (gaussian blur parameter)')
59 plt.ylabel('run time (seconds)')
60 plt.legend(lines, ('fft-gaussian', 'conv-gaussian'))
61 plt.title('Comparision of Gaussian Blur Implementations')

```

listings/hfft.py

```

1 #!/usr/bin/env python3
2
3 import numpy as np
4 from scipy import signal
5 import scipy.fftpack as fftpack
6 from scipy.special import iv, ive
7 from scipy.ndimage import gaussian_filter
8 from itertools import combinations_with_replacement
9
10 # for demos
11 import matplotlib.pyplot as plt
12
13 from skimage.data import camera
14 from skimage.util import img_as_float
15 from skimage.measure import compare_mse, compare_nrmse
16 """
17 hfft.py is the implementation of calculating the hessian of a real
18 image based in frequency space (rather than direct convolution with a gaussian
19 as is standard in scipy, for example).
20
21 TODO: PROVIDE MAIN USAGE NOTES
22 """
23
24 def fft_gaussian(img, sigma, kernel=None):
25     """
26     https://docs.scipy.org/doc/scipy/reference/generated/scipy.signal.fftconvolve.html
27     in particular the example in which a gaussian blur is implemented.
28
29
30
31

```

```

32 along with the comment:
33 "Gaussian blur implemented using FFT convolution. Notice the dark borders
34 around the image, due to the zero-padding beyond its boundaries. The
35 convolve2d function allows for other types of image boundaries, but is far
36 slower"
37
38 (i.e. doesn't use FFT).
39
40 note that here, you actually take the FFT of a gaussian (rather than
41 build it in frequency space). there are ~6 ways to do this.
42 """
43 #create a 2D gaussian kernel to take the FFT of
44 # output of signal.gaussian is normalized to 1 so you need to scale
45 # it back to work
46 #A = 1 / (2*np.pi*sigma**2) # scale factor for 2D
47
48 if kernel in ('discrete', None):
49     kern_x = discrete_gaussian_kernel(img.shape[0], sigma)
50     kern_y = discrete_gaussian_kernel(img.shape[1], sigma)
51 elif kernel == 'sampled':
52     A = 1 / (np.sqrt((2*np.pi)*sigma**2))
53     kern_x = A*signal.gaussian(img.shape[0], sigma)
54     kern_y = A*signal.gaussian(img.shape[1], sigma)
55 else:
56     raise ValueError("Key must be 'discrete' or 'sampled'")
57
58 kernel = np.outer(kern_x, kern_y)
59
60 return signal.fftconvolve(img, kernel, mode='same')
61
62 def discrete_gaussian_kernel(n_samples, sigma):
63 """
64 sigma is the scale, n_samples is the number of samples to compute
65 will return a window centered a zero
66 i.e. arange(-n_samples//2, n_samples//2+1)
67
68 note! to make this work similarly to fft_gaussian, this uses
69 sigma = np.sqrt(t). Usually you'll find this in terms of t
70
71 by using scipy.special.iv instead we prevent blowups
72 """
73 dom = np.arange(-(n_samples//2), (n_samples//2) + 1)
74 #there should be a scaling parameter alpha but whatever
75 #return np.exp(-t) * iv(dom,t)
76 return iv(dom,sigma**2)
77
78 def fft_dgk(img, sigma, order=0, A=None):
79 """
80 This is the discrete gaussian kernel which is supposedly less crappy
81 than using a sampled gaussian.
82 """
83 m,n = img.shape
84 # i don't know if this will suck if there are odd dimensions
85 kernel = np.outer(discrete_gaussian_kernel(m,sigma**2),
86                   discrete_gaussian_kernel(n,sigma**2))
87
88 return signal.fftconvolve(img, kernel, mode='same')
89
90 def fft_fdgk(img, sigma):
91 """
92 convolve with discrete gaussian kernel in freq. space
93 """
94 # this would be a lot better since you wouldn't have to deal
95 # with an arbitrary cutoff of size of the discrete kernel

```

```

96     # since the freq. space version is just
97     #  $\exp\{\alpha^*t(\cos\theta - 1)\}$ 
98     # see formula 22 of lindeberg discrete paper
99
100    pass
101
102  def fft_hessian(image, sigma=1., kernel=None):
103      """
104          a reworking of skimage.feature.hessian_matrix that uses
105          FFT to compute gaussian, which results in a considerable speedup
106
107      INPUT:
108          image - a 2D image (which type?)
109          sigma - coefficient for gaussian blur
110          kernel - input to fft_gaussian
111          gradient - if you've already computed this
112
113      OUTPUT:
114          (Lxx, Lxy, Lyy) - a triple containing three arrays
115              each of size image.shape containing the xx, xy, yy derivatives
116              respectively at each pixel. That is, for the pixel value given
117              by image[j][k] has a calculated 2x2 hessian of
118              [ [Lxx[j][k], Lxy[j][k]],
119                [Lxy[j][k], Lyy[j][k]] ]
119
120
121
122      gaussian_filtered = fft_gaussian(image, sigma=sigma, kernel=kernel)
123
124      gradients = np.gradient(gaussian_filtered)
125
126      axes = range(image.ndim)
127
128      H_elems = [np.gradient(gradients[ax0], axis=ax1)
129                  for ax0, ax1 in combinations_with_replacement(axes, 2)]
130
131      return H_elems
132
133
134  def fft_gradient(image, sigma=1.):
135      """ returns gradient norm """
136
137      gaussian_filtered = fft_gaussian(image, sigma=sigma)
138
139      Lx, Ly = np.gradient(gaussian_filtered)
140
141      return np.sqrt(Lx**2 + Ly**2)
142
143
144  def demo(img=None):
145      """
146          old main function for testing.
147
148          This simply tests fft_gaussian on a test image,
149
150      if img is None:
151          img = img_as_float(camera())
152      else:
153          img = img_as_float(img)
154
155      sample_sigmas = (.5, 2, 8, 30)
156      #sample_sigmas = (.2, 2)
157
158      # build the graphs here side by side

```

```

160 # show regular blur, sampled blur, discrete blur, 1d plot of signals
161 # so a 4 by 4 grid
162
163 fig, axes = plt.subplots(nrows=len(sample_sigmas), ncols=4,
164                         figsize=(10, 10))
165
166 for cax, sigma in enumerate(sample_sigmas):
167
168     # convolve the image with a gaussian kernel, one of three ways
169     fft_dgk = fft_gaussian(img, sigma, kernel='discrete')
170     fft_sampled = fft_gaussian(img, sigma, kernel='sampled')
171     xy_sampled = gaussian_filter(img, sigma, mode='constant', cval=0)
172
173     # make the fancy sample
174     N = 80
175     dom = np.arange(-(N//2), N//2 + 1)
176     dgk = discrete_gaussian_kernel(N, sigma)
177     A = np.sqrt(2*np.pi*sigma**2)
178     A = 1 / A
179     sgk = A * signal.gaussian(N+1, sigma)
180
181     axes[cax, 0].imshow(xy_sampled, cmap='gray', vmin=0, vmax=1)
182     axes[cax, 0].set_ylabel(r'$\sigma$ = .format(sigma))')
183     #axes[cax, 0].set_title(f'ndi.gaussian_filter, $\sigma$={sigma}'))
184     #axes[cax, 0].axis('off')
185     axes[cax, 0].set_xticks([])
186     axes[cax, 0].set_yticks([])
187
188     axes[cax, 1].imshow(fft_sampled, cmap='gray', vmin=0, vmax=1)
189     #axes[cax, 1].imshow(fft_sampled, cmap='gray')
190     #axes[cax, 1].set_title(f'fft sampled kernel, $\sigma$={sigma}'))
191     axes[cax, 1].axis('off')
192
193     axes[cax, 2].imshow(fft_dgk, cmap='gray', vmin=0, vmax=1)
194     #axes[cax, 2].set_title(f'fft discrete kernel, $\sigma$={sigma}'))
195     axes[cax, 2].axis('off')
196
197
198     axes[cax, 3].plot(dom, sgk, 'k', dom, dgk, 'g:')
199     #axes[cax, 3].set_title(f'discrete vs. sampled kernel $\sigma$={sigma}'))
200     #axes[cax, 3].axes.set_aspect('equal')
201
202     # set titles for the first column
203     axes[0,0].set_title('(a)')
204     axes[0,1].set_title('(b)')
205     axes[0,2].set_title('(c)')
206     axes[0,3].set_title('(d)')
207
208 plt.tight_layout()
209 plt.show()
210
211 def compare_mae(arr1, arr2):
212
213     assert arr1.shape == arr2.shape
214     return np.abs(arr1 - arr2).sum() / arr1.size
215
216
217 def semigroup_demo(img=None):
218     """
219     the step ones don't look anywhere near as blurred as the initial image
220     in any case! don't use this till it's good!
221     """
222     if img is None:
223         img = img_as_float(camera())

```

```

224
225     img = img_as_float(img)
226
227     sigma = 45.
228     n_steps = 2
229     sigmas = (10, 35)
230
231     fft_discrete = fft_gaussian(img, sigma, kernel='discrete')
232     fft_sampled = fft_gaussian(img, sigma, kernel='sampled')
233     xy_sampled = gaussian_filter(img, sigma, mode='constant', cval=0)
234
235     step_discrete = img.copy()
236     step_fft_sampled = img.copy()
237     step_xy_sampled = img.copy()
238
239     #sigma_n = sigma / n_steps
240     #sigma_n = np.power(sigma, 1/n_steps)
241     counter = 0
242     for sigma_n in sigmas:
243         step_discrete = fft_gaussian(step_discrete, sigma_n, kernel='discrete')
244         step_fft_sampled = fft_gaussian(step_fft_sampled, sigma_n,
245                                         kernel='sampled')
246         step_xy_sampled = gaussian_filter(step_xy_sampled, sigma_n,
247                                           mode='constant', cval=0)
248         counter += sigma_n
249         #print(counter, end=' ')
250
251     print()
252     er = int(sigma)
253     crop = np.s_[er:-er, er:-er]
254
255     fft_discrete = fft_discrete[crop]
256     fft_sampled = fft_sampled[crop]
257     xy_sampled = xy_sampled[crop]
258     step_discrete = step_discrete[crop]
259     step_fft_sampled = step_fft_sampled[crop]
260     step_xy_sampled = step_xy_sampled[crop]
261
262     fig, axes = plt.subplots(ncols=3, nrows=2)
263     axes[0,0].imshow(xy_sampled, vmin=0, vmax=1, cmap='gray')
264     axes[0,0].set_title('(a)')
265     axes[0,0].set_xticks([]), axes[0,0].set_yticks([])
266
267     axes[0,1].imshow(fft_sampled, vmin=0, vmax=1, cmap='gray')
268     axes[0,1].set_title('(b)')
269     axes[0,1].set_xticks([]), axes[0,1].set_yticks([])
270
271     axes[0,2].imshow(fft_discrete, vmin=0, vmax=1, cmap='gray')
272     axes[0,2].set_title('(c)')
273     axes[0,2].set_xticks([]), axes[0,2].set_yticks([])
274
275     axes[1,0].imshow(step_xy_sampled, vmin=0, vmax=1, cmap='gray')
276     axes[1,0].axis('off')
277     axes[1,1].imshow(step_fft_sampled, vmin=0, vmax=1, cmap='gray')
278     axes[1,1].axis('off')
279     axes[1,2].imshow(step_discrete, vmin=0, vmax=1, cmap='gray')
280     axes[1,2].axis('off')
281
282     MSE_sampled = compare_mse(xy_sampled, step_xy_sampled)
283     MSE_fft_sampled = compare_mse(fft_sampled, step_fft_sampled)
284     MSE_discrete = compare_mse(fft_discrete, step_discrete)
285
286     print(f'MSE sampled:{MSE_sampled}')
287     print(f'MSE fft_sampled:{MSE_fft_sampled}')

```

```

288 print(f'MSE discrete:{MSE_discrete}')
289 print()
290 #NRMSE_sampled = compare_nrmse(xy_sampled, step_xy_sampled)
291 #NRMSE_fft_sampled = compare_nrmse(fft_sampled, step_fft_sampled)
292 #NRMSE_discrete = compare_nrmse(fft_discrete, step_discrete)
293
294 #print(f'NRMSE sampled:{NRMSE_sampled}')
295 #print(f'MSE fft_sampled:{NRMSE_fft_sampled}')
296 #print(f'NRMSE discrete:{NRMSE_discrete}')
297 #for ax, title in zip(axes.ravel(), ['(a)', '(b)', '(c)', '(d)']):
298 #    ax.axis('off')
299 #    ax.set_title(title)
300
301
302 MAE_sampled = compare_mae(xy_sampled, step_xy_sampled)
303 MAE_fft_sampled = compare_mae(fft_sampled, step_fft_sampled)
304 MAE_discrete = compare_mae(fft_discrete, step_discrete)
305
306 print(f'MAE sampled:{MAE_sampled}')
307 print(f'MAE fft_sampled:{MAE_fft_sampled}')
308 print(f'MAE discrete:{MAE_discrete}')
309
310 plt.show()
311
312 if __name__ == "__main__":
313     from skimage.io import imread
314     from placenta import list_by_quality, get_named_placenta
315     #A = list_by_quality(0)[0]
316     #A = get_named_placenta(A)
317     #A = imread('samples/5.3.02.tif')
318     A = None
319     demo(A)
320     semigroup_demo(A)

```

listings/make_output_montage.py

```
1 #!/usr/bin/env python3
```

listings/merging.py

```

1 #!/usr/bin/env python3
2
3 import numpy as np
4 import numpy.ma as ma
5 from scipy.ndimage import label
6 from skimage.morphology import remove_small_objects
7 import matplotlib.pyplot as plt
8
9 def nz_percentile(A, q, axis=None, interpolation='linear'):
10     """calculate np.percentile(...,q) on an array's nonzero elements only
11
12     Parameters
13     -----
14     A : ndarray
15         matrix from which percentiles will be calculated. Percentiles
16         are calculated on an elementwise basis, so the shape is not important
17     q : a float
18         Percentile to compute, between 0 and 100.0 (inclusive).
19
20     (other arguments): see numpy.percentile docstring
21     """

```

```

22
23     Returns
24     -----
25     out: float
26
27     """
28
29     if ma.is_masked(A):
30         A = A.filled(0)
31
32     return np.percentile(A[A > 0], q, axis=axis, interpolation=interpolation)
33
34
35 def apply_threshold(targets, alphas, return_labels=True):
36     """Threshold targets at each scale, then return max target over all scales.
37
38     A unique alpha can be given for each scale (see below). Return a 2D boolean
39     array, and optionally another array representing what at what scale the max
40     filter response occurred.
41
42     Parameters
43     -----
44     targets : ndarray
45         a 3D array, where targets[:, :, k] is the result of the Frangi filter
46         at the kth scale.
47     alphas : float or array_like
48         a list / 1d array of length targets.shape[-1]. each alphas[k] is a
49         float which thresholds the Frangi response at the kth scale. Due to
50         broadcasting, this can also be a single float, which will be applied
51         to each scale.
52     return_labels : bool, optional
53         If True, return another ndarray representing the scale (see Notes
54         below). Default is True.
55
56     Returns
57     -----
58     out : ndarray, dtype=bool
59         if return labels is true, this will return both the final
60         threshold and the labels as two separate matrices. This is
61         a convenience, since you could easily find labels with
62     labels : ndarray, optional, dtype=uint8
63         The scale at which the largest filter response was found after
64         thresholding. Element is 0 if no scale passed the threshold,
65         otherwise an int between 1 and targets.shape[-1] See Notes below.
66
67     Notes / Examples
68     -----
69     Despite the name, this does *NOT* return the thresholded targets itself,
70     but instead the maximum value after thresholding. If you wanted the
71     thresholded filter responses alone, you should simply run
72
73     >>>(targets > alphas)*targets
74
75     The optional output 'labels' is a 2D matrix indicating where the max filter
76     response occurred. For example, if the label is K, the max filter response
77     will occur at targets[:, :, K-1]. In other words,
78
79     >>>passed, labels = apply_threshold(targets, alphas)
80     >>>targets.max(axis=-1) == targets[:, :, labels - 1 ]
81     True
82
83     It should be noted that returning labels is really just for convenience
84     only; you could construct it as shown in the following example:
85

```

```

86     >>>manual_labels = (targets.argmax(axis=-1) + 1)*np.invert(passed)
87     >>>labels == manual_labels
88     True
89
90     Similarly, the standard boolean output could just as easily be obtained.
91     >>>passed == (labels != 0)
92     True
93     """
94
95     # threshold as an array (even if it's a single element) to broadcast
96     alphas = np.array(alphas)
97
98     # if input's just a MxN matrix, expand it trivially so it works below
99     if targets.ndim == 2:
100         targets = np.expand_dims(targets, 2)
101
102     # either there's an alpha for each channel or there's a single
103     # alpha to be broadcast across all channels
104     assert (targets.shape[-1] == alphas.size) or (alphas.size == 1)
105
106     # pixels that passed the threshold at any level
107     passed = (targets >= alphas).any(axis=-1)
108
109     if not return_labels:
110         return passed # we're done already
111
112     wheres = targets.argmax(axis=-1) # get label of where maximum occurs
113     wheres += 1 # increment to reserve 0 label for no match
114
115     # then remove anything that didn't pass the threshold
116     wheres[np.invert(passed)] = 0
117
118     assert np.all(passed == (wheres > 0))
119
120     return passed, wheres
121
122
123 def sieve_scales(multiscale, high_percentile, low_percentile, min_size=None,
124                  axis=0):
125     """
126     multiscale is a 3 dimensional where 2 dimensions are image and 'axis'
127     parameter is which one is the scale space (i.e. resolution). hopefully
128     axis is 0 or 1 (this won't handle stupider cases)
129
130     this gathers points contiguous points at a low threshold and adds them
131     to the output it contains at least only if that blob contains at least one
132     high percentile point.
133
134     min_size is a size requirement can either be an integer or an array of
135     integers """
136
137     assert multiscale.ndim == 3
138
139     if axis in (-1, 2):
140         # this won't change the input, just creates a view
141         V = np.transpose(multiscale, axes=(2, 0, 1))
142
143     elif axis == 0:
144         V = multiscale # just to use the same variable name
145     else:
146         raise ValueError('Please make resolution the first or last dimension.')
147
148     if np.isscalar(min_size):
149         min_size = [min_size for x in range(multiscale.shape[0])]
```

```

150
151 # label matrix the size of one of the images
152 sieved = np.zeros(V.shape[1:], dtype=np.int32)
153
154 print('sieving ', end='')
155 for n, v in enumerate(V):
156     print('σ', end=' ', flush=True)
157
158     if min_size is not None:
159         z = remove_small_objects(v, min_size=min_size[n])
160     else:
161         z = v # relabel to use same variable
162
163     high_thresh = nz_percentile(v, high_percentile)
164     low_thresh = nz_percentile(v, low_percentile)
165
166     labeled, n_labels = label(z > low_thresh)
167     high_passed = (z > high_thresh)
168
169     for lab in range(n_labels):
170         if lab == 0:
171             continue
172         if np.any(high_passed[labeled == lab]):
173             sieved[labeled == lab] = n
174
175 print()
176 return sieved
177
178 def view_slices(multiscale, axis=0, scales=None, cmap='nipy_spectral',
179                 vmin=0, vmax=1.0, outnames=None, show_colorbar=True):
180     """ scales is just to use for a figure title
181     crop before you get in here.
182
183     if outname is an iterable returning filenames, then we'll assume
184     non-interative mode
185     """
186     assert multiscale.ndim == 3
187
188     if axis in (-1, 2):
189         # this won't change the input, just creates a view
190         V = np.transpose(multiscale, axes=(2, 0, 1))
191
192     elif axis == 0:
193         V = multiscale # just to use the same variable name
194     else:
195         raise ValueError('Please make resolution the first or last dimension.')
196
197     if scales is None:
198         scales = [None for x in range(multiscale.shape[0])]
199     if outnames is None:
200         outnames = [None for x in range(multiscale.shape[0])]
201
202     plt.close('all')
203     for v, sigma, outname in zip(V, scales, outnames):
204
205         if outname is None:
206             plt.imshow(v, cmap=cmap, vmin=vmin, vmax=vmax)
207             mng = plt.get_current_fig_manager()
208             mng.window.showMaximized()
209             plt.tight_layout()
210             if sigma is not None:
211                 plt.title(r'σ=:2f'.format(sigma))
212                 plt.axis('off')
213                 if show_colorbar:

```

```

214         plt.colorbar()
215         plt.tight_layout()
216         plt.show()
217         plt.close()
218
219     else:
220         # save them non interactively with imsave
221         plt.imsave(outname, v, cmap=cmap, vmin=vmin, vmax=vmax)

```

listings/pcsvn.py

```

1 #!/usr/bin/env python3
2
3 """
4 the contents of this file should be split up between frangi (multiscale)
5 and scoring/output
6 """
7 from placenta import get_named_placenta
8 from diffgeo import principal_directions
9 from frangi import frangi_from_image
10 from skimage.util import img_as_float
11 import numpy as np
12 from preprocessing import inpaint_hybrid
13
14 from merging import nz_percentile
15
16 from plate_morphology import dilate_boundary
17
18 import matplotlib.pyplot as plt
19 import matplotlib as mpl
20 import numpy.ma as ma
21
22 import os.path
23 import json
24 import datetime
25
26
27 def make_multiscale(img, scales, beta=0.5, gamma=0.5, c=None, dark_bg=True,
28                     find_principal_directions=False, dilate_per_scale=True,
29                     signed_frangi=False, kernel=None, verbose=True,
30                     rescale_frangi=False, gradient_filter=False):
31     """Returns an ordered list of dictionaries for each scale of Frangi info.
32
33     beta, gamma, and c can all be vectors as long as scales or constants
34     if c is None it will be set.
35
36     Each element in the output contains the following info:
37     {'sigma': sigma,
38      'beta': beta,
39      'gamma': gamma,
40      'H': hesh,
41      'F': targets,
42      'k1': k1,
43      'k2': k2,
44      't1': t1, # if find_principal_directions
45      't2': t2 # if find_principal_directions
46      }
47
48     is it necessary to lug all this shit around?
49     """
50
51     # store results of each scale (create as empty list)
52     multiscale = list()

```

```

53
54     img = ma.masked_array(img_as_float(img), mask=img.mask)
55
56     vectorize = lambda x: np.repeat(x, len(scales)) if (x is None or np.isscalar(x)) else np.array([vectorize(x) for x in scales])
57
58     # vectorize any scalar inputs here
59     beta = vectorize(beta)
60     gamma = vectorize(gamma)
61     c = vectorize(c)
62     print('finding multiscale targets ', end='')
63     for i, (sigma, b, g, cx) in enumerate(zip(scales, beta, gamma, c)):
64
65         print('σ', end=' ', flush=True)
66
67         if dilate_per_scale:
68             if sigma > 20:
69                 radius = int(2*sigma)
70             elif sigma < 3:
71                 radius = 12
72             else:
73                 radius = int(4*sigma)
74         else:
75             radius = None
76
77         targets, this_scale = frangi_from_image(img, sigma=sigma, beta=b, gamma=g,
78                                                 c=cx, dark_bg=dark_bg,
79                                                 dilation_radius=radius,
80                                                 kernel=kernel,
81                                                 signed_frangi=signed_frangi,
82                                                 return_debug_info=True,
83                                                 rescale_frangi=rescale_frangi,
84                                                 gradient_filter=gradient_filter)
85
86         if find_principal_directions:
87             # principal directions should only be computed for critical regions
88             # this mask is where PD's will *NOT* be calculated
89             # is targets a masked array?
90             cutoff = nz_percentile(targets, 80)
91             pd_mask = np.bitwise_or(targets < cutoff, img.mask).filled(1)
92             percent_calculated = (pd_mask.size - pd_mask.sum()) / pd_mask.size
93
94             if verbose:
95                 print(f"finding PD's for {percent_calculated:.2%} of image"
96                      f"anything above vesselness score {cutoff:.6f}")
97             t1, t2 = principal_directions(img, sigma=sigma, H=this_scale['H'],
98                                           mask=pd_mask)
99
100            # add them to this scale's output
101            this_scale['t1'] = t1
102            this_scale['t2'] = t2
103
104        else:
105            if verbose:
106                print('skipping principal direction calculation')
107
108        # store results as a list of dictionaries
109        multiscale.append(this_scale)
110
111    print()
112    return multiscale
113
114
115    def extract_pcsvn(img, filename, scales, beta=0.5, gamma=0.5, c=None,
116

```

```

117     dark_bg=True, dilate_per_scale=True, verbose=True,
118     generate_json=True, output_dir=None, kernel=None,
119     signed_frangi=False, rescale_frangi=False,
120     gradient_filter=False):
121 """Run PCSVN extraction on the sample given in the file.
122
123 Despite the name, this simply returns the Frangi filter responses at
124 each provided scale without explicitly making any decisions about what
125 is or is not part of the PCSVN.
126
127 As a matter of fact, this function currently just is a wrapper for
128 make_multiscale that logs some output
129 The original main use of this function has kind of bled into
130 extract_NCS_pcsvn.py. that needs fixing. You should load the image
131 outside of this function, do post processing there, pass it inside here
132 with a dictionary of things to add to the json file
133
134 """
135
136 # Multiscale Frangi Filter#####
137
138 # output is a dictionary of relevant info at each scale
139 multiscale = make_multiscale(img, scales, beta=beta, gamma=gamma, c=None,
140                             find_principal_directions=False,
141                             dilate_per_scale=dilate_per_scale,
142                             kernel=kernel, signed_frangi=signed_frangi,
143                             dark_bg=dark_bg, verbose=verbose,
144                             rescale_frangi=rescale_frangi,
145                             gradient_filter=gradient_filter)
146
147 # extract these for logging
148 c = [scale['c'] for scale in multiscale]
149 border_radii = [scale['border_radius'] for scale in multiscale]
150
151 # ignore targets too close to edge of plate
152 # wait are we doing this twice?
153 if dilate_per_scale:
154     if verbose:
155         print('trimming collars of plates (per scale)')
156
157     for i in range(len(multiscale)):
158         f = multiscale[i]['F']
159         # twice the buffer (be conservative!)
160         radius = int(multiscale[i]['sigma'] * 2)
161         if verbose:
162             print('dilating plate for radius={}'.format(radius))
163             f = dilate_boundary(f, radius=radius, mask=img.mask)
164             # get rid of mask
165             multiscale[i]['F'] = f.filled(0)
166     else:
167         for i in range(len(multiscale)):
168             # get rid of mask
169             multiscale[i]['F'] = multiscale[i]['F'].filled(0)
170 # Make Composite#####
171
172 # get a M x N x n_scales array of Frangi targets at each level
173 F_all = np.dstack([scale['F'] for scale in multiscale])
174
175 if generate_json:
176
177     time_of_run = datetime.datetime.now()
178     timestamp = time_of_run.strftime("%y%m%d_%H%M")
179
180     # numpy arrays have to be turned into lists first

```

```

181     vectorize = lambda x: x if x is None or np.isscalar(x) else list(x)
182
183     logdata = {'time': timestamp,
184                'filename': filename,
185                'betas': vectorize(beta),
186                'gammas': vectorize(gamma),
187                'c': vectorize(c),
188                'sigmas': list(scales)
189            }
190
191     if dilate_per_scale:
192         logdata['border_radii'] = border_radii
193
194     if output_dir is None:
195         output_dir = 'output'
196
197     base = os.path.basename(filename)
198     *base, suffix = base.split('.')
199     dumpfile = os.path.join(output_dir,
200                            '_'.join(base) + '_' + str(timestamp)
201                            + '.json')
202
203     with open(dumpfile, 'w') as f:
204         json.dump(logdata, f, indent=True)
205
206     return F_all, dumpfile
207
208
209 def get_outname_lambda(filename, output_dir=None, timestamp=None):
210     """
211     return a lambda function which can build output filenames
212     """
213
214     if output_dir is None:
215         output_dir = 'output'
216
217     base = os.path.basename(filename)
218     *base, suffix = base.split('.')
219
220     if timestamp is None:
221         time_of_run = datetime.datetime.now()
222         timestamp = time_of_run.strftime("%y%m%d_%H%M")
223
224     outputstub = '_'.join(base) + '_' + timestamp + '_{}.' + suffix
225     return lambda s: os.path.join(output_dir, outputstub.format(s))
226
227
228 def _build_scale_colormap(N_scales, base_colormap, basecolor=(0,0,0,1)):
229     """
230     returns a mpl.colors.ListedColormap with N samples,
231     based on the colormap named "default_colormap" (a string)
232
233     the N colors are given by the default colormap, and
234     basecolor (default black) is added to map to 0.
235     (you could change this, for example, to (1,1,1,1) for white)
236
237     reversed colormaps often work better if the basecolor is black
238     you should make sure there's good contrast between the basecolor
239     and the first color in the colormap
240     """
241
242     map_range = np.linspace(0, 1, num=N_scales)
243
244     colormap = plt.get_cmap(base_colormap)

```

```

245 colorlist = colormap(map_range)
246
247 # add basecolor as the first entry
248 colorlist = np.vstack((basecolor, colorlist))
249
250 return mpl.colors.ListedColormap(colorlist)
251
252
253
254 def scale_label_figure(whereis, scales, savefilename=None,
255                         crop=None, show_only=False, image_only=False,
256                         base_cmap='viridis_r', save_colorbar_separate=False,
257                         basecolor=(0, 0, 0, 1), savecolorbarfile=None,
258                         output_dir=None):
259     """
260     crop is a slice object.
261     if show_only, then just plt.show (interactive).
262     if image_only, then this will *not* be printed with the colorbar
263
264     if save_colormap_separate, then the colormap will be saved as a separate
265     file
266     """
267     if crop is not None:
268         whereis = whereis[crop]
269
270     fig, ax = plt.subplots() # not sure about figsize
271     N = len(scales) # number of scales / labels
272
273     tabemap = _build_scale_colormap(N, base_cmap, basecolor)
274
275     if image_only:
276         plt.imsave(savefilename, whereis, cmap=tabemap, vmin=0, vmax=N)
277         plt.close()
278     else:
279         imgplot = ax.imshow(whereis, cmap=tabemap, vmin=0, vmax=N)
280         # discrete colorbar
281         cbar = plt.colorbar(imgplot)
282
283         # this is apparently hackish, beats me
284         tick_locs = (np.arange(N+1) + 0.5)*(N-1)/N
285
286         cbar.set_ticks(tick_locs)
287         # label each tick with the sigma value
288         scalelabels = [r" $\sigma$ ={:2f}".format(s) for s in scales]
289         scalelabels.insert(0, "(no match)")
290         # label with their sigma value
291         cbar.set_ticklabels(scalelabels)
292         # ax.set_title(r"Scale ( $\sigma$ ) of maximum vesselness ")
293         plt.tight_layout()
294         # plt.savefig(outname('labeled'), dpi=300)
295         if show_only or (savefilename is None):
296             plt.show()
297         else:
298             plt.savefig(savefilename, dpi=300)
299
300     plt.close()
301
302     if save_colorbar_separate:
303         if savecolorbarfile is None:
304             savecolorbarfile = os.path.join(output_dir, "scale_colorbar.png")
305         fig = plt.figure(figsize=(1, 8))
306         ax1 = fig.add_axes([0.05, 0.05, 0.15, 0.9])
307         tick_locs = (np.arange(N+1) + 0.5)*(N-1)/N
308         scalelabels = [r" $\sigma$ ={:2f}".format(s) for s in scales]

```

```

309     scalelabels.insert(0, "n/a")
310     cbar = mpl.colorbar.ColorbarBase(ax1, cmap=tabemap,
311                                         norm=mpl.colors.Normalize(vmin=0,
312                                                       vmax=N),
313                                         orientation='vertical',
314                                         ticks=tick_locs)
315     cbar.set_ticklabels(scalelabels)
316     plt.savefig(savecolorbarfile, dpi=300)

```

listings/pd_demo_uniscale.py

```

1 #!/usr/bin/env python3
2
3 import numpy as np
4 import numpy.ma as ma
5
6 import matplotlib.pyplot as plt
7 import matplotlib as mpl
8
9 from skimage.io import imread
10 from skimage.util import img_as_float
11
12 from placenta import (get_named_placenta, list_by_quality, cropped_args,
13                         img_as_float)
14
15 from frangi import frangi_from_image
16 from hfft import fft_gradient, fft_hessian, fft_gaussian
17 from merging import nz_percentile
18 from plate_morphology import dilate_boundary
19 import os.path, os
20
21 from diffgeo import principal_curvatures, principal_directions
22
23
24 filename = list_by_quality(N=1)[0]
25 img = get_named_placenta(filename)
26 crop = cropped_args(img)
27
28 sigma = 1.5
29 img = img_as_float(img)
30
31 print('calculating frangi filter')
32
33 f = frangi_from_image(img, sigma=1.5, dark_bg=False, dilation_radius=20,
34                       beta=0.35)
35
36 print('calculating hessian again (oops)')
37 H = fft_hessian(img, sigma=1.5)
38 print('calculating pd where f > .05')
39 v1, v2 = principal_directions(img, 1.5, H=H, mask=(f < 0.05))
40 print('done')
41 vm = ma.masked_array(v2, mask=f<.05)
42
43 # this colormap doesn't have any black in it!
44 cmap = mpl.cm.hsv
45 # so set the mask to black
46
47 cmap.set_bad(color=(0,0,0), alpha=1)
48
49 fig, ax = plt.subplots()
50 cax = ax.imshow(vm[crop], cmap=cmap, vmin=0, vmax=np.pi)
51 ax.axis('off')
52 cbar = fig.colorbar(cax, ticks=[0, np.pi/3, np.pi/2, 2*np.pi/3, np.pi])

```

```

53 cbar.ax.set_yticklabels(['0', r' $\frac{\pi}{3}$ ', r' $\frac{\pi}{2}$ ',  

54                         r' $\frac{2\pi}{3}$ ', r' $\pi$ '])
55
56 ax.set_title(r'leading (local) principal direction,  $\sigma=1.5$ ')
57 fig.tight_layout()
58
59 plt.show() # save manually with the name pd_demo_uniscale.png

```

listings/placenta.py

```

1 #!/usr/bin/env python3
2
3 """
4 Get registered, unpreprocessed placental images. No automatic registration
5 (i.e. segmentation of placental plate) takes place here. The background,
6 however, *is* masked.
7
8 Again, there is no support for unregistered placental pictures.
9 A mask file must be provided.
10
11 There is currently no support for color images.
12 """
13
14 import numpy as np
15 import numpy.ma as ma
16 import os.path
17 import os
18 import json
19 from scipy.ndimage import imread
20 from skimage import morphology
21
22 from numpy.ma import is_masked
23 from skimage.color import gray2rgb
24 from skimage.util import img_as_float
25 import matplotlib.pyplot as plt
26 from hfft import fft_gradient
27 from skimage.segmentation import watershed
28 from skimage.morphology import binary_erosion, disk
29 import scipy.ndimage as ndi
30
31
32 def open_typefile(filename, filetype, sample_dir=None, mode=None):
33     """
34     filetype is either 'mask' or 'trace'
35     mask -> 'L' mode
36     trace -> 'RGB' mode
37     use mode keyword to override this behavior (for example if you
38     want a binary trace)
39
40     typefiles that aren't the above will be treated as 'L'
41     """
42     # try to open what the mask *should* be named
43     # this should be done less hackishly
44     # for example, if filename is 'ncs.1029.jpg' then
45     # this would set the maskfile as 'ncs.1029.mask.jpg'
46
47     #if filetype not in ("mask", "trace"):
48     #    raise NotImplementedError("Can only deal with mask or trace files.")
49
50     # get the base of filename and build the type filename
51     *base, suffix = filename.split('.')
52     base = ''.join(base)

```

```

53     typefile = '.'.join((base, filetype, suffix))
54
55     if sample_dir is None:
56         sample_dir = 'samples'
57
58     typefile = os.path.join(sample_dir, typefile)
59
60     if mode is not None:
61         if filetype == 'mask':
62             mode = 'L'
63         elif filetype in ('ctrace', 'veins', 'arteries'):
64             mode = 'RGB'
65         else:
66             # handle this if you need to?
67             mode = 'L'
68     try:
69         img = imread(typefile, mode=mode)
70
71     except FileNotFoundError:
72         print('Could not find file', typefile)
73         return None
74
75     return img
76
77
78 def open_tracefile(base_filename, as_binary=True,
79                     sample_dir=None):
80     """
81
82     ###width parsing is no longer done here. instead, this function
83     should handle the venous/arterial difference.
84
85     this currently only serves to open the RGB traces as binary
86     files instead of RGB, which is processed later
87
88     #TODO: expand this later to handle arterial traces and venous traces
89     INPUT:
90         base_filename: the name of the base file, not the tracefile itself
91         as_binary: if True
92     """
93
94
95     if as_binary:
96         mode = 'L'
97     else:
98         mode = 'RGB'
99
100    T = open_typefile(base_filename, 'trace', sample_dir=sample_dir, mode=mode)
101
102    if as_binary:
103
104        return np.invert(T != 0)
105
106    else:
107        return T
108
109 def mimg_as_float(mimg):
110
111     if not ma.is_masked(mimg):
112
113         return img_as_float(mimg)
114
115     else:
116         return ma.masked_array(img_as_float(mimg.data),

```

```

117                         mask=mimg.mask)
118
119 def get_named_placenta(filename, sample_dir=None, masked=True,
120                         maskfile=None, mode='L'):
121     """
122     This function is to be replaced by a more ingenious/natural
123     way of accessing a database of unregistered and/or registered
124     placental samples.
125
126     Parameters
127     -----
128
129     filename: name of file (including suffix?) but NOT directory
130     masked: return it masked.
131     maskfile: if supplied, this use the file will use a supplied 1-channel
132                 mask (where 1 represents an invalid/masked pixel, and 0
133                 represents a valid/unmasked pixel. the supplied image must be
134                 the same shape as the image. if not provided, the mask is
135                 calculated (unless masked=False)
136                 the file must be located within the sample directory
137
138     If maskfile is 'None' then this function will look for
139     a default maskname with the following pattern:
140
141         test.jpg -> test.mask.jpg
142         ncs.1029.jpg -> ncs.1029.mask.jpg
143
144     sample_directory: Relative path where sample (and mask file) is located.
145                 defaults to './samples'
146
147     if masked is true (default), this returns a masked array.
148
149     NOTE: A previous logical incongruity has been corrected. Masks should have
150           1 as the invalid/background/mask value (to mask), and 0 as the
151           valid/plate/foreground value (to not mask)
152     """
153     if sample_dir is None:
154         sample_dir = 'samples'
155
156     full_filename = os.path.join(sample_dir, filename)
157
158     if mode.lower() in ('g', 'green'):
159         # first channel of RGBA (or RGB!)
160         raw_img = imread(full_filename)[...,1]
161
162     else:
163         raw_img = imread(full_filename, mode=mode)
164
165     if maskfile is None:
166         # try to open what the mask *should* be named
167         # this should be done less hackishly
168         # for example, if filename is 'ncs.1029.jpg' then
169         # this would set the maskfile as 'ncs.1029.mask.jpg'
170         base, suffix = filename.split('.')
171         test_maskfile = ''.join(base) + '.mask.' + suffix
172         test_maskfile = os.path.join(sample_dir, test_maskfile)
173
174         try:
175             mask = imread(test_maskfile, mode='L')
176         except FileNotFoundError:
177             print('Could not find maskfile', test_maskfile)
178             print('Please supply a maskfile. Autogeneration of mask',
179                  'files is slow and buggy and therefore not supported.')
180             raise
181             #return mask_background(raw_img)

```

```

181     else:
182         # set maskfile name relative to path
183         maskfile = os.path.join(sample_dir, maskfile)
184         mask = imread(maskfile, mode='L')
185
186     if filename.startswith('T-BN'):
187         if filename not in FAILS:
188             print('tightening the mask')
189             raw = open_typefile(filename, 'raw')
190             plate = find_plate_in_raw(raw)
191
192             stuff = ma.masked_array(raw_img, mask=mask)
193             return ma.masked_array(stuff, mask=plate)
194         else:
195             print('leaving this mask as it is')
196     return ma.masked_array(raw_img, mask=mask)
197
198
199 def list_by_quality(quality=0, N=None, json_file=None, return_empty=False):
200     """
201     returns a list of filenames that are of quality 'quality'
202
203     quality is either "good" or 0
204         "OK" or 1
205         "fair" or 2
206         "poor" or 3
207
208     N is the number of placentas to return (will return # of placentas
209     of that quality or N, whichever is smaller)
210
211     if json_name is not None just use that filename directly
212
213     if return_empty then silently failing is OK
214     """
215
216     quality_keys = ('good', 'okay', 'fair', 'poor')
217
218     if quality in quality_keys:
219         pass
220     elif quality in (0, 1, 2, 3):
221         quality = quality_keys[quality]
222     else:
223         try:
224             quality = quality.lower()
225         except AttributeError:
226             if return_empty:
227                 return list()
228             else:
229                 print(f'unknown quality {quality}')
230                 raise
231         else:
232             # if no json file is provided, and quality is a string,
233             # just assume it follows a template format
234             if json_file is None:
235                 json_file = f"{quality}-mccs.json"
236
237     # if it's still not provided in the main file, it's in the main file
238     if json_file is None:
239         json_file = 'sample-qualities.json'
240
241     try:
242         with open(json_file, 'r') as f:
243             D = json.load(f)
244     except FileNotFoundError:

```

```

245     if return_empty:
246         return list()
247     else:
248         print('cannot find', json_file)
249         raise FileNotFoundError
250
251     if json_file == 'sample-qualities.json':
252         # go one level deep
253         placentas = [k for k in D[quality].keys()]
254     else:
255         placentas = [k for k in D.keys()]
256
257     if N is not None:
258         return placentas[:N]
259     else:
260         return placentas
261
262 def check_filetype(filename, assert_png=True, assert_standard=False):
263     """
264     'T-BN8333878.raw.png' returns 'raw'
265     'T-BN8333878.mask.png' returns 'mask'
266     'T-BN8333878.png' returns 'base'
267
268     if assert_png is True, then raise assertion error if the file
269     is not of type png
270
271     if assert_standard, then assert the filetype is
272     mask, base, trace, or raw.
273
274     etc.
275     """
276     basename, ext = os.path.splitext(filename)
277
278     if ext != '.png':
279         if assert_png:
280             assert ext == '.png'
281
282     sample_name, typestub = os.path.splitext(basename)
283
284     if typestub == '':
285         # it's just something like 'T-BN8333878.png'
286         return 'base'
287     elif typestub in ('.mask', '.trace', '.raw', '.ctrace', '.arteries', '.veins', '.ucip'):
288         # return 'mask' or 'trace' or 'raw'
289         return typestub.strip('.')
290     else:
291         print('unknown filetype:', typestub)
292         print('is it a weird filename?')
293
294         print('warning: lookup failed, unknown filetype:' + typestub)
295
296     return typestub
297
298 def list_placentas(label='T-BN', sample_dir=None):
299     """
300     label is the specifier, basically just ''.startswith()
301
302     only real use is to find all the T-BN* files
303
304     this is hackish, if you ever decide to use a file other than
305     png then this needs to change
306     """
307
308

```

```

309     if sample_dir is None:
310         sample_dir = 'samples'
311
312     if label is None:
313         label = '' # str.startswith('') is always True
314
315     placentas = list()
316
317     for f in os.listdir(sample_dir):
318
319         if f.startswith(label):
320             # oh man they gotta be png files
321             if check_filetype(f) == 'base':
322                 placentas.append(f)
323
324     return sorted(placentas)
325
326
327 def show_mask(img, mask=None, interactive=False, mask_color=None):
328     """
329     rename this color_mask since showing the mask is just a secondary feature
330     show a masked grayscale image with a dark blue masked region
331
332     custom version of imshow that shows grayscale images with the right
333     colormap and, if they're masked arrays, sets makes the mask a dark blue) a
334     better function might make the grayscale value dark blue (so there's no
335     confusion)
336
337     if interactive, this operates like "plt.imshow"
338     if interactive==False, return the RGB matrix
339
340     if mask provided, add it to the image. (pass img.data instead if you don't
341     want to use the original mask)
342     """
343
344     if mask_color is None:
345         mask_color = (0, 0, 60)
346
347     # if there's no mask at all
348     if (mask is None) and (not is_masked(img)):
349         if interactive:
350             plt.imshow(img, cmap=plt.cm.gray)
351             return # we're done
352         else:
353             # return as an rgb image so output is uniform
354             return gray2rgb(img)
355
356     elif not is_masked(img):
357         # add mask to the image / add to existing mask
358         # if i just rewrite img will it change outside this function?
359         new_img = ma.masked_array(img, mask=mask)
360     else:
361         new_img = img.copy()
362
363     # otherwise, get an RGB array, black where the mask is
364     mimg = gray2rgb(new_img.filled(0))
365
366     # fill masked regions with the mask color
367     mimg[new_img.mask, :] = mask_color
368
369     if interactive:
370         plt.imshow(mimg)
371     else:
372         return mimg

```

```

373
374 def _cropped_bounds(img, mask=None):
375
376     if mask is not None:
377
378         img = ma.masked_array(img, mask=mask)
379
380     X, Y = (np.argwhere(np.invert(img.mask)).any(axis=k)).squeeze()
381         for k in (0, 1)
382             )
383
384     if X.size == 0:
385         X = [None, None] # these will slice correctly
386     if Y.size == 0:
387         Y = [None, None]
388
389     return Y[0], Y[-1], X[0], X[-1]
390
391
392 def cropped_args(img, mask=None):
393     """
394     get a slice that would crop image
395     i.e. img[cropped_args(img)] would be a cropped view
396     """
397
398
399     x0, x1, y0, y1 = _cropped_bounds(img, mask=None)
400
401     return np.s_[x0:x1, y0:y1]
402
403
404 def cropped_view(img, mask=None):
405     """
406     removes entire masked rows and columns from the borders of a masked array.
407     will return a masked array of smaller size
408
409     don't ask me about data
410
411     the name sucks too
412     """
413
414     # find first and last row with content
415     x0, x1, y0, y1 = _cropped_bounds(img, mask=mask)
416
417     return img[x0:x1, y0:y1]
418
419
420 CYAN = [0, 255, 255]
421 YELLOW = [255, 255, 0]
422
423 def find_plate_in_raw(raw, sigma=.01):
424     g = fft_gradient(raw[...,1], sigma=.01)
425     marks=np.zeros(g.shape, np.int32)
426     marks[0,0] = 1
427     marks[g > g.mean()] = 2
428     #marks[g > np.percentile(g,25)] = 2
429     w = watershed(g,marks)
430
431     eroded = binary_erosion(w==2, disk(15))
432
433     labeled, n_labs = ndi.label(eroded)
434
435     # get largest object (0 is gonna be background)
436     # sort labels by decreasing magnitude

```

```

437     labs_by_size = sorted(list(range(1,n_labs+1)),
438                           key=lambda l: np.sum(labeled==l), reverse=True)
439
440     # unless something went horribly wrong
441     plate_index = labs_by_size[0]
442
443     return ~(labeled == plate_index)
444
445
446 FAILS = [
447     "T-BN0687730.png",
448     "T-BN1629357.png",
449     "T-BN2050224.png",
450     "T-BN6381701.png",
451     "T-BN7476220.png",
452     "T-BN7644170.png",
453     "T-BN7767693.png",
454 ]
455 def measure_ncs_markings(ucip_img=None, filename=None, verbose=False):
456     """
457         find location of ucip and resolution of image based on input
458         (similar to perimeter layer in original NCS data set
459
460     Parameters
461     -----
462
463     ucip_img: an RGB ndarray or None
464             The perimeter layer of an NCS sample (colorations according to the
465             tracing protocol). if None, filename must be included. Default is None.
466     filename:
467             the filename of the SAMPLE (not the ucip image file itself)
468
469     Returns
470     -----
471     m : tuple of ints
472             the coordinates of (the center of) of the umbilical cord point
473             (depicted as a yellow dot) in the original image.
474     resolution: a float
475             measured distance between the two cyan dots
476     """
477
478     if ucip_img is None:
479         ucip_img = open_typefile(filename, 'ucip')
480
481     if ucip_img is None:
482         # if it's still none (no file), return None
483         return None, None
484
485     # just in case it's got an alpha channel, remove it
486     img = ucip_img[:, :, 0:3]
487
488     # given the image img (make sure no alpha channel)
489     # find all cyan pixels (there are two boxes of 3 pixels each and we
490     # just want to extract the middle of each
491     if verbose:
492         print('the image size is {}x{}'.format(img.shape[0], img.shape[1]))
493
494     rulemarks = np.all(img == CYAN, axis=-1)
495
496     # turn into two pixels (these should each be shape (18,))
497     X, Y = np.where(rulemarks)
498
499     assert X.shape == Y.shape
500

```

```

501 # if they followed the protocol correctly...
502 if X.size == 18:
503     # get the two pixels at the center of each box
504     A, B = (X[4], Y[4]), (X[13], Y[13])
505 else:
506     # dots are a nonstandard size for some reason. this works too.
507     thinned = morphology.thin(rulemarks)
508     X, Y = np.where(thinned)
509     assert(thinned.sum() == 2) # there should be just two pixels now.
510     A, B = (X[0], Y[0]), (X[1], Y[1])
511
512 ruler_distance = np.sqrt((A[0] - B[0])**2 + (A[1] - B[1])**2)
513 if verbose:
514     print(f'one cm equals {ruler_distance} pixels')
515
516 # the umbilical cord insertion point (UCIP) is a yellow circle, radius 19
517 ucipmarks = np.all(img == YELLOW, axis=-1)
518 X, Y = np.where(ucipmarks)
519
520 # find midpoint of the x & y coordinates
521 assert X.max() - X.min() == Y.max() - Y.min()
522 radius = (X.max() - X.min()) // 2
523
524 mid = (X.min() + radius, Y.min() + radius)
525
526 if verbose:
527     print('the middle of the UCIP location is', mid)
528     print('the radius outward is', radius)
529     print('the total measurable diameter is', radius*2 + 1)
530
531 return mid, ruler_distance
532
533
534 def add_ucip_to_mask(m, radius=100, mask=None, size_like=None):
535     """
536     - m is a tuple (2x1) representing the (coordinate) midpoint of the UCIP
537     - radius around which to dilate the UCIP is the dilation radius as it
538     works in morphology--this is passed directly to skimage.morphology.disk.
539     thus a circle centered at point m with diameter 2*radius + 1
540     - if no mask is supplied, dilate the point in an array of zeros the shape
541     of 'size_like' (would be the same as passing mask=np.zeros_like(size_like))
542
543     Note: this behaves much faster than binary dilation on the point
544     """
545     if mask is None:
546         if size_like is not None:
547             mask = np.zeros_like(size_like)
548         else:
549             raise ValueError("No mask info supplied!")
550
551     # an empty mask (since we need to merge--we don't want to copy the
552     # zeros of the dilated UCIP -- just the ones!)
553     to_add = np.zeros_like(mask)
554
555     # this is way faster than dilating the point in the matrix,
556     # just set this at the centered point
557
558     # doesn't check for out of bounds stuff. use at your own peril
559     D = morphology.disk(radius)
560     to_add[m[0]-radius:m[0]+radius+1, m[1]-radius:m[1]+radius+1] = D
561
562     # merge with supplied mask
563     return mask | to_add
564

```

```

565
566 if __name__ == "__main__":
567     """test that this works on an easy image."""
568     test_filename = 'barium1.png'
569
570     img = get_named_placenta(test_filename, maskfile=None)
571
572     print('showing the mask of', test_filename)
573     print('run plt.show() to see masked output')
574
575
576     show_mask(img, interactive=True)

```

listings/plate_morphology.py

```

1 #!/usr/bin/env python3
2
3 from skimage.morphology import (disk, binary_erosion, binary_dilation,
4                                 convex_hull_image, thin)
5 from skimage.segmentation import find_boundaries, watershed
6
7 from placenta import open_typefile, get_named_placenta
8
9 import numpy as np
10 import numpy.ma as ma
11
12 def dilate_boundary(img, radius=10, mask=None):
13     """
14     grows the mask by a specified radius of a masked 2D array
15     Manually remove (erode) the outside boundary of a plate.
16     The goal is remove any influence of the zeroed background
17     on reporting derivative information.
18
19     There is varying functionality here (maybe should be multiple functions
20     instead?)
21
22     If img is a masked array and mask=None, the mask will be dilated and a
23     masked array is outputted.
24
25     If img is any 2D array (masked or unmasked), if mask is specified, then
26     the mask will be dilated and the original image will be returned as a
27     masked array with a new mask.
28
29     If the img is None, then the specified mask will be dilated and returned
30     as a regular 2D array.
31
32     """
33
34     if mask is None:
35         # grab the mask from input image
36         # if img is None this will break too but not handled
37         try:
38             mask = img.mask
39         except AttributeError:
40             raise('Need to supply mask information')
41
42     perimeter = find_boundaries(mask, mode='inner')
43
44     maskpad = np.zeros_like(perimeter)
45
46     M,N = maskpad.shape
47     for i,j in np.argwhere(perimeter):

```

```

48     # just make a cross shape on each of those points
49     # these will silently fail if slice is OOB thus ranges are limited.
50     maskpad[max(i-radius,0):min(i+radius,M),j] = 1
51     maskpad[i,max(j-radius,0):min(j+radius,N)] = 1
52
53 new_mask = np.bitwise_or(maskpad, mask)
54
55 if img is None:
56     return new_mask # return a 2D array
57 else:
58     # replace the original mask or create a new masked array
59     return ma.masked_array(img, mask=new_mask)
60
61
62 def l2_dist(p,q):
63     return int(np.round(np.sqrt((p[0]-q[0])**2 + (p[1]-q[1])**2)))
64
65
66 def mask_cuts_simple(img, ucip, mask_only=False, in_place=False,
67                      return_success=False):
68     """
69     this covers up the cut with a disc originating at the perimeter of
70     significant radius
71     """
72
73     cutmarks = np.all(ucip==(0,0,255), axis=-1)
74     B = np.all(ucip==(0,0,255), axis=-1)
75     dilcut = img.copy()
76
77     if not np.any(cutmarks):
78
79         #print("no cutmarks found on image")
80
81         if return_success:
82             return img, False
83         else:
84             return img
85     else:
86         #print("found a cutmark!")
87         pass
88
89     cutmarks = np.nonzero(cutmarks)
90     # get the first pixel of it (we don't need to be too precise here)
91     G = np.all(ucip==(0,255,0), axis=-1) # perimeter elements
92     cutmarks = np.nonzero(thin(B))
93     perimeter = np.nonzero(G)
94
95     cutinds = np.stack(cutmarks).T
96
97     for P in cutinds:
98
99         # consider larger and larger window sizes
100        for W in [100,200,300]:
101            # consider all perimeter elements within these bounds
102
103            rmin, rmax = max(0, P[0]-W), min(img.shape[0], P[0]+W)
104            cmin, cmax = max(0, P[1]-W), min(img.shape[1], P[1]+W)
105            #window = np.s_[rmin:rmax, cmin:cmax]
106
107            # perimeter indices within the window
108            pinds = [(x,y) for x, y in zip(*perimeter)
109                      if x > rmin and x < rmax and y > cmin and y < cmax
110                      ]
111            if pinds:

```

```

112             break #otherwise increase the size of the window
113
114     if pinds:
115
115         # max distance to boundary point in the window
116         # we really only need to keep the largest; deque?
117         dists = sorted([(pp, l2_dist(P, pp)) for pp in pinds],
118                         key=lambda t: t[1])
119         r = 2*int(dists[0][1]) + 1 # get largest radius but closest point
120         P = dists[0][0]
121         B = np.zeros_like(img.mask)
122
123     B[cutmarks] = True
124
125     # center a disk of found radius there
126     D = disk(r)
127     winx = max(P[0]-r,0), min(P[0]+r+1,B.shape[0])
128     winy = max(P[1]-r,0), min(P[1]+r+1,B.shape[1])
129     try:
130         B[winx[0]:winx[1], winy[0]:winy[1]] = D
131     except ValueError:
132         # they're out of bounds so it's a size mismatch. fix it
133         # by starting/ending D index with opposite sign of the initial
134         # p +/- radius that was out of bounds
135         # for example P[0]-r was -9 and everything else was fine
136         # so you just need to set left side to D[9,:,:]
137         # but you should wrap this up in a function so the three times
138         # you do it here and the one time in ucip all gets the same
139         # code
140         print("too close to the boundary or size mismatch?")
141         success = False
142     else:
143         dilcut[B] = ma.masked
144         success = True
145     else:
146         print("we completely failed to mask the cut. too close to the",
147               "boundary to fit an unmodified disk in. fix this")
148         success = False
149
150     return dilcut, success
151
152
153 def mask_cuts_watershed(img, ucip, mask_only=False, in_place=False,
154                         return_success=False):
155     """
156
157     this doesn't handle any image, io. just provide the ucip img and the
158     base (masked) image and we'll fix the mask
159
160     ucip is the actual RGB array, not the file. do io elsewhere.
161
162     if mask_only, this will simply return the new mask as a 2D boolean array.
163     Otherwise, it returns a masked_array.
164     The cut region will be added to the img's mask. If you really want just the
165     difference, you'll have to run
166     >>>(cut_mask & ~img.mask) yourself.
167
168     yourself.
169
170     If in_place, this changes the mask of the image directly (but still returns
171     a masked array. If mask_only is True, in_place will automatically be set to
172     False to prevent hideous side effects
173
174     if return_success, this function returns True if there was a cutmark found,
175     otherwise false as a second output

```

```

176 """
177 # get indices where the blue square indicating center of a cut appears
178 cutmarks = np.all(ucip==(0,0,255), axis=-1)
179
180 if not np.any(cutmarks):
181     #print("no cutmarks found on image")
182
183     if return_success:
184         return img, False
185     else:
186         return img
187
188 else:
189     #print("found a cutmark!")
190     pass
191
192 cutmarks = np.nonzero(cutmarks)
193 # get the first pixel of it (we don't need to be too precise here)
194 X, Y = cutmarks[0][0], cutmarks[1][0]
195
196 # get a value somewhat lower than the value of bg in the cut
197 # (this should be a high number before we take 85%)
198 # sometimes this is in a shadowy region which fucks everything up though
199 #threshold = max(img[cutmarks].mean() * .85, 175)
200 # get the brightest value in a smallish window around the cut * .85
201 threshold = np.max(img[X-10:X+10, Y-10:Y+10])
202
203 rmin, rmax = max(0, X-100), min(img.shape[0], X+100)
204 cmin, cmax = max(0, Y-100), min(img.shape[1], Y+100)
205 cutregion = np.s_[rmin:rmax, cmin:cmax] # get a window around the mark
206
207 # mark inside of the placenta with label 2, original mask and cutmarks with
208 # label 1, and the rest with 0 (i dunno)
209 markers = np.zeros(img.shape, dtype='int32')
210 markers[img.filled(255) < threshold] = 2
211 markers[img.mask] = 1
212 markers[cutmarks] = 1
213
214 # perform watershedding on the thresholded image to fill in the cut with
215 # label 1
216 cutfix = watershed(img.filled(255) < threshold, markers=markers)
217
218 # this is a waste considering the in_place, but eh
219 new_mask = img.mask.copy()
220
221 new_mask[cutregion] = (cutfix[cutregion] == 1)
222
223 if mask_only:
224     out = new_mask
225
226 elif not in_place:
227     out = ma.masked_array(img, mask=new_mask)
228
229 else:
230
231     # will this work?
232     img[new_mask] = ma.masked
233
234     out = img
235
236
237 # now return succeed if asked to
238 if return_success:

```

```

240         return out, True
241
242     else:
243         return out
244
245
246 if __name__ == "__main__":
247
248     # DEMO FOR SHOWING OFF DILATE_BOUNDARY EFFECT
249
250     from placenta import get_named_placenta
251     from frangi import frangi_from_image
252     import matplotlib.pyplot as plt
253
254     import os.path
255
256     dest_dir = 'demo_output'
257     img = get_named_placenta('T-BN0164923.png')
258
259     sigma = 3
260     radius = 25
261
262     inset = np.s_[800:1000, 500:890]
263
264     D = dilate_boundary(img, radius=radius)
265
266     Fimg = frangi_from_image(img, sigma, dark_bg=False, dilation_radius=None)
267     FD = frangi_from_image(D, sigma, dark_bg=False)
268     FDinv = frangi_from_image(D, sigma, dark_bg=True)
269     Finv = frangi_from_image(img, sigma, dark_bg=True, dilation_radius=None)
270
271     fig, axes = plt.subplots(ncols=2, nrows=3)
272
273     axes[0,0].imshow(img[inset].filled(0), cmap=plt.cm.gray)
274     axes[0,1].imshow(D[inset].filled(0), cmap=plt.cm.gray)
275     axes[1,0].imshow(Fimg[inset].filled(0), cmap=plt.cm.nipy_spectral)
276     axes[1,1].imshow(FD[inset].filled(0), cmap=plt.cm.nipy_spectral)
277     axes[2,0].imshow(Finv[inset].filled(0), cmap=plt.cm.nipy_spectral)
278     axes[2,1].imshow(FDinv[inset].filled(0), cmap=plt.cm.nipy_spectral)
279
280     for a in axes.ravel():
281         # get rid of all the labels
282         plt.setp(a.get_xticklabels(), visible=False)
283         plt.setp(a.get_yticklabels(), visible=False)
284
285     # lol matlab
286     for i in range(5):
287         fig.tight_layout()
288
289     plt.savefig(os.path.join(dest_dir, "boundary_dilation_demo.png"), dpi=300)

```

listings/postprocessing.py

```

1#!/usr/bin/env python3
2
3"""
4 doing things to the Frangi targets, i.e. feeding them into other algorithms
5"""
6
7from skimage.filters import sobel
8from skimage.morphology import remove_small_holes, remove_small_objects, thin
9from frangi import frangi_from_image
10from merging import apply_threshold, nz_percentile

```

```

11 from plate_morphology import dilate_boundary
12 from skimage.segmentation import random_walker
13 import numpy as np
14
15 def random_walk_fill(img, Fmax, high_thresh, low_thresh, dark_bg):
16     """
17     # this is deprecated, it's trash
18     """
19
20     s = sobel(img)
21     s = dilate_boundary(s, mask=img.mask, radius=20)
22
23     finv = frangi_from_image(img, sigma=0.8, beta=0.5, dark_bg=(not dark_bg),
24                             dilation_radius=20)
25
26     finv_thresh = (finv > nz_percentile(finv, 50)).filled(0)
27     margins = remove_small_objects(finv_thresh, min_size=32)
28
29     markers = np.zeros(img.shape, dtype=np.int32)
30     markers[Fmax < low_thresh] = 1
31
32     margins_added = (margins | (Fmax > high_thresh))
33     #margins_added = remove_small_holes(margins_added, area_threshold=50)
34
35     markers[Fmax < low_thresh] = 1
36
37     markers[margins_added] = 2
38
39     rw = random_walker(1-Fmax, markers, beta=1000)
40
41     approx_rw = (rw == 2)
42
43     return approx_rw, markers, margins_added
44
45
46 def random_walk_scalewise(F, high_thresh=0.4, rw_beta=130,
47                           return_labels=False):
48     """Random walker on each a multiscale Frangi result"""
49     print('doing scalewise random walk', end=' ')
50     V = np.transpose(F, axes=(2, 0, 1))
51     W = np.zeros(V.shape, np.bool)
52     for n, v in enumerate(V):
53         print('σ', end=' ', flush=True)
54         markers = np.zeros(v.shape, np.int32)
55         markers[v == 0] = 1
56         # this could be a vector too
57         markers[v > high_thresh] = 2
58         # or 1-v
59         W[n] = (random_walker(v, markers, rw_beta) == 2)
60     print()
61     if not return_labels:
62         return W.any(axis=0)
63     else:
64         # argmax grabs the first scale where it was satisfied
65         # so this will grab the lowest scale that matches
66         return W.any(axis=0), W.argmax(axis=0)

```

listings/preprocessing.py

```

1 #!/usr/bin/env python3
2
3 # TODO: refactor this so inpaint_glare is the main function that takes
4 #        a keyword argument strategy='hybrid' or whatever then you can run

```

```

5 #         >>>for s in ['mean_window', 'median_boundary', 'biharmonic', 'hybrid']:
6 #             timeit.timeit('inpaint_glare(img, strategy=s)', globals=globals())
7 #
8 #     ... but it's annoying since you'll need a way to pass args to the
9 #         particular strategy
10
11 from skimage.morphology import (binary_dilation, disk, remove_small_objects,
12                                 convex_hull_object)
13 from skimage.restoration import inpaint_biharmonic
14 import numpy as np
15 import numpy.ma as ma
16 from scipy.ndimage import label
17 from skimage.util import img_as_float
18 from skimage.segmentation import find_boundaries
19 from plate_morphology import dilate_boundary
20
21 import scipy.ndimage as ndi
22 import matplotlib.pyplot as plt
23
24 def inpaint_glare(img, threshold=175, window_size=15, mask=None):
25     """
26     img is a masked array type uint [0,255]
27     """
28
29     # bool array, true where glare
30     if mask is None:
31         glared = mask_glare(img, threshold=threshold, mask_only=True)
32     else:
33         glared = mask
34
35     B = ma.masked_array(img, mask=glared) # masked background *and* glare
36     new_img = img.copy() # copy values of original image (will rewrite)
37     d = int(window_size)
38
39     for j, k in zip(*np.where(glared)):
40         # rewrite all glared pixels with the mean of nonmasked elements
41         # in a window_size window. (this doesn't check OoB, be careful!)
42         new_img[j, k] = B[j-d:j+d, k-d:k+d].compressed().mean()
43
44     return new_img
45
46
47 def inpaint_with_boundary_median(img, threshold=175, mask=None):
48     """
49     mask glare pixels, then replace by the median value on the mask's boundary
50     """
51     if mask is None:
52         glared = mask_glare(img, threshold=threshold, mask_only=True)
53     else:
54         glared = mask
55
56     B = ma.masked_array(img, mask=glared)
57
58     new_img = img.copy() # copy values of original image (will rewrite)
59     bounds = find_boundaries(glared)
60     lb, _ = label(bounds)
61     fill_vals = np.zeros_like(img.data)
62
63     # for each boundary of masked region, find the median value of the img
64     for lab in range(1, lb.max()+1):
65         inds = np.where(lb == lab)
66         fill_vals[inds] = nz_median(B[inds])
67
68     # label masked regions together with their boundaries (they'll be

```

```

69     # connected)
70     lm, _ = label(np.logical_or(glared, lb != 0))
71
72     # fill the masked areas with the corresponding fill value
73     for lab in range(1, lm.max()+1):
74         inds = np.where(lm == lab)
75         # find locations of filled values corresponding to this label
76         # median in case there's overlapped regions? (sloppy)
77         replace_value = nz_median(fill_vals[inds])
78
79         if replace_value == 0:
80             raise
81
82         fill_vals[inds] = replace_value
83
84     # now fill in the values
85     new_img[glared] = fill_vals[glared]
86
87     return new_img
88
89 def nz_median(A):
90
91     if ma.is_masked(A):
92         relevant = A[A > 0].compressed()
93     else:
94         relevant = A[A > 0]
95
96     return np.median(relevant)
97
98
99 def inpaint_hybrid(img, threshold=175, min_size=64, boundary_radius=10):
100    """
101    use biharmonic inpainting in larger, inner areas (important stuff)
102    and median inpainting in smaller areas and along boundary
103    """
104
105    glare = mask_glare(img, threshold=threshold, mask_only=True)
106
107    glare_inside = dilate_boundary(glare, mask=img.mask,
108                                    radius=boundary_radius).filled(0)
109
110    large_glare = remove_small_objects(glare_inside, min_size=min_size,
111                                       connectivity=2)
112    small_glare = np.logical_and(glare, np.invert(large_glare))
113
114    # inpaint smaller and less important values with less expensive method
115    inpainted = inpaint_with_boundary_median(img, mask=small_glare)
116    hybrid = img_as_float(inpainted) # scale 0 to 1
117
118    # inpaint larger regions with biharmonic inpainting
119    large_inpainted = inpaint_biharmonic(img.filled(0), mask=large_glare)
120
121    # now overwrite with these values
122    hybrid[large_glare] = large_inpainted[large_glare]
123
124    # put on old image mask
125    return ma.masked_array(hybrid, mask=img.mask)
126
127 def inpaint_with_biharmonic(img, threshold=175):
128    """
129    use biharmonic inpainting *all* glare
130    """
131    glare = mask_glare(img, threshold=threshold, mask_only=True)
132    inpainted = inpaint_biharmonic(img_as_float(img.filled(0)), mask=glare)

```

```

133
134     if ma.is_masked(img):
135         return ma.masked_array(inpainted, mask=img.mask)
136     else:
137         return inpainted
138
139 def mask_glare(img, threshold=175, mask_only=False):
140     """
141     for demoing purposes, with placenta.show_mask
142
143     if mask_only, just return the mask. Otherwise return a copy of img with
144     that added to the mask. If you want the original mask to be ignored,
145     just pass img.filled(0) ya doofus
146
147     threshold is expected to be of the same dtype as img *unless# it assumes
148     its default value, in which case the threshold will be converted to a float
149
150     """
151     # if img.dtype is floating but threshold value is still the default
152     # this could be generalized
153     if np.issubdtype(img.dtype, np.floating) and (threshold == 175):
154         threshold = 175 / 255
155     # region to inpaint
156     inp = (img > threshold)
157
158     # get a larger area around the specks
159     inp = binary_dilation(inp, selem=disk(2))
160
161     # remove anything large
162     #inp = white_tophat(inp, selem=disk(3))
163
164     if mask_only:
165         return inp
166     else:
167         # both the original background *and* these new glared regions
168         # are masked
169         return ma.masked_array(img, mask=inp)
170
171
172 def mask_stump(img, mask=None, mask_only=True):
173
174     if img.ndim < 3:
175         print('better to pass the raw image')
176         channel = img
177     else:
178         channel = img[...,0]
179
180     C = channel.copy()
181     if mask is not None:
182         C[mask] = 0
183     elif ma.is_masked(img):
184         C[img.mask] = 0
185         mask = img.mask
186     else:
187         mask = np.zeros(img.shape, np.bool)
188
189     thresh = (170/255)*C.max()
190     b = ndi.white_tophat(C > thresh, 90)
191     b = remove_small_objects(b, 1000)
192     b = convex_hull_object(b)
193     b[mask] = 0
194
195     plt.imshow(b)
196     labs, n_labs = ndi.label(b)

```

```

197
198 # sort by size of object (largest first)
199
200 #     incl_count = 0 #objects used
201 #     mags = sorted(list(range(1,n_labs+1)), key=lambda lb: np.sum(labs==lb),
202 #                     reverse=True)
203 #     print(mags)
204 #     for l in mags:
205 #         # big things get weird
206 #         if np.sum(b==l) > 5000:
207 #             print('skipping very large object')
208 #             # get rid of it, whatever
209 #             plt.imshow(b==l)
210 #             b[b==l] = 0
211 #         else:
212 #             incl_count += 1
213 #
214 #     if incl_count > 4:
215 #         print('only removing a few things here')
216 #         b[b==l] = 0
217 #
218 #     print('b after')
219 #     plt.imshow(b)
220 #     b = ndi.binary_dilation(b, disk(15))
221 #
222 if mask_only:
223     return b
224
225 else:
226     # will add to existing mask
227     return ma.masked_array(img, mask=b)
228
229
230
231 DARK_RED = np.array([103, 15, 23]) / 255.
232
233 # test it on a particularly bad sample
234 if __name__ == "__main__":
235
236     from placenta import get_named_placenta, show_mask
237     import matplotlib.pyplot as plt
238
239     filename = 'T-BN0204423.png' # a particularly glary sample
240     img = get_named_placenta(filename)
241
242     img = ma.masked_array(img_as_float(img), mask=img.mask)
243     crop = np.s_[150:500, 150:800] # indices to zoom in on the region
244     zoom = np.s_[300:380, 300:380] # even smaller region
245
246     inset = zoom # which view to use
247
248     masked = mask_glare(img) # for viewing
249     inpainted = inpaint_glare(img)
250     minpainted = inpaint_with_boundary_median(img)
251     hinpainted = inpaint_hybrid(img)
252     binpainted = inpaint_with_biharmonic(img)
253
254     # view the closeup like this
255     minpainted_view = show_mask(minpainted, interactive=False,
256                                 mask_color=DARK_RED)
257     inpainted_view = show_mask(inpainted, interactive=False,
258                                mask_color=DARK_RED)
259     masked_view = show_mask(masked, interactive=False,
260                             mask_color=DARK_RED)

```

```

261 img_view = show_mask(img, interactive=False,
262                     mask_color=DARK_RED)
263 hinpainted_view = show_mask(hinpainted, interactive=False,
264                             mask_color=DARK_RED)
265 binpainted_view = show_mask(binpainted, interactive=False,
266                             mask_color=DARK_RED)
267
268 # view them all next to each other
269
270 fig, axes = plt.subplots(ncols=3, nrows=2)
271
272 axes[0,0].imshow(img_view[inset])
273 axes[0,1].imshow(masked_view[inset])
274 axes[0,2].imshow(inpainted_view[inset])
275 axes[1,0].imshow(minpainted_view[inset])
276 axes[1,1].imshow(binpainted_view[inset])
277 axes[1,2].imshow(hinpainted_view[inset])
278
279 for a in axes.ravel():
280     # get rid of all the labels
281     plt.setp(a.get_xticklabels(), visible=False)
282     plt.setp(a.get_yticklabels(), visible=False)
283
284 # lol matlab
285 for i in range(5):
286     fig.tight_layout()
287
288 IMGS = np.vstack((
289     np.hstack((img_view, masked_view, inpainted_view)),
290     np.hstack((minpainted_view, binpainted_view, hinpainted_view))))
291
292 # THEN IMSAVE
293
294 # plt.imsave('preprocessing_comparison_cropped.png', IMGS)
295 # plt.imsave('preprocessing_comparison_zoomed.png', IMGS)
296
297 # if it's zoomed, then rescale the output in GIMP to 4x

```

listings/process_NCS_xcfs.py

```

1 # -*- coding: utf-8 -*-
2 #!/usr/bin/env python
3
4 """
5 This should be a plugin to take images from the folder NCS_vessel_GIMP_xcf
6 and create trace, mask, and backgrounded images from each xcf file.
7
8 to use:
9 chmod +x and then copy or link to ~/gimp-2.x/plug-ins/
10 """
11
12 from gimpfu import *
13 import os.path
14 from functools import partial
15
16 #basefile, ext = os.path.splitext(xcffile)
17
18 def _outname(base, s=None):
19
20     #base = base.split("_", maxsplit=1)[0]
21     if s is None:
22         stubs = (base, 'png')
23     else:

```

```

24         stubs = (base, s, 'png')
25     file
26     filename = '.'.join(stubs)
27
28     return os.path.join(os.getcwd(), filename)
29
30 # get active image
31 def process_NCS_xcf(timg, tdrawable):
32     img = timg
33     basename, _ = os.path.splitext(img.name) # split off extension .xcf
34     basename = basename.split("_")[0] # only get T-BN-kjlksf part
35     print "*" * 80
36     print '\n\n'
37
38     print "Processing " , img.name
39     # generate output names easier
40     outname = partial(_outname, base=basename)
41
42     # get coordinates of the center
43     cx, cy = img.height // 2 , img.width // 2
44
45     # disable the undo buffer
46     img.disable_undo()
47
48     #perimeter = pdb.gimp_image_get_layer_by_name(img, 'perimeter')
49
50     for layer in img.layers:
51         if layer.name.lower() in ('perimeter', 'perimeters'):
52             # .copy() has optional arg of "add_alpha_channel"
53             mask = layer.copy()
54             break
55     else:
56         print "Could not find a perimeter layer."
57         print "Layers of this image are:"
58         for n,layer in enumerate(img.layers):
59             print "\t", n, ":", layer.name
60         print "Skipping this file."
61
62     return
63
64     for layer in img.layers:
65         layer.visible = False
66
67     mask.name = "mask" # name the new layer
68     img.add_layer(mask,0) # add in position 0 (top)
69
70     pdb.gimp_layer_flatten(mask) # Remove Alpha Channel.
71
72     # save the annotated perimeter file (for calculations later)
73     pdb.gimp_file_save(img,mask, outname(s="ucip"), '')
74
75     # remove unneeded annotations from mask layer
76     # color exchange yellow & blue to black
77     pdb.plug_in_exchange(img,mask,255,255,0,0,0,0,1,1,1)
78     pdb.plug_in_exchange(img,mask,0,0,255,0,0,0,1,1,1)
79
80     # set FG color to black (for tools, not of image)
81     gimp.set_foreground(0,0,0)
82
83     # Bucket Fill Inside black (center pixel is hopefully fine,
84     # do rest manually
85     pdb.gimp_edit_bucket_fill(mask,0,0,100,0,0,cx,cy)
86
87     # Color Exchange Green to White.

```

```

88     pdb.plug_in_exchange(img,mask,0,255,0,255,255,255,1,1,1)
89
90     # Color Exchange Cyan (00ffff) to White.
91     pdb.plug_in_exchange(img,mask,0,255,255,255,255,255,1,1,1)
92
93     # Export Layer as Image called "f".mask.png
94     pdb.gimp_file_save(img,mask, outname(s="mask"), '')
95
96     # invert (so exterior is now black)
97     pdb.gimp_invert(mask)
98     mask.mode = DARKEN_ONLY_MODE # the constant 9
99
100    # set bottom layer (placenta) to visible
101    raw = img.layers[-1]
102    raw.visible = True
103
104    # now make a new layer called 'raw_img' from visible
105    base = pdb.gimp_layer_new_from_visible(img,img,'base')
106    img.add_layer(base,0)
107    pdb.gimp_file_save(img , base, outname(s=None) , '')
108
109    # now get rid of mask and save the raw image
110    mask.visible = False
111    pdb.gimp_file_save(img, base, outname(s='raw') , '')
112
113
114    # now make the other one visible (this is dumb)
115    for layer in img.layers:
116        if layer.name.lower() in ("arteries", "veins"):
117            layer.visible = True
118        else:
119            layer.visible = False
120
121    # now with these two visible, merge them and add layer
122    trace = pdb.gimp_layer_new_from_visible(img,img,'trace')
123    img.add_layer(trace,0)
124
125    pdb.gimp_layer_flatten(trace) # remove alpha channel
126
127    # don't turn binary anymore
128    #pdb.gimp_desaturate(trace) # turn to grayscale
129    #pdb.gimp_threshold(trace,255,255) # anything not 255 turns black
130
131    pdb.gimp_file_save(img, trace, outname(s='ctrace') , '')
132
133    # now extract an each type individually.
134    found = 0
135    for subtype in ("arteries", "veins"):
136        for layer in img.layers:
137            if layer.name.lower() == subtype:
138                layer.visible = True
139                pdb.gimp_layer_flatten(layer) # remove alpha channel
140                pdb.gimp_file_save(img, layer, outname(s=subtype), '')
141                layer.mode = 9 # set to darken only (for merging)
142                found += 1
143            else:
144                layer.visible = False
145
146    if found < 2:
147        print "WARNING! Could not find appropriate artery/vein layers."
148
149
150    print "Saved. "
151 register(

```

```

152 "process_NCS_xcf",
153 "Create base image + trace + mask from an NCS xcf file",
154 "Create base image + trace + mask from an NCS xcf file",
155 "Luke Wukmer",
156 "Luke Wukmer",
157 "2018",
158 "<Image>/Image/Process_NCS_xcf...",
159 "RGB*, GRAY*",
160 [],
161 [],
162 process_NCS_xcf)
163
164 main()

```

listings/scaleddecay.py

```

1 # coding: utf-8
2 from placenta import get_named_placenta, list_by_quality
3 list_by_quality(0)
4 filename = _[-2]
5 img = get_named_placenta(filename)
6 import matplotlib.pyplot as plt
7 import numpy as np
8 plt.imshow(img)
9 plt.show()
10 plt.show()
11 filename = list_by_quality(0)[0]
12 img = get_named_placenta(filename)
13 from placenta import cropped_args
14 crop = cropped_args(img)
15 img[crop]
16 plt.imshow(img[crop])
17 plt.show()
18 from hfft import fft_gaussian
19 get_ipython().run_line_magic('pinfo', 'fft_gaussian')
20 C = fft_gaussian(img, 32, 'discrete')
21 B = fft_gaussian(img, 5, 'discrete')
22 A = fft_gaussian(img, .12, 'discrete')
23 plt.imshow(A)
24 plt.show()
25 A = fft_gaussian(img, .25, 'discrete')
26 plt.imshow(A)
27 plt.show()
28 plt.imshow(B)
29 plt.show()
30 plt.imshow(C)
31 plt.show()
32 gA = np.gradient(A)
33 gA
34 gB = np.gradient(B)
35 gC = np.gradient(C)
36 gA.shape
37 gA[0].shape
38 aa = lambda g: np.sqrt((1+g[0]*g[0] + g[1]*g[1]))
39 plt.imshow(aa(gA))
40 plt.show()
41 from plate_morphology import dilate_boundary
42 from functools import partial
43 dilate = partial(dilate_boundary, mask=img.mask)
44 dilate(aa(gA), 20)
45 plt.imshow(_)
46 plt.show()
47 dilate(aa(gA), 20).filled(0)

```

```

48 plt.show()
49 plt.imshow(_)
50 plt.show()
51 Aaa = dilate(aa(gA), 20).filled(0)
52 Aaa.max()
53 Aaa.min()
54 Aaa[~img.mask].min()
55 Aaa[img.mask].min()
56 Aaa[img.mask].max()
57 Aaa[~img.mask].max()
58 Baa = dilate(aa(gB), 20).filled(0)
59 Caa = dilate(aa(gC), 20).filled(0)
60 plt.imshow(Baa)
61 plt.show()
62 plt.imshow(Caa)
63 plt.show()
64 Caa.min()
65 Caa[~img.mask].min()
66 Caa == 0
67 plt.imshow(_)
68 plt.show()
69 Caa[~img.mask].max()
70 Caa[~img.mask].min()
71 Caa[~img.mask].argmin()
72 dilate_boundary(img.mask, 20)
73 dilate_boundary(img.mask, 20, mask_only=True)
74 get_ipython().run_line_magic('pinfo', 'dilate_boundary')
75 dilate_boundary(img, radius=20)
76 dil = _.mask.copy()
77 dil
78 plt.imshow(dil)
79 plt.show()
80 Caa[~dil].argmin()
81 Caa[~dil]
82 Caa[~dil].min()
83 Caa[~dil].max()
84 Baa[~dil].max()
85 Baa[~dil].min()
86 Aaa[~dil].min()
87 Aaa[~dil].max()
88 plt.imshow(Caa)
89 plt.show()
90 plt.imshow(Aaa)
91 plt.show()
92 #for sigma in np.logspace(-3, 8, base=2, num=20):
93 #    D = fft_gaussian(img, sigma, 'discrete')
94 #    gD = np.gradient(D)
95 #    Daa = dilate(aa(dG), 20).filled(1)
96 #    print(Daa[~dil].min(), Daa[~dil].max())
97 aas = list()
98 for sigma in np.logspace(-3, 8, base=2, num=20):
99    D = fft_gaussian(img, sigma, 'discrete')
100   gD = np.gradient(D)
101   Daa = dilate(aa(dG), 20).filled(1)
102   aas.append(Daa)
103   print(f"sigma={sigma:.3f}", "min: {:.6f}, max:{:.6f}".format(
104     Daa[~dil].min(), Daa[~dil].max()))
105
106
107 for sigma in np.logspace(-3, 8, base=2, num=20):
108    D = fft_gaussian(img, sigma, 'discrete')
109    gD = np.gradient(D)
110    Daa = dilate(aa(gD), 20).filled(1)
111    aas.append(Daa)

```

```

112 print(f"sigma={sigma:.3f}", "min: {:.6f}, max:{:.6f}" .format(
113     Daa[~dil].min(), Daa[~dil].max())
114 )
115
116 for sigma in np.logspace(-4, 8, base=2, num=50):
117     D = fft_gaussian(img, sigma, 'discrete')
118     gD = np.gradient(D)
119     Daa = dilate(aa(gD), 20).filled(1)
120     aas.append(Daa)
121     print(f"sigma={sigma:.3f}", "min: {:.6f}, max:{:.6f}" .format(
122         Daa[~dil].min(), Daa[~dil].max())
123     )
124
125 bb = lambda g: np.linalg.norm(np.array([
126     [[1+g[1]**2, -g[0]*g[1]],
127      [-g[0]*g[1], 1 + g[0]**2]]))
128 bb = lambda g: np.linalg.norm(np.array([
129     [[1+g[1]**2, -g[0]*g[1]],
130      [-g[0]*g[1], 1 + g[0]**2]]))
131 bb(gA)
132 get_ipython().set_next_input('man np.linalg.norm');get_ipython().run_line_magic('pinfo', 'bb')
133 ginv = lambda g: np.array([
134     [[1+g[1]**2, -g[0]*g[1]],
135      [-g[0]*g[1], 1 + g[0]**2]])
136 ginv(gA)
137 _.shape
138 G[:, :, 34, 289]
139 ginvA = _101
140 ginvA[:, :, 340, 289]
141 bb = lambda g: np.sqrt((1+g[1]**2)**2 + 2*(g[0]*g[1])**2 + (1+g[0]**2)**2)
142 bb(gA)
143 _.shape
144 plt.imshow(bb)
145 _.shape
146 bb(gA)
147 plt.imshow(_)
148 plt.show()
149 bb(gA) / aa(gA)
150 plt.imshow(_)
151 plt.show()
152 dilate(bb(gA) / aa(gA))
153 plt.imshow(dilate(bb(gA) / aa(gA)).filled(0))
154 plt.show()
155 bb = lambda g: np.sqrt((1+g[1]**2)**2 + 2*(g[0]*g[1])**2 + (1+g[0]**2)**2)
156 plt.imshow(dilate(bb(gA), 20))
157 plt.show()
158 bb(gA)[~dil].min()
159 bb(gA)[~dil].max()
160 (bb(gA) / aa(gA))[~dil].min()
161 (bb(gA) / aa(gA))[~dil].max()
162 (bb(gA) / aa(gA))
163 plt.imshow(dilate(_, 20).filled(1.414))
164 plt.show()
165 for sigma in np.logspace(-4, 8, base=2, num=50):
166     D = fft_gaussian(img, sigma, 'discrete')
167     gD = np.gradient(D)
168     Daa, Dbb = aa(gD), bb(gD)
169     Dcc = Daa / Dbb
170     aas = Daa[~dil].min(), Daa[~dil].max()
171     bbs = Dbb[~dil].min(), Dbb[~dil].max()
172     ccs = Dcc[~dil].min(), Dcc[~dil].max()
173     print(f"sigma={sigma:.3f}",
174           "\tmin: {:.6f},\tmax:{:.6f}" .format(aas),
175           "\tmin: {:.6f},\tmax:{:.6f}" .format(bbs),

```

```

176     "\tmin: {:.6f},\tmax:{:.6f}" .format(ccs), sep='\n')
177
178 for sigma in np.logspace(-4, 8, base=2, num=50):
179     D = fft_gaussian(img, sigma, 'discrete')
180     gD = np.gradient(D)
181     Daa, Dbb = aa(gD), bb(gD)
182     Dcc = Daa / Dbb
183     aas = Daa[~dil].min(), Daa[~dil].max()
184     bbs = Dbb[~dil].min(), Dbb[~dil].max()
185     ccs = Dcc[~dil].min(), Dcc[~dil].max()
186     print(f"sigma={sigma:.3f}",
187           "\tmin: {:.6f},\tmax:{:.6f}" .format(*aas),
188           "\tmin: {:.6f},\tmax:{:.6f}" .format(*bbs),
189           "\tmin: {:.6f},\tmax:{:.6f}" .format(*ccs), sep='\n')
190
191
192
193 for sigma in np.logspace(-4, 8, base=2, num=50):
194     D = fft_gaussian(img, sigma, 'discrete')
195     gD = np.gradient(D)
196     Daa, Dbb = aa(gD), bb(gD)
197     Dcc = Dbb / Daa
198     aas = Daa[~dil].min(), Daa[~dil].max()
199     bbs = Dbb[~dil].min(), Dbb[~dil].max()
200     ccs = Dcc[~dil].min(), Dcc[~dil].max()
201     print(f"sigma={sigma:.3f}",
202           "\tmin: {:.6f},\tmax:{:.6f}" .format(*aas),
203           "\tmin: {:.6f},\tmax:{:.6f}" .format(*bbs),
204           "\tmin: {:.6f},\tmax:{:.6f}" .format(*ccs), sep='\n')
205
206 data = []
207 data = list()
208 for sigma in np.logspace(-4, 8, base=2, num=50):
209     D = fft_gaussian(img, sigma, 'discrete')
210     gD = np.gradient(D)
211     Daa, Dbb = aa(gD), bb(gD)
212     Dcc = Dbb / Daa
213     aas = Daa[~dil].min(), Daa[~dil].max()
214     bbs = Dbb[~dil].min(), Dbb[~dil].max()
215     ccs = Dcc[~dil].min(), Dcc[~dil].max()
216     print(f"sigma={sigma:.3f}",
217           "\tmin: {:.6f},\tmax:{:.6f}" .format(*aas),
218           "\tmin: {:.6f},\tmax:{:.6f}" .format(*bbs),
219           "\tmin: {:.6f},\tmax:{:.6f}" .format(*ccs), sep='\n')
220     data.append(
221         [sigma, *aas, *bbs, *ccs])
222
223 import pandas
224 table = pandas.DataFrame(data)
225 print(table)
226 from hfft import fft_hessian
227 get_ipython().run_line_magic('pinfo', 'fft_hessian')
228 helems = fft_hessian(img, sigma=1, kernel='discrete')
229 np.sqrt(helems[0]**2 + 2*helems[1]**2 + helems[2]**2)
230 _ .shape
231 plt.imshow(np.sqrt(helems[0]**2 + 2*helems[1]**2 + helems[2]**2))
232 plt.show()
233 data = list()
234 for sigma in np.logspace(-4, 8, base=2, num=50):
235     D = fft_gaussian(img, sigma, 'discrete')
236     gD = np.gradient(D)
237     Daa, Dbb = aa(gD), bb(gD)
238     Dcc = Dbb / Daa

```

```

240 h = fft_hessian(img, sigma, 'discrete')
241 hnorm = np.sqrt(h[0]**2 + 2*h[1]**2 + h[2]**2)
242 Lnorm = hnorm*Dcc
243 aas = Daa[~dil].min(), Daa[~dil].max()
244 bbs = Dbb[~dil].min(), Dbb[~dil].max()
245 ccs = Dcc[~dil].min(), Dcc[~dil].max()
246 dds = hnorm[~dil].min(), hnorm[~dil].max()
247 lls = Lnorm[~dil].min(), Lnorm[~dil].max()
248 print(f"sigma={sigma:.3f}",
249      "\tmin: {:.6f},\tmax:{:.6f}" .format(*aas),
250      "\tmin: {:.6f},\tmax:{:.6f}" .format(*bbs),
251      "\tmin: {:.6f},\tmax:{:.6f}" .format(*ccs),
252      "\tmin: {:.6f},\tmax:{:.6f}" .format(*dds),
253      "\tmin: {:.6f},\tmax:{:.6f}" .format(*lls), sep='\n')
254 data.append(
255     [sigma, *aas, *bbs, *ccs, *dds, *lls])
256
257
258 data
259 table = pandas.DataFrame(data)
260 table
261 table.columns
262 help(table.columns)
263 plt.imshow(Lnorm)
264 plt.show()
265 Ls = list()
266 for sigma in np.logspace(-4, 8, base=2, num=50):
267     D = fft_gaussian(img, sigma, 'discrete')
268     gD = np.gradient(D)
269     Daa, Dbb = aa(gD), bb(gD)
270     Dcc = Dbb / Daa
271     h = fft_hessian(img, sigma, 'discrete')
272     hnorm = np.sqrt(h[0]**2 + 2*h[1]**2 + h[2]**2)
273     Lnorm = hnorm*Dcc
274     Ls.append(Lnorm)
275     aas = Daa[~dil].min(), Daa[~dil].max()
276     bbs = Dbb[~dil].min(), Dbb[~dil].max()
277     ccs = Dcc[~dil].min(), Dcc[~dil].max()
278     dds = hnorm[~dil].min(), hnorm[~dil].max()
279     lls = Lnorm[~dil].min(), Lnorm[~dil].max()
280     print(f"sigma={sigma:.3f}",
281           "\tmin: {:.6f},\tmax:{:.6f}" .format(*aas),
282           "\tmin: {:.6f},\tmax:{:.6f}" .format(*bbs),
283           "\tmin: {:.6f},\tmax:{:.6f}" .format(*ccs),
284           "\tmin: {:.6f},\tmax:{:.6f}" .format(*dds),
285           "\tmin: {:.6f},\tmax:{:.6f}" .format(*lls), sep='\n')
286 #data.append(
287 #    [sigma, *aas, *bbs, *ccs, *dds, *lls])
288
289 L[0]
290 Ls[0]
291 plt.imshow(_)
292 plt.show()
293 for Lnorm, sigma in zip(Ls, np.logspace(-4,8, base=2, num=50)):
294     plt.imshow(Lnorm[crop], cmap='nipy_spectral')
295     mng = plt.get_current_fig_manager()
296     mng.window.showMaximized()
297     plt.colorbar()
298     plt.title(r'Lnorm σ =:3f' .format(sigma))
299     plt.axis('off')
300     plt.tight_layout()
301     plt.show()
302     plt.close('all')
303

```

```

304 for Lnorm, sigma in zip(Ls, np.logspace(-4,8, base=2, num=50)):
305     L = dilate(Lnorm, min(20,int(sigma))).filled(0)
306     plt.imshow(Lnorm[crop], cmap='nipy_spectral')
307     mng = plt.get_current_fig_manager()
308     mng.window.showMaximized()
309     plt.colorbar()
310     plt.title(r'Lnorm  $\sigma = :.3f$ '.format(sigma))
311     plt.axis('off')
312     plt.tight_layout()
313     plt.show()
314     plt.close('all')
315
316 for Lnorm, sigma in zip(Ls, np.logspace(-4,8, base=2, num=50)):
317     L = dilate(Lnorm, min(20,int(sigma))).filled(0)
318     plt.imshow(L[crop], cmap='nipy_spectral')
319     mng = plt.get_current_fig_manager()
320     mng.window.showMaximized()
321     plt.colorbar()
322     plt.title(r'Lnorm  $\sigma = :.3f$ '.format(sigma))
323     plt.axis('off')
324     plt.tight_layout()
325     plt.show()
326     plt.close('all')
327
328 for Lnorm, sigma in zip(Ls, np.logspace(-4,8, base=2, num=50)):
329     L = dilate(Lnorm, max(20,int(sigma))).filled(0)
330     plt.imshow(L[crop], cmap='nipy_spectral')
331     mng = plt.get_current_fig_manager()
332     mng.window.showMaximized()
333     plt.colorbar()
334     plt.title(r'Lnorm  $\sigma = :.3f$ '.format(sigma))
335     plt.axis('off')
336     plt.tight_layout()
337     plt.show()
338     plt.close('all')
339
340 for Lnorm, sigma in zip(Ls, np.logspace(-4,8, base=2, num=50)):
341     L = dilate(Lnorm, max(20,int(sigma))).filled(0)
342     plt.imshow(L[crop], cmap='nipy_spectral')
343     mng = plt.get_current_fig_manager()
344     mng.window.showMaximized()
345     plt.colorbar()
346     plt.title(r'Lnorm  $\sigma = :.3f$ '.format(sigma))
347     plt.axis('off')
348     plt.tight_layout()
349     plt.show()
350     plt.close('all')
351
352 for Lnorm, sigma in zip(Ls, np.logspace(-4,8, base=2, num=50)):
353     L = dilate(Lnorm, max(20,int(2*sigma))).filled(0)
354     plt.imshow(L[crop], cmap='nipy_spectral')
355     mng = plt.get_current_fig_manager()
356     mng.window.showMaximized()
357     plt.colorbar()
358     plt.title(r'Lnorm  $\sigma = :.3f$ '.format(sigma))
359     plt.axis('off')
360     plt.tight_layout()
361     plt.show()
362     plt.close('all')
363
364 print(table)
365 table
366 table + 2
367 table[:,0]

```

```

368 table[0]
369 table / table[0]
370 T = np.array(table)
371 T
372 T.shape
373 T.dtype
374 T / T[:,0]
375 T / T[:,0]
376 T[:, -1] / T[:,0]
377 T[:, -1] / np.sqrt(T[:,0])
378 T[:, -1] * np.sqrt(T[:,0])
379 T[:, -1] * T[:,0]
380 T[:, -1] * T[:,0]**2
381 table
382 T[:, -3] * T[:,0]**2
383 T[:, -3] * T[:,0]
384 T[:, -4] * T[:,0]
385 T[:, -4] / T[:,0]
386 T[:, -4] / T[:,0] > .01
387 which =_
388 T[:,0][which]
389 (T[:, -4] / T[:,0]) > .001
390 scales
391 scales = np.logspace(-4,8,num=50,base=2)
392 scales
393 (T[:, -3] / T[:,0]) > .001
394 (T[:, -3] / T[:,0]) > .005
395 scales[_]
396 (T[:, -3] / T[:,0]) > .001
397 scales
398 scales
399 (T[:, -3] / T[:,0]) > .001
400 scales[_]
401 (T[:, -3] / T[:,0]) > .05
402 T[:, -3]
403 (T[:, -3] / T[:,0])
404 (T[:, -3] / T[:,0]**2)
405 (T[:, -3] * np.sqrt(1/T[:,0]))
406 (T[:, -4] / T[:,0]) > .05
407 table
408 from frangi import frangi_from_image
409 g[0]g[1]
410 g[0]*g[1]
411 gA[0]*gA[1]
412 plt.imshow(_)
413 plt.show()

```

listings/scale_sweep_demo.py

```

1 #!/usr/bin/env python3
2
3 from placenta import (get_named_placenta, list_placentas, _cropped_bounds,
4                        cropped_view, cropped_args, show_mask)
5 from frangi import frangi_from_image
6
7 import numpy as np
8 import numpy.ma as ma
9
10 from plate_morphology import dilate_boundary
11
12 import os.path
13 import matplotlib.pyplot as plt
14 import matplotlib as mpl

```

```

15 from itertools import product
16
17 # pick two samples and two insets (should be the same size)
18 demo1 = 'BN2315363', np.s_[370:670, 530:930]
19 demo2 = 'BN5280796', np.s_[150:450, 530:930]
20
21 make_individual = False
22
23 for sample_name, inset_slice in (demo1, demo2):
24     img = get_named_placenta(f'T-{sample_name}.png')
25
26     crop = cropped_args(img)
27
28     F, fi = list(), list() # make some empty lists to store for inspection
29
30     scales = [0.2, 0.8, 1.0, 2.0, 4.0, 6.0, 8.0, 16.0]
31     CMAP = plt.cm.nipy_spectral
32     cmin, cmax = (0, 0.4)
33
34     for n, sigma in enumerate(scales):
35         R = max(int(sigma**3), 10) # only really necessary for signed
36         target = frangi_from_image(img, sigma, dark_bg=False,
37                                     signed_frangi=False, dilation_radius=R)
38         plate = target[crop].filled(0)
39         inset = target[inset_slice].filled(0)
40         F.append(plate)
41         fi.append(inset)
42
43     if not make_individual:
44         continue
45
46     # else this might be nice for the actual thesis defense
47     for label in ['plate', 'inset']:
48         if label == 'inset':
49             printable = inset
50         else:
51             printable = plate
52
53         plt.imshow(printable, cmap=CMAP)
54         plt.title(r'$\sigma$={:.2f}'.format(sigma))
55         plt.tight_layout()
56         c = plt.colorbar()
57         c.set_ticks = np.linspace(cmin, cmax, num=len(scales)+1)
58         plt.clim(cmin, cmax)
59         plt.axis('off')
60         outname = f'demo_output/scale_sweep_{sample_name}_{label}_{n}.png'
61         plt.savefig(outname, dpi=300, bbox_inches='tight')
62         print('saved', outname)
63         plt.close()
64
65     # now make a stitched together version
66     for label in ['plate', 'inset']:
67         if label == 'inset':
68             L = fi
69             imgview = img[inset_slice].filled(0)
70             figsize = (12, 6)
71
72         else:
73             L = F
74             imgview = img[crop].filled(0)
75             figsize = (12, 9)
76
77         # adjust this manually depending on how many scales you end up using!
78         nrows, ncols = 2, 4
79         fig, axes = plt.subplots(nrows=nrows, ncols=ncols, figsize=figsize)

```

```

79
80     for n, (i, j) in enumerate(product(range(nrows), range(ncols))):
81
82         if n == 0:
83             axes[i,j].imshow(imgview, cmap=plt.cm.gray)
84             axes[i,j].set_title('raw')
85         else:
86             im = axes[i,j].imshow(L[n], cmap=CMAP, vmin=cmin, vmax=cmax)
87             axes[i,j].set_title(r'$\sigma = :.2f$'.format(scales[n]))
88
89             plt.setp(axes[i,j].get_xticklabels(), visible=False)
90             plt.setp(axes[i,j].get_yticklabels(), visible=False)
91
92         fig.subplots_adjust(top=0.954, bottom=0.025, left=0.010,
93                             right=0.989, hspace=0.0, wspace=0.0)
94
95         plt.savefig(f'demo_output/scalesweep_stitch_{sample_name}_{label}.png',
96                     dpi=300)
97
98         cfile = 'demo_output/scalesweep_colorbar.png'
99         if os.path.isfile(cfile):
100             continue # no need to make another
101
102         fig = plt.figure(figsize=(figsize[0],2))
103         ax1 = fig.add_axes([0.15, 0.25, 0.75, 0.5])
104         cbar = mpl.colorbar.ColorbarBase(ax1, cmap=CMAP,
105                                         norm=matplotlib.colors.Normalize(cmin,cmax),
106                                         orientation='horizontal')
107         plt.savefig(cfile) # don't set dpi maybe it won't be so small and weird

```

listings/scoring.py

```

1 #!/usr/bin/env python3
2
3 import numpy as np
4 from placenta import open_typefile, open_tracefile
5 from skimage.morphology import thin
6
7 import matplotlib as mpl
8 import matplotlib.pyplot as plt
9
10 import itertools
11 from collections import deque
12
13 def rgb_to_widths(T):
14     """
15         this will take an RGB trace image (MxNx3) and return a 2D (MxN)
16         "labeled" trace corresponding to the traced pixel length.
17         there is no distinguishing between arteries and vessels
18
19         it's preferable to do this in real-time so only one tracefile
20         needs to be stored (making the sample folder less cluttered)
21         although obviously at the expense of storing a larger image
22         which is only needed for visualization purposes.
23
24     Input:
25         T: a MxNx3 RGB (uint8) array, where the colorations are
26         assumed as described in NOTES below.
27
28     Output:
29         widthtrace: a MxN array whose inputs describe the width of the
30         vessel (in pixels), see NOTES.

```

```

31
32 Notes:
33
34     The correspondence is as follows:
35     3 pixels: "#ff006f", # magenta
36     5 pixels: "#a80000", # dark red
37     7 pixels: "#a800ff", # purple
38     9 pixels: "#ff00ff", # light pink
39     11 pixels: "#008aff", # blue
40     13 pixels: "#8aff00", # green
41     15 pixels: "#ffc800", # dark yellow
42     17 pixels: "#ff8a00", # orange
43     19 pixels: "#ff0015" # bright red
44
45 According to the original tracing protocol, the traced vessels are
46 binned into these 9 sizes. Vessels with a diameter smaller than 3px
47 are not traced (unless they're binned into 3px).
48
49 Note: this does *not* deal with collisions. If you pass anything
50 with addition (blended colors) as the ctraces are, you will have
51 trouble, as those will not be registered as any of the colors above
52 and will thus be ignored. If you want to handle data from both
53 arterial *and* venous layers, you should do so outside of this
54 function.
55 """
56
57 # a 2D picture to fix in with the pixel widths
58 W = np.zeros_like(T[:, :, 0])
59
60 for pix, color in TRACE_COLORS.items():
61
62     #ignore pixelwidths outside the specified range
63     # get the 2D indices that are that color
64     idx = np.where(np.all(T == color, axis=-1))
65     W[idx] = pix
66
67
68 return W
69
70 def merge_widths_from_traces(A_trace, V_trace, strategy='minimum'):
71 """
72 combine the widths from two RGB-traces A_trace and V_trace
73 and return one width matrix according to 'strategy'
74
75 Parameters
76 -----
77 A_trace: ndarray
78     an MxNx3 matrix, where each pixel (along the
79     last dimension) is an RGB triplet (i.e. each entry
80     is an integer between [0,256]). The colors each
81     correspond to those in TRACE_COLORS, and (255,255,255)
82     signifies "no vessel". This will normally correspond to
83     the sample's arterial trace.
84 V_trace: ndarray
85     an MxNx3 matrix the same shape and other
86     requirements as A_trace (see above). This will normally
87     correspond to the sample's venous trace.
88 strategy: keyword string
89     when A_trace and V_trace coincide at some entry,
90     this is the merging strategy. It should be a keyword
91     of one of the following choices:
92
93     "minimum": take the minimum width of the two traces
94     (default). this is the sensible option if you

```

```

95     are filtering out larger widths.
96     "maximum": take the maximum width of the two traces
97     "artery" or "A" or "top": take the width from A_trace
98     "vein" or "V" or "bottom": take the width from V_trace
99
100    Returns
101    -----
102        W : ndarray
103        a width-matrix where each entry is a number 0 (no vessel), 3,5,7,...19
104
105    Notes
106    -----
107    Since arteries grow over the veins on the PCSVN and are generally easier
108    to extract, it might be preferable to indicate "arteries". In reality,
109    each strategy is a compromise, and only by keeping track of both would
110    you get the complete picture.
111
112    No filtering out widths is done here.
113    """
114    assert A_trace.shape == V_trace.shape
115
116    A = rgb_to_widths(A_trace)
117    V = rgb_to_widths(V_trace)
118
119    # collisions (where are widths both reported)
120    c = (A!=0)& (V!=0)
121
122    W = np.maximum(A,V) # get the nonzero value
123    if strategy == 'maximum':
124        pass # already done, else rewrite the collisions
125    elif strategy in ('arteries', 'A', 'top'):
126        W[c] = A[c]
127    elif strategy in ('veins', 'V', 'bottom'):
128        W[c] = V[c]
129    else:
130        if strategy != 'minimum':
131            print(f"Warning: unknown merge strategy: {strategy}")
132            print("Defaulting to minimum strategy")
133
134    W[c] = np.minimum(A[c], V[c])
135
136    return W
137
138 def filter_widths(W, widths=None, min_width=3, max_width=19):
139     """
140     Filter a width matrix, removing widths according to rules.
141
142     This function will take a 2D matrix of vessel widths and
143     remove any widths outside a particular range (or alternatively,
144     that are not included in a particular list)
145
146     Should be roughly as easy as doing it by hand, except that you
147     won't have to rewrite the code each time.
148
149     Inputs:
150
151     W: a width matrix (2D matrix with elements 0,3,5,7,...19
152
153     min_width: widths below this will be excluded (default is
154         3, the min recorded width). assuming these
155         are ints
156
157     max_width: widths above this will be excluded (default is
158         19, the max recorded width)

```

```

159
160     widths: an explicit list of widths that should be returned.
161         in this case the above min & max are ignored.
162         this way you could include widths = [3, 17, 19] only
163         """
164
165     Wout = W.copy()
166     if widths is None:
167         Wout[W < min_width] = 0
168         Wout[W > max_width] = 0
169
170     else:
171         # use numpy.isin(T, widths) but that's only in version 1.13 and up
172         # of numpy this is basically the code for that though
173         to_keep = np.in1d(W, widths, assume_unique=True).reshape(W.shape)
174         Wout[~to_keep] = 0
175
176     return Wout
177
178 TRACE_COLORS = {
179     3: (255, 0, 111),
180     5: (168, 0, 0),
181     7: (168, 0, 255),
182     9: (255, 0, 255),
183     11: (0, 138, 255),
184     13: (138, 255, 0),
185     15: (255, 200, 0),
186     17: (255, 138, 0),
187     19: (255, 0, 21)
188 }
189
190
191 def widths_to_rgb(w, show_non_matches=False):
192     """Convert width matrix back to RGB values.
193
194     For display purposes/convenience. Return an RGB matrix
195     converting back from [3,5,7, ... , 19] -> TRACE_COLORS
196
197     this doesn't do any rounding (i.e. it ignores anything outside of
198     the default widths), but maybe you'd want to?
199     """
200
201     B = np.zeros((w.shape[0], w.shape[1], 3))
202
203     for px, rgb_triplet in TRACE_COLORS.items():
204         B[w == px, :] = rgb_triplet
205
206     if show_non_matches:
207         # everything in w not found in TRACE_COLORS will be black
208         B[w == 0, :] = (255, 255, 255)
209     else:
210         non_filled = (B == 0).all(axis=-1)
211
212         B[non_filled, :] = (255, 255, 255) # make everything white
213
214     # matplotlib likes the colors as [0,1], so....
215     return B / 255.
216
217 def _hex_to_rgb(hexstring):
218     """
219     there's a function that does this in matplotlib.colors
220     but its scaled between 0 and 1 but not even as an
221     array so this is just as much work
222

```

```

223 ##TODO rewrite everything so this is useful if it's not been
224 rewritten already.
225 """
226     triple = hexstring.strip("#")
227     return tuple(int(x, 16) for x in (triple[:2], triple[2:4], triple[4:]))
228
229
230 def skeletonize_trace(T, T2=None):
231     """
232         if T is a boolean matrix representing a trace, then thin it
233
234         if T is an RGB trace, then register it according to the
235             tracing protocol then thin it
236
237         if T2 is provided, do the same thing to T2 and then merge the two
238     """
239     if T.ndim == 3:
240         trace = (rgb_to_widths(T) > 0) # booleanize it
241     else:
242         trace = T.astype('bool')
243
244     thinned = thin(trace)
245
246     if T2 is None:
247         return thinned
248
249     else:
250         # do the same thing to second trace and merge it
251         if T2.ndim == 3:
252             trace_2 = (rgb_to_widths(T2) > 0) # booleanize it
253             thinned_2 = thin(trace_2)
254
255         return np.logical_or(thinned, thinned_2)
256
257
258 def confusion(test, truth, bg_mask=None, colordict=None, tint_mask=True):
259     """
260         distinct coloration of false positives and negatives.
261
262         colors output matrix with
263             true_pos if test[-] == truth[-] == 1
264             true_neg if test[-] == truth[-] == 0
265             false_neg if test[-] == 0 and truth[-] == 1
266             false_pos if test[-] == 1 and truth[-] == 0
267
268         if colordict is supplied: you supply a dictionary of how to
269             color the four cases. Spec given by the default below:
270
271         if tint mask, then the mask is overlaid on the image, not replacing totally
272         colordict = {
273             'TN': (247, 247, 247), # true negative
274             'TP': (0, 0, 0) # true positive
275             'FN': (241, 163, 64), # false negative
276             'FP': (153, 142, 195), # false positive
277             'mask': (247, 200, 200) # mask color (not used in MCC calculation)
278         }
279     """
280
281     if colordict is None:
282         colordict = {
283             'TN': (247, 247, 247), # true negative# 'f7f7f7'
284             'TP': (0, 0, 0), # true positive # '000000',
285             'FN': (241, 163, 64), # false negative # 'f1a340' orange
286             'FP': (153, 142, 195), # false positive # '998ec4' purple

```

```

287 #         'mask': (247, 200, 200) # mask color (not used in MCC calculation)
288 #
289 #
290 #colordict = {
291 #    'TN': (49,49,49), # true negative# 'f7f7f7'
292 #    'TP': (0, 0, 0), # true positive # '000000'
293 #    'FN': (201,53,108), # false negative # 'f1a340' orange
294 #    'FP': (0,112,163), # false positive # '998ec4' purple
295 #    'mask': (247, 200, 200) # mask color (not used in MCC calculation)
296 #
297 colordict = {
298     'TP': (0,0,0),
299     'TN': (226,226,226),
300     'FN': (201,152,152),
301     'FP': (30,69,230),
302     'mask': (209,209,209)
303 }
304
305 #TODO: else check if mask is specified and add it as color of TN otherwise
306
307 true_neg_color = np.array(colordict['TN'], dtype='f')/255
308 true_pos_color = np.array(colordict['TP'], dtype='f')/255
309 false_neg_color = np.array(colordict['FN'], dtype='f')/255
310 false_pos_color = np.array(colordict['FP'], dtype='f')/255
311 mask_color = np.array(colordict['mask'], dtype='f')/255
312
313 assert test.shape == truth.shape
314
315 # convert to bool
316 test, truth = test.astype('bool'), truth.astype('bool')
317
318 # RGB array size of test and truth for output
319 output = np.zeros((test.shape[0], test.shape[1], 3), dtype='f')
320
321 # truth conditions
322 true_pos = (test==truth & truth)
323 true_neg = (test==truth & ~truth)
324 false_neg = (truth & ~test)
325 false_pos = (test & ~truth)
326
327 output[true_pos,:,:] = true_pos_color
328 output[true_neg,:,:] = true_neg_color
329 output[false_pos,:,:] = false_pos_color
330 output[false_neg,:,:] = false_neg_color
331
332 # try to find a mask
333 if bg_mask is None:
334     try:
335         bg_mask = test.mask
336     except AttributeError:
337         # no mask is specified, we're done.
338         return output
339
340 # color the mask
341 if tint_mask:
342     output[bg_mask,:,:] += mask_color
343     output[bg_mask,:,:] /= 2
344 else:
345     output[bg_mask,:,:] = mask_color
346
347 return output
348
349 def compare_trace(approx, trace=None, filename=None,

```

```

351         sample_dir=None, colordict=None):
352     """
353     compare approx matrix to trace matrix and output a confusion matrix.
354     if trace is not supplied, open the image from the tracefile.
355     if tracefile is not supplied, filename must be supplied, and
356     tracefile will be opened according to the standard pattern
357
358     colordict are parameters to pass to confusion()
359
360     returns a matrix
361     """
362
363     # load the tracefile if not supplied
364     if trace is None:
365         if filename is not None:
366             try:
367                 trace = open_typefile(filename, 'trace')
368             except FileNotFoundError:
369                 print("No trace file found matching ", filename)
370                 print("no trace found. generating dummy trace.")
371                 trace = np.zeros_like(approx)
372         else:
373             print("no trace supplied/found. generating dummy trace.")
374             trace = np.zeros_like(approx)
375
376     C = confusion(approx, trace, colordict=colordict)
377
378     return C
379
380
381 def mcc(test, truth, bg_mask=None, score_bg=False, return_counts=False):
382     """
383     Matthews correlation coefficient
384     returns a float between -1 and 1
385     -1 is total disagreement between test & truth
386     0 is "no better than random guessing"
387     1 is perfect prediction
388
389     bg_mask is a mask of pixels to ignore from the statistics
390     for example, things outside the placental plate will be counted
391     as "TRUE NEGATIVES" when there wasn't any chance of them not being
392     scored as negative. therefore, it's not really a measure of the
393     test's accuracy, but instead artificially pads the score higher.
394
395     setting bg_mask to None when test and truth are not masked
396     arrays should give you this artificially inflated score.
397     Passing score_bg=True makes this decision explicit, i.e.
398     any masks (even if supplied) will be ignored, and your count of
399     false positives will be inflated.
400
401     """
402
403     true_pos = ((test == truth) & truth)
404     true_neg = ((test == truth) & ~truth)
405     false_neg = (truth & ~test)
406     false_pos = (test & ~truth)
407
408     if score_bg:
409         # take the classifications above as they are (nothing is masked)
410         pass
411     else:
412         # if no specified mask, check the test array itself?
413         if bg_mask is None:
414             try:

```

```

415         bg_mask = test.mask
416     except AttributeError:
417         # no mask is specified, we're done.
418         bg_mask = np.zeros_like(test)
419
420     # only get stats in the plate
421     true_pos[bg_mask] = 0
422     true_neg[bg_mask] = 0
423     false_pos[bg_mask] = 0
424     false_neg[bg_mask] = 0
425
426     # now tally
427     TP = true_pos.sum()
428     TN = true_neg.sum()
429     FP = false_pos.sum()
430     FN = false_neg.sum()
431
432     if not score_bg:
433         total = np.sum(~bg_mask)
434     else:
435         total = test.size
436
437     #print('TP: {}\\t TN: {}\\nFP: {}\\tFN: {}'.format(TP,TN,FP,FN))
438     #print('TP+TN+FN+FP={}\\ntotal pixels={}'.format(TP+TN+FP+TN,total))
439     # prevent potential overflow
440     denom = np.sqrt(TP+FP)*np.sqrt(TP+FN)*np.sqrt(TN+FP)*np.sqrt(TN+FN)
441
442     if denom == 0:
443         # set MCC to zero if any are zero
444         m_score = 0
445     else:
446         m_score = ((TP*TN) - (FP*FN)) / denom
447
448     if return_counts:
449         return m_score, (TP,TN,FP,FN)
450     else:
451         return m_score
452
453 def mean_squared_error(A,B):
454     """
455     get mean squared error between two matrices of the same size
456
457     input:
458         A, B : two ndarrays of the same size.
459
460     output:
461
462         mse:    a single number.
463     """
464
465     try:
466         mse = ((A-B)**2).sum() / A.size
467
468     except ValueError:
469         print("inputs must be of the same size")
470         raise
471
472     return mse
473
474 def chain_lengths(iterable):
475     pos, s = 0, 0
476
477
478

```

```

479     for b, g in itertools.groupby(iterable):
480
481         if not b:
482             # alternative if the bottom doesn't work or something
483             #d = deque(enumerate(g,1), maxlen=1)
484             #pos += d[0][0] if d else 0
485
486             pos += sum((1 for i in g if not i))
487
488         else:
489
490             s = sum(g)
491
492             yield pos, s
493
494             pos += s
495
496         if not s:
497             # so it will return something even if iterable is empty
498             yield 0, 0
499
500
501 def longest_chain_1d(iterable):
502     """ will return a tuple of ind, length
503     where ind is the position in the iterable the chain starts and length is the
504     length of the chain
505     """
506     return max(chain_lengths(iterable), key=lambda x: x[1])
507
508
509 def longest_chain(arr, axis):
510     """Find where the longest chain of boolean values and occurs across an array
511     and also return its length
512     """
513
514     C = np.apply_along_axis(_longest_chain_1d, axis, arr.astype('bool'))
515
516     start_inds, chain_lens = np.split(C, 2, axis)
517
518     return np.squeeze(start_inds), np.squeeze(chain_lens)
519
520
521 def _bunch_hists(H, bunches):
522
523     return np.stack((np.sum(np.atleast_2d(H[b,:]), axis=0) for b in bunches))
524
525
526 def scale_to_width_plots(multiscale_approx, max_labels, widths, scales,
527                         bunches=None, cmap=None, approx_method=None,
528                         figsize=(13,14), style='seaborn', bunch_until=None):
529     """
530     multiscale_approx is a 3d boolean array whose first dimension is scale
531     max_labels is a 2d array of integers that say where the max value of
532     F occurred. you can get max_labels by running V.argmax(axis=0)
533
534     in widths, each pixel has a unique width
535
536     bunches.flatten() should be the same as arange(scales)
537     but can be something like
538     ( (0,1,2,3), (4,5), 6, 7, 8, (9,10,11) )
539
540     or even
541
542     (2,3,4,5,(0,1,6,7))

```

```

543
544     this is to prevent similar scales from clogging, you can just bin them
545     all together.
546
547     approx method is a label to use in the fig titles
548     """
549
550     if bunches is None:
551         if bunch_until is not None:
552             indices = list(range(len(scales)))
553             bunches = [indices[:bunch_until],] + indices[bunch_until:]
554
555     plt.style.use(style)
556
557     fig, ax = plt.subplots(nrows=2, ncols=1, figsize=figsize)
558
559     A = multiscale_approx # easier to work with
560
561     wbins = np.arange(3,20,2) # bins of widths in ground truth
562
563     max_hists = [[np.sum((max_labels == s) & (widths==w)) for w in wbins]
564                   for s in range(len(scales))]
565
566     hists = np.array([[np.sum((widths==w) & A[n]) for w in wbins]
567                       for n in range(len(scales))])
568
569
570     if cmap is None:
571         # this will just use the default cycle of colors
572         colors = np.repeat(None, len(scales))
573     else:
574         if not isinstance(cmap, mpl.colors.LinearSegmentedColormap):
575             # try this
576             cmap = plt.get_cmap(cmap)
577
578         colors = cmap(np.linspace(0,1,len(scales)))
579
580     labels = [rf'\sigma_k=\sigma_{k:.2f}'
581               for k, sigma in enumerate(scales,1)]
582
583     # number of true positives, false negatives for each width
584     tp_hists = [np.sum((widths==w) & A.any(axis=0)) for w in wbins]
585     fn_hists = [np.sum((widths==w) & ~A.any(axis=0)) for w in wbins]
586
587     if bunches is not None:
588         hists = _bunch_hists(hists, bunches)
589
590         # just return \sigma_{1,2,3} or something rather than listing
591         bunch_label = lambda b: r"\sigma".format(',').join([
592             str(x+1)
593             for x in b])
594
595     labels = [labels[b] if np.isscalar(b) else bunch_label(b)
596               for b in bunches]
597
598     if cmap is None:
599         # just make it the appropriate length
600         cmap = np.repeat(None, len(bunches))
601     else:
602         colors = [colors[b] if np.isscalar(b) else colors[b[0]]
603                   for b in bunches]
604
605     ax[0].bar(wbins, tp_hists, color=(0.6,0.6,0.6),

```

```

607     label='# true positives')
608 ax[0].bar(wbins, fn_hists, bottom=tp_hists, color=(1,.8,.8),
609             label='# false negatives')
610
611 for h, mh, label, color in zip(hists, max_hists, labels, colors):
612     ax[0].plot(wbins, h, label=label, color=color)
613     ax[1].plot(wbins, mh, label=label, color=color)
614
615
616 ax[0].set_xticks(wbins)
617 ax[0].set_xlabel('vessel widths (ground truth), pixels')
618 ax[0].set_ylabel('# pixels')
619 ax[0].set_xlim(2,21)
620
621 ax[1].set_xticks(wbins)
622 ax[1].set_xlabel('vessel widths (ground truth), pixels')
623 ax[1].set_ylabel('# pixels')
624 ax[1].set_xlim(2,21)
625
626 title = 'pixels reported per scale'
627 max_title = r'pixel widths of true positives by scale of  $V_{max}$ '
628 if approx_method is not None:
629     title += f'({approx_method})'
630     max_title += f'({approx_method})'
631
632 ax[0].set_title(title)
633 ax[1].set_title(max_title)
634 ax[0].legend(loc='best', labelspacing=0.2)
635 ax[1].legend(loc='best', labelspacing=0.2)
636
637 fig.tight_layout()
638 return fig, ax
639
640
641 def scale_to_argmax_plot(max_labels, widths, scales, normalize=False,
642                         bunches=None, cmap=None, figsize=(13,10),
643                         style='seaborn-paper', bunch_until=None):
644     """
645     if normalize, normalize each scale over columns (i.e. all widths)
646     multiscale_approx is a 3d boolean array whose first dimension is scale
647     max_labels is a 2d array of integers that say where the max value of
648     F occurred. you can get max_labels by running V.argmax(axis=0)
649
650     in widths, each pixel has a unique width
651
652     bunches.flatten() should be the same as arange(scales)
653     but can be something like
654     ( (0,1,2,3), (4,5), 6, 7, 8, (9,10,11) )
655
656     or even
657
658     (2,3,4,5,(0,1,6,7))
659
660     this is to prevent similar scales from clogging, you can just bin them
661     all together.
662
663     approx method is a label to use in the fig titles
664     """
665
666     if bunches is None:
667         if bunch_until is not None:
668             indices = list(range(len(scales)))
669             bunches = [indices[:bunch_until],] + indices[bunch_until:]

```

```

671 plt.style.use(style)
672 fig, ax = plt.subplots(figsize=figsize)
674 wbins = np.arange(3,20,2) # bins of widths in ground truth
676 max_hists = np.array([[np.sum((max_labels == s) & (widths==w)) for w in wbins]
677                         for s in range(len(scales))])
678 if normalize:
679     max_hists = max_hists / max_hists.sum(axis=1, keepdims=True)
681
682 if cmap is None:
683     # this will just use the default cycle of colors
684     colors = np.repeat(None, len(scales))
685 else:
686     if not isinstance(cmap, mpl.colors.LinearSegmentedColormap):
687         # try this
688         cmap = plt.get_cmap(cmap)
689
690     colors = cmap(np.linspace(0,1,len(scales)))
691
692 labels = [rf' $\sigma_k = \sigma$ :{2f}'
693             for k, sigma in enumerate(scales,1)]
694
695 # number of true positives, false negatives for each width
696
697 if bunches is not None:
698
699     # just return \sigma_{1,2,3} or something rather than listing
700     bunch_label = lambda b: r" $\sigma$ ".format(','.join((str(x+1)
701                                         for x in b
702                                         )))
703
704     labels = [labels[b] if np.isscalar(b) else bunch_label(b)
705               for b in bunches]
706
707     if cmap is None:
708         # just make it the appropriate length
709         cmap = np.repeat(None, len(bunches))
710     else:
711         colors = [colors[b] if np.isscalar(b) else colors[b[0]]
712                   for b in bunches]
713
714 #ax.bar(wbins, tp_hists, color=(0.6,0.6,0.6),
715 #        label='# true positives')
716 #ax.bar(wbins, fn_hists, bottom=tp_hists, color=(1,.8,.8),
717 #        label='# false negatives')
718
719 for mh, label, color in zip(max_hists, labels, colors):
720     ax.plot(wbins, mh, label=label, color=color)
721
722
723 ax.set_xticks(wbins)
724 ax.set_xlabel('vessel widths (ground truth), pixels')
725 if normalize:
726     ax.set_ylabel('# pixels identified by scale /'
727                  '# pixels identified by all scales')
728 else:
729     ax.set_ylabel('# pixels')
730
731 ax.set_xlim(2,21)
733 max_title = r'pixel widths of true positives by scale of  $V_{\max}$ '
```

```

735     ax.set_title(max_title)
736     ax.legend(loc='best', labelspacing=0.2)
737
738     fig.tight_layout()
739     return fig, ax
740
741
742
743 if __name__ == "__main__":
744
745     import matplotlib.pyplot as plt
746     from skimage.data import binary_blobs
747
748     A = binary_blobs()
749     B = binary_blobs()
750
751     true_neg_color = np.array([247, 247, 247], dtype='f') # 'f7f7f7'
752     true_pos_color = np.array([0, 0, 0], dtype='f') # '000000'
753     false_neg_color = np.array([241, 163, 64], dtype='f')# 'f1a340'
754     false_pos_color = np.array([153, 142, 195], dtype='f') # '998ec4'
755
756     C = confusion(A,B)
757
758     fig, (ax0, ax1, ax2) = plt.subplots(nrows=1,
759                                         ncols=3,
760                                         figsize=(8, 2.5),
761                                         sharex=True,
762                                         sharey=True)
763
764     ax0.imshow(A, cmap='gray')
765     ax0.set_title('A')
766     ax0.axis('off')
767     ax0.set_adjustable('box-forced')
768
769     ax1.imshow(B, cmap='gray')
770     ax1.set_title('B')
771     ax1.axis('off')
772     ax1.set_adjustable('box-forced')
773
774     ax2.imshow(C)
775     ax2.set_title('confusion matrix of A and B')
776     ax2.axis('off')
777     ax2.set_adjustable('box-forced')
778
779     fig.tight_layout()

```

listings/signed_sweep_demo.py

```

1 #!/usr/bin/env python3
2
3 from placenta import (get_named_placenta, list_placentas, _cropped_bounds,
4                       cropped_view, cropped_args, show_mask)
5 from frangi import frangi_from_image
6
7 import numpy as np
8 import numpy.ma as ma
9
10 from plate_morphology import dilate_boundary
11
12 import os.path
13 import matplotlib.pyplot as plt
14 import matplotlib as mpl
15 from itertools import product

```

```

16
17 # pick two samples and two insets (should be the same size)
18 demo1 = 'BN2315363', np.s_[370:670, 530:930]
19 demo2 = 'BN5280796', np.s_[150:450, 530:930]
20
21 for sample_name, inset_slice in (demo1, demo2):
22     img = get_named_placenta(f'T-{sample_name}.png')
23
24     crop = cropped_args(img)
25
26 F, fi = list(), list() # make some empty lists to store for inspection
27
28 #scales = np.logspace(-3, 4, num=8, base=2)
29 scales = [0.2, 0.8, 1.0, 2.0, 4.0, 6.0, 8.0, 16.0]
30 CMAP = plt.cm.Spectral
31 cmin, cmax = (-0.4, 0.4)
32
33 for n, sigma in enumerate(scales):
34     R = max(int(sigma**3), 10)
35     target = frangi_from_image(img, sigma, dark_bg=False,
36                                signed_frangi=True, dilation_radius=R)
37     plate = target[crop].filled(0)
38     inset = target[inset_slice].filled(0)
39     F.append(plate)
40     fi.append(inset)
41     #for label in ['plate', 'inset']:
42     #    if label == 'inset':
43     #        printable = inset
44     #    else:
45     #        printable = plate
46
47     # plt.imshow(printable, cmap=CMAP)
48     # plt.title(r'$\sigma$=:2f'.format(sigma))
49     # plt.tight_layout()
50     # c = plt.colorbar()
51     # c.set_ticks = np.linspace(cmin, cmax, num=len(scales)+1)
52     # plt.clim(cmin, cmax)
53     # plt.axis('off')
54     # outname = f'demo_output/signsweep_{sample_name}_{label}_{n}.png'
55     # plt.savefig(outname, dpi=300, bbox_inches='tight')
56     # print('saved', outname)
57     # plt.close()
58
59 # now make a stitched together version
60 for label in ['plate', 'inset']:
61     if label == 'inset':
62         L = fi
63         imgview = img[inset_slice].filled(0)
64         figsize = (12, 6)
65
66     else:
67         L = F
68         imgview = img[crop].filled(0)
69         figsize = (12, 9)
70     #adjust this manually depending on how many scales you end up using!
71
72     nrows, ncols = 2, 4
73     fig, axes = plt.subplots(nrows=nrows, ncols=ncols, figsize=figsize)
74
75     for n, (i, j) in enumerate(product(range(nrows), range(ncols))):
76
77         if n == 0:
78             axes[i,j].imshow(imgview, cmap=plt.cm.gray)
79             axes[i,j].set_title('raw')

```

```

80
81     else:
82         im = axes[i,j].imshow(L[n], cmap=CMAP, vmin=cmin, vmax=cmax)
83         axes[i,j].set_title(r' $\sigma = :.2f$ '.format(scales[n]))
84
85         plt.setp(axes[i,j].get_xticklabels(), visible=False)
86         plt.setp(axes[i,j].get_yticklabels(), visible=False)
87
88 #for i in range(5):
89 #    fig.tight_layout()
90
91 #fig.subplots_adjust(right=0.8)
92 #cax = fig.add_axes([.85,.15,.05,.7])
93 #c = fig.colorbar(im, ax=cax)
94
95 fig.subplots_adjust(top=0.954, bottom=0.025, left=0.010,
96                     right=0.989, hspace=0.0, wspace=0.0)
97
98 plt.savefig(f'demo_output/signsweep_stitch_{sample_name}_{label}.png',
99             dpi=300)
100
101 cfile = 'demo_output/signsweep_colorbar.png'
102 if os.path.isfile(cfile):
103     continue # no need to make another
104
105 fig = plt.figure(figsize=(figsize[0],2))
106 ax1 = fig.add_axes([0.15, 0.25, 0.75, 0.5])
107 cbar = mpl.colorbar.ColorbarBase(ax1, cmap=CMAP,
108                                 norm=mpl.colors.Normalize(cmin,cmax),
109                                 orientation='horizontal')
110 plt.savefig(cfile, dpi=300)
111 #top = np.concatenate(L[:4],axis=1)
112 #bottom = np.concatenate(L[4:],axis=1)
113 #stitched = np.concatenate((top,bottom),axis=0)
114 #imga = plt.imshow(stitched, cmap=CMAP)
115 #plt.imsave(f'demo_output/signsweep_stitch_{sample_name}_{label}.png',
116 #            stitched, cmap=CMAP, vmin=cmin, vmax=cmax)
117
118 # also save the original pic
119 #plt.imsave(f'demo_output/signsweep_{sample_name}_{label}_raw',
120 #            imgview, cmap=plt.cm.gray)

```

APPENDIX B
3D VISUALIZATION OF THE FRANGI FILTER

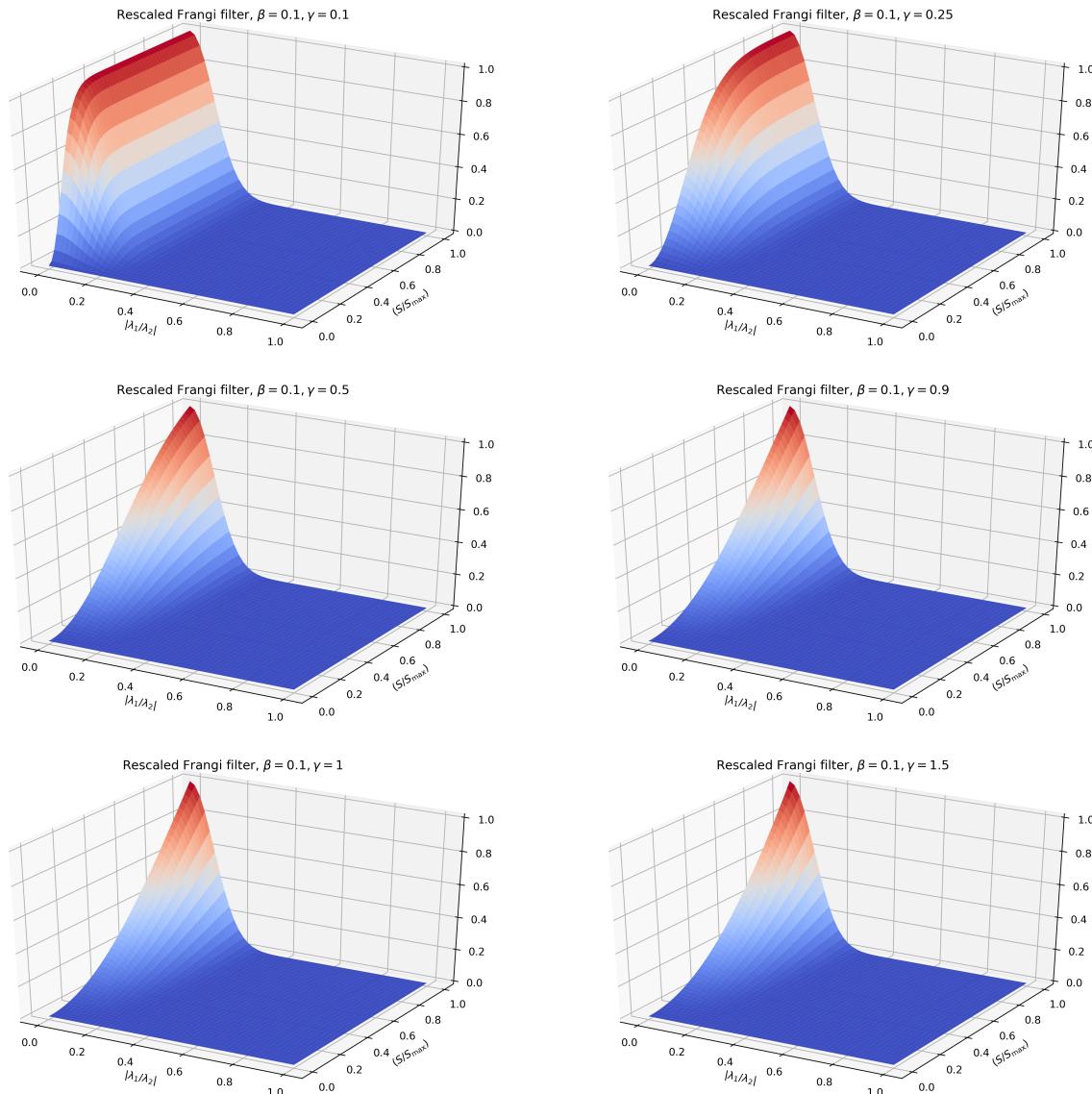


FIGURE 42: 3D graph of the Frangi Vesselness Measure, variable γ , $\beta = 0.1$

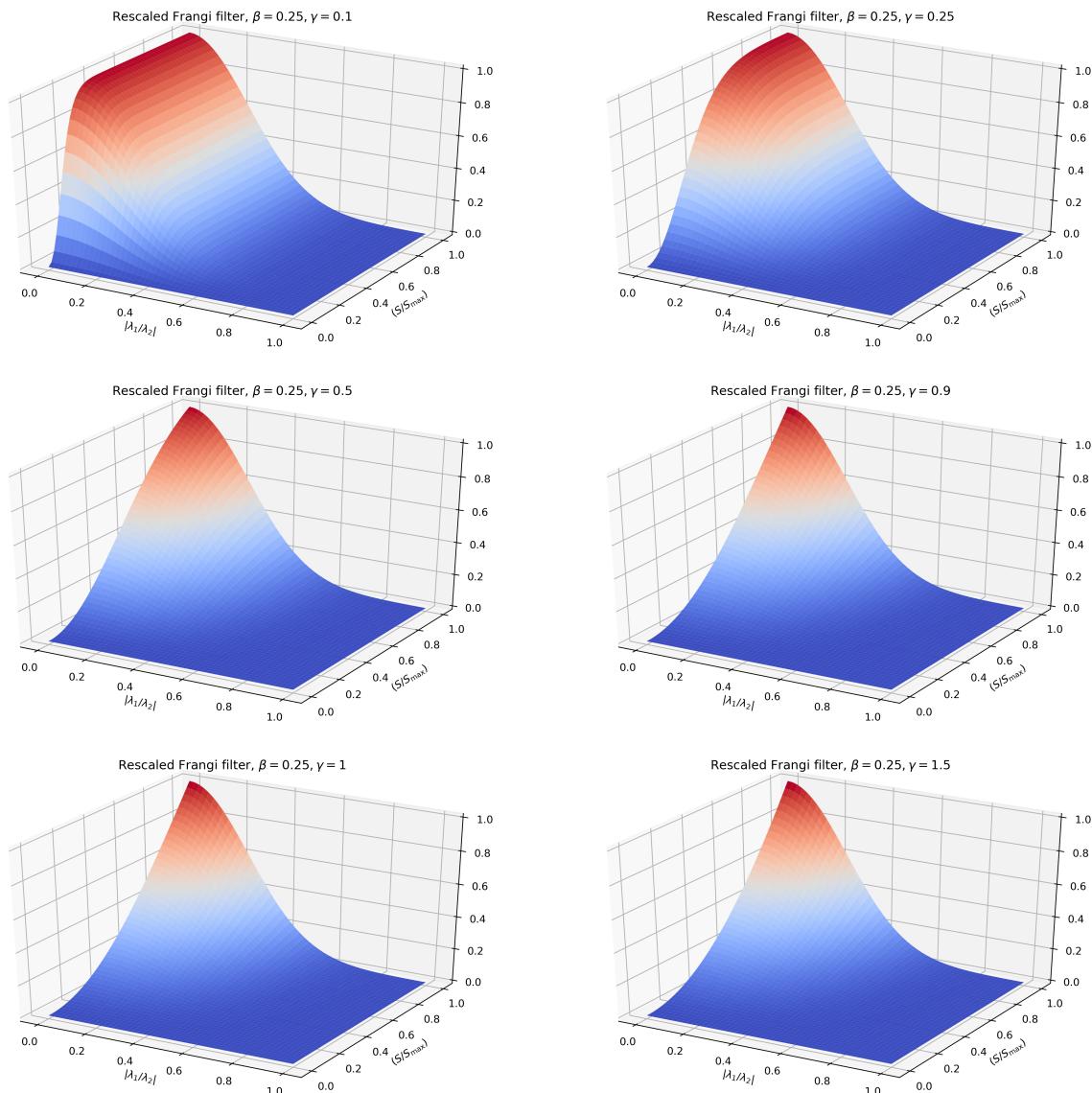


FIGURE 43: 3D graph of the Frangi Vesselness Measure, variable γ , $\beta = 0.25$

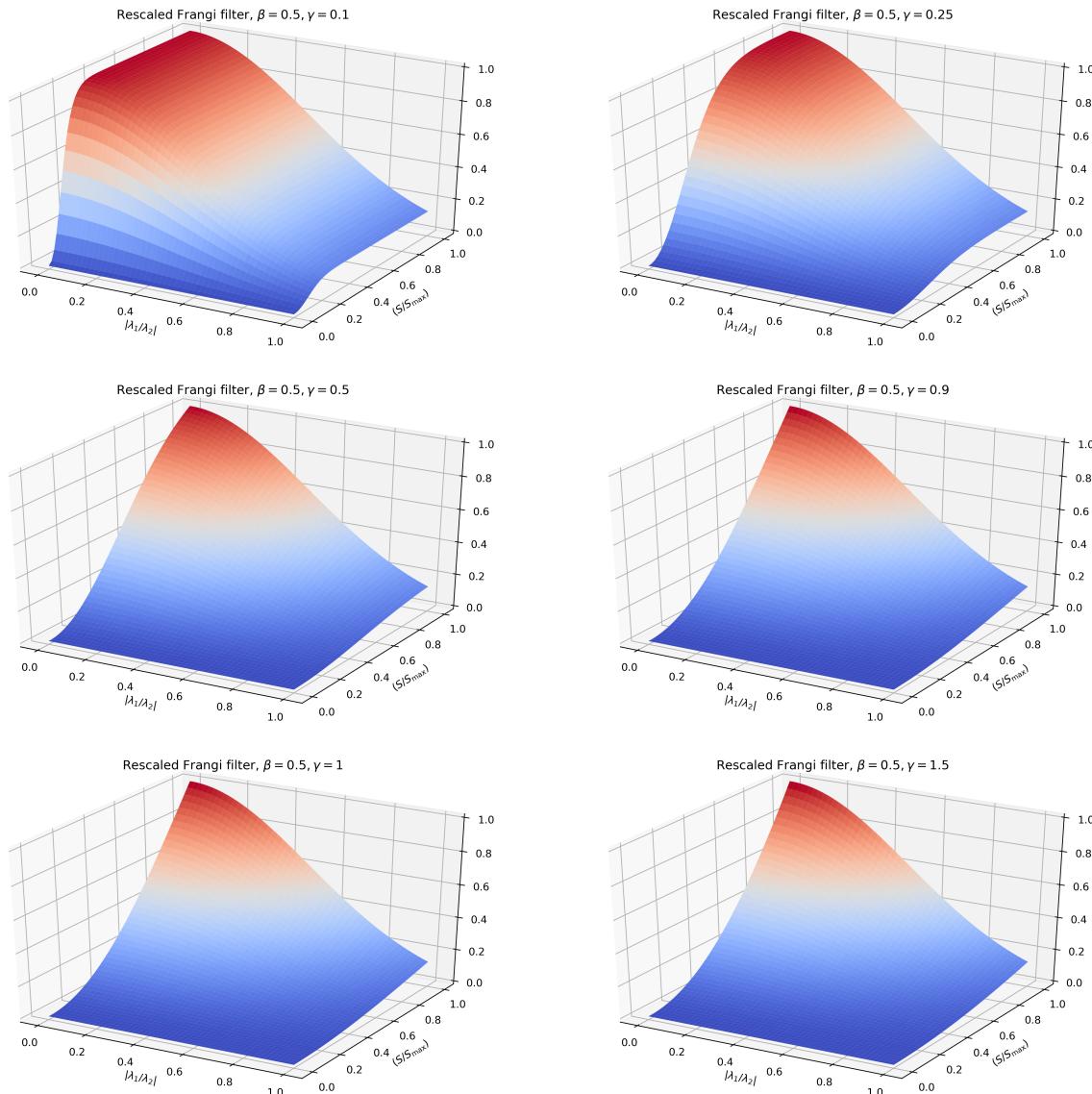


FIGURE 44: 3D graph of the Frangi Vesselness Measure, variable γ , $\beta = 0.5$

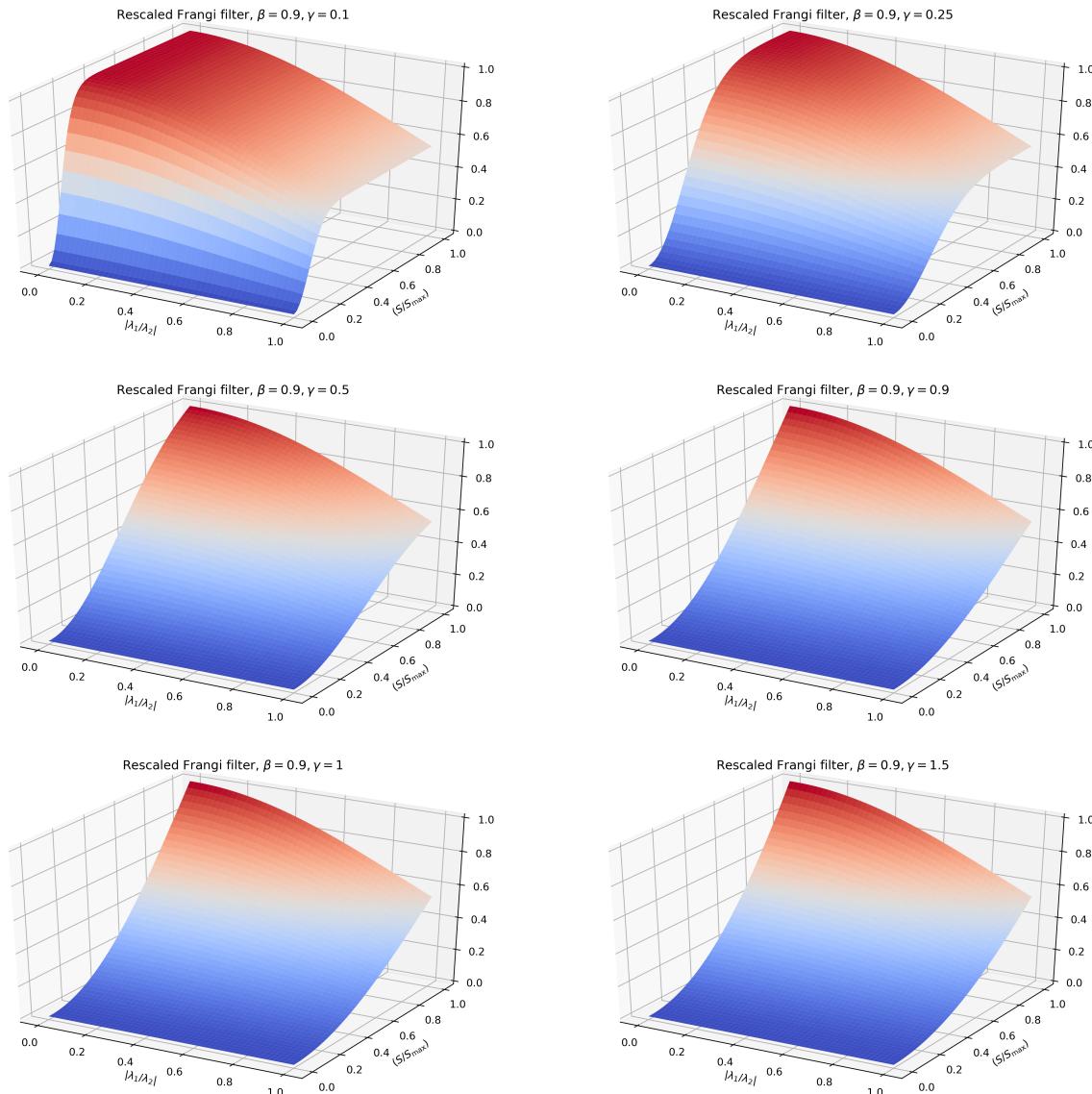


FIGURE 45: 3D graph of the Frangi Vesselness Measure, variable γ , $\beta = 0.9$

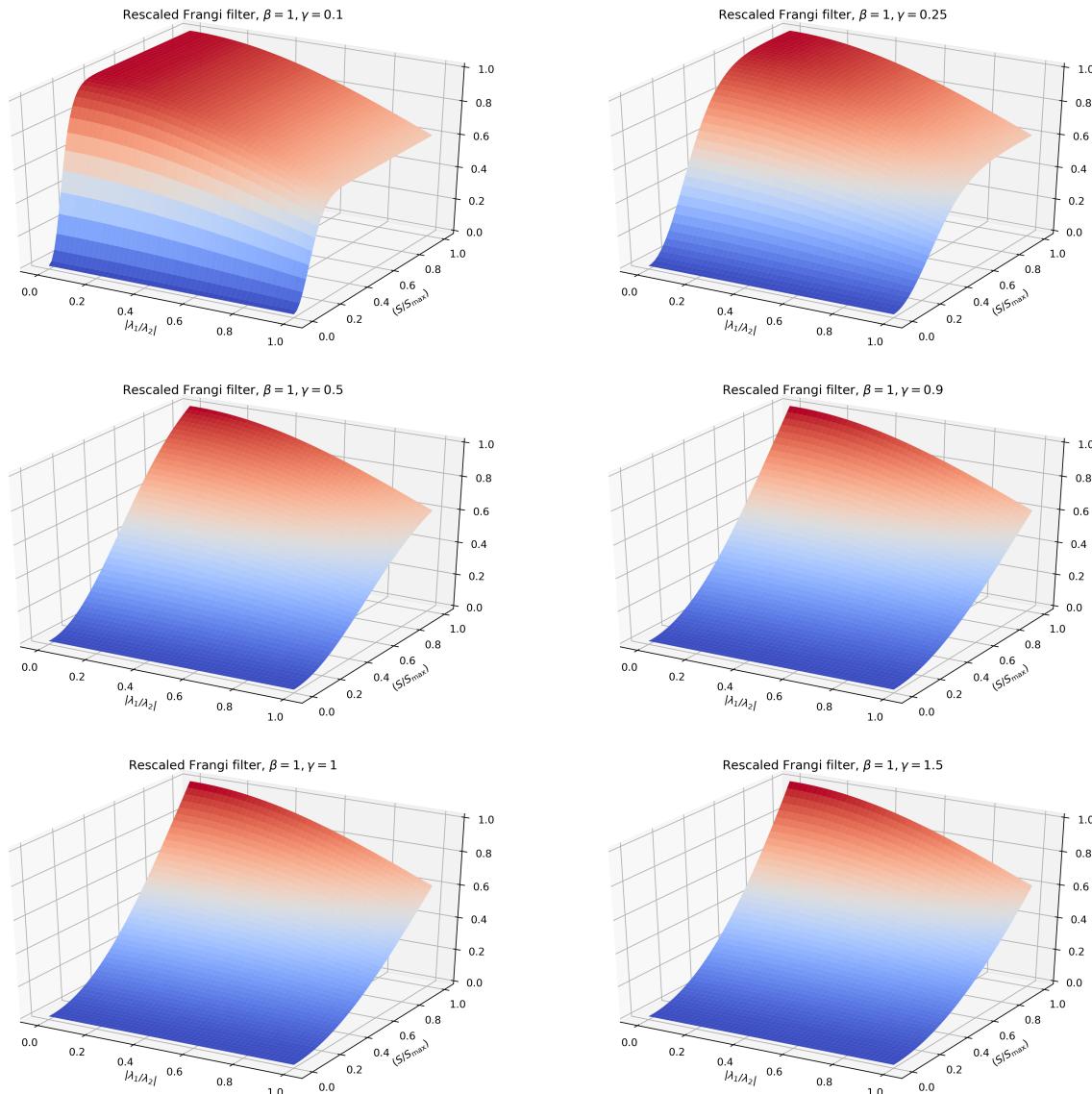


FIGURE 46: 3D graph of the Frangi Vesselness Measure, variable γ , $\beta = 1$

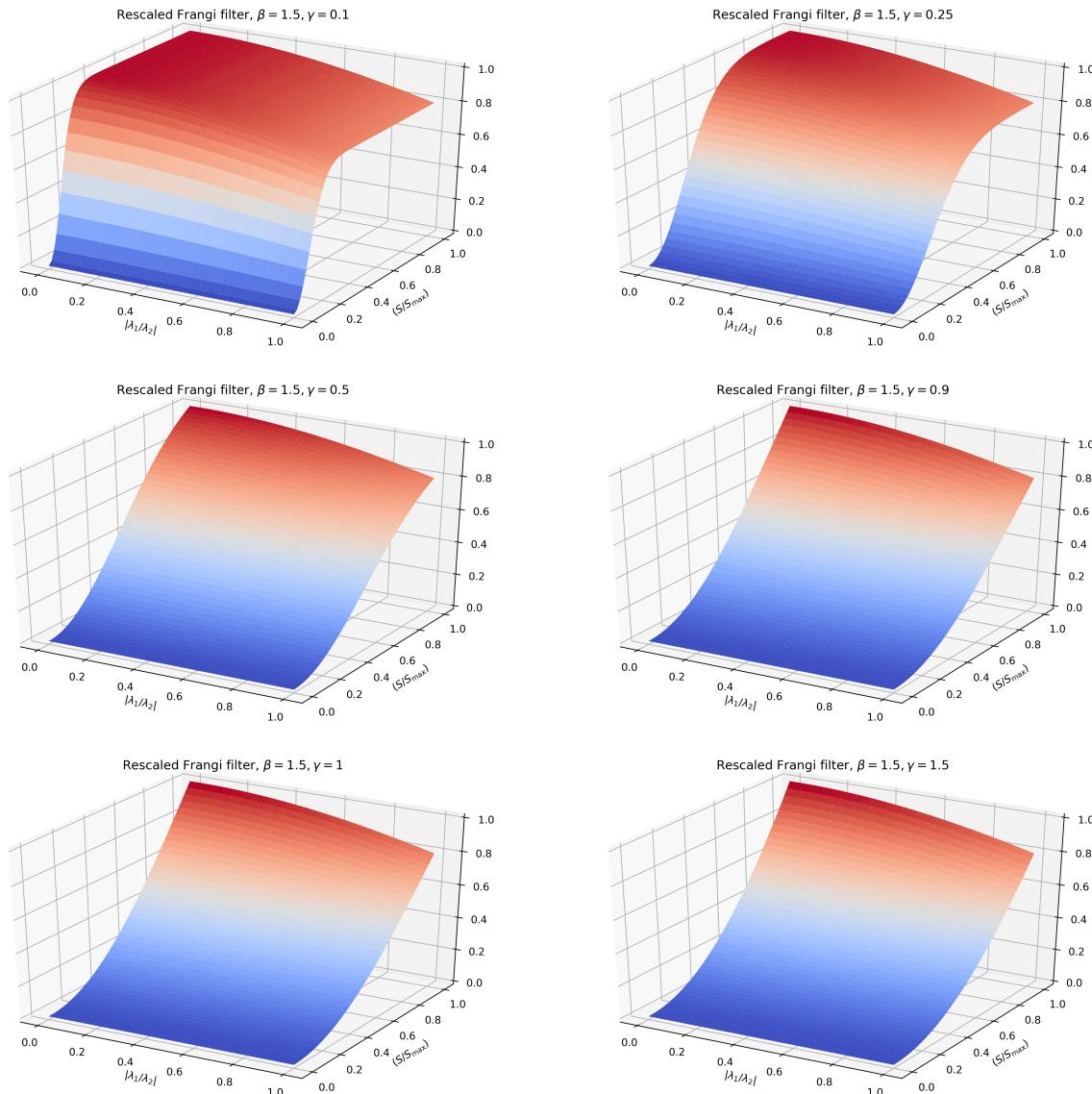


FIGURE 47: 3D graph of the Frangi Vesselness Measure, variable γ , $\beta = 1.5$

BIBLIOGRAPHY

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- [1] J.-M. Chang, H. Zeng, R. Han, Y.-M. Chang, R. Shah, C. M. Salafia, C. Newschaffer, R. K. Miller, P. Katzman, J. Moye, *et al.*, BMC medical informatics and decision making **17**, 162 (2017).
- [2] N. Huynh, Ph.D. thesis, California State University, Long Beach, 2013.
- [3] Y.-M. Chang, R. Han, H. Zeng, R. Shah, C. Newschaffer, R. Miller, P. Katzman, J. Moye, C. Salafia, *et al.*, Placenta **45**, 75 (2016).
- [4] N. Almoussa, B. Dutra, B. Lampe, P. Getreuer, T. Wittman, C. Salafia, and L. Vese, in *Medical Imaging 2011: Image Processing*, International Society for Optics and Photonics (PUBLISHER, ADDRESS, 2011), Vol. 7962, p. 79621L.
- [5] K. Y. Djima, C. Salafia, R. K. Miller, R. Wood, P. Katzman, C. Stodgell, and J.-M. Chang, Placenta **57**, 292 (2017).
- [6] R. C. Gonzalez and R. E. Woods, Upper Saddle River, NJ (2002).
- [7] W. Kühnel, B. Hunt, and A. M. Society, *Differential Geometry: Curves - Surfaces - Manifolds, Student mathematical library* (American Mathematical Society, ADDRESS, 2006).
- [8] *The Algebraic Eigenvalue Problem*, edited by J. H. Wilkinson (Oxford University Press, Inc., New York, NY, USA, 1988).
- [9] R. Horn and C. Johnson, *Matrix Analysis, Matrix Analysis* (Cambridge University Press, ADDRESS, 2012).
- [10] X. Jiao and H. Zha, in *Proceedings of the 2008 ACM symposium on Solid and physical modeling*, ACM (PUBLISHER, ADDRESS, 2008), pp. 159–170.
- [11] R. Burden and J. Faires, *Numerical Analysis*, 9 ed. (Brooks/Cole, ADDRESS, 2011).
- [12] A. F. Frangi, W. J. Niessen, K. L. Vincken, and M. A. Viergever, in *International Conference on Medical Image Computing and Computer-Assisted Intervention*, Springer (PUBLISHER, ADDRESS, 1998), pp. 130–137.
- [13] Y. Sato, S. Nakajima, N. Shiraga, H. Atsumi, S. Yoshida, T. Koller, G. Gerig, and R. Kikinis, Medical image analysis **2**, 143 (1998).

- [14] C. Lorenz, I. C. Carlsen, T. M. Buzug, C. Fassnacht, and J. Weese, in *CVRMed-MRCAS'97*, edited by J. Troccaz, E. Grimson, and R. Mösges (Springer Berlin Heidelberg, Berlin, Heidelberg, 1997), pp. 233–242.
- [15] S. D. Olabarriaga, M. Breeuwer, and W. Niessen, in *International Congress Series*, Elsevier (PUBLISHER, ADDRESS, 2003), Vol. 1256, pp. 1191–1196.
- [16] J. J. Koenderink, *Biological Cybernetics* **50**, 363 (1984).
- [17] J. Sporrings, in *Gaussian Scale-Space Theory*, edited by L. Florack, M. Nielsen, and P. Johansen (Kluwer Academic Publishers, Norwell, MA, USA, 1997).
- [18] J. Babaud, M. Baudin, R. O. Duda, and A. P. Witkin, *IEEE Transactions on Pattern Analysis & Machine Intelligence* **8**, 26 (1986).
- [19] T. Lindeberg, *IEEE transactions on pattern analysis and machine intelligence* **12**, 234 (1990).
- [20] T. Lindeberg, *On the construction of a scale-space for discrete images* (KTH Royal Institute of Technology, ADDRESS, 1988).
- [21] M. Abramowitz and I. A. Stegun, *Handbook of Mathematical Functions with Formulas, Graphs, and Mathematical Tables*, ninth dover printing, tenth gpo printing ed. (Dover, New York, 1964).
- [22] T. Lindeberg, *Journal of Mathematical Imaging and Vision* **3**, 349 (1993).
- [23] T. Lindeberg, *International journal of computer vision* **30**, 79 (1998).
- [24] B. Fornberg, *Mathematics of computation* **51**, 699 (1988).
- [25] A. Morar, F. Moldoveanu, and E. Gröller, in *2012 IEEE 8th International Conference on Intelligent Computer Communication and Processing*, IEEE (PUBLISHER, ADDRESS, 2012), pp. 213–220.
- [26] E. Jones, T. Oliphant, P. Peterson, *et al.*, SciPy: Open source scientific tools for Python, 2001–, [Online; accessed <today>].
- [27] S. Damelin and N. Hoang, *International Journal of Mathematics and Mathematical Sciences* **2018**, (2018).
- [28] H. Lange, in *Medical Imaging 2005: Image Processing*, International Society for Optics and Photonics (PUBLISHER, ADDRESS, 2005), Vol. 5747, pp. 2183–2193.
- [29] B. Matthews, *Biochimica et Biophysica Acta (BBA) - Protein Structure* **405**, 442 (1975).
- [30] L. Grady, *IEEE Trans. Pattern Anal. Mach. Intell.* **28**, 1768 (2006).

- [31] Z. Guo and R. W. Hall, Communications of the ACM **32**, 359 (1989).
- [32] I. Laptev, H. Mayer, T. Lindeberg, W. Eckstein, C. Steger, and A. Baumgartner, Machine Vision and Applications **12**, 23 (2000).