

ABSTRACT

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

By

Lucas Allen Wukmer

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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 ($N=40$) 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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Committee Members:

Jen-Mei Chang, Ph.D. (Chair)
James von Brecht, Ph.D.
William Ziemer, Ph.D.

College Designee:
Tangan Gao, Ph.D.

By Lucas Allen Wukmer
B.S., 2013, University of California, Los Angeles
December 2018

WE, THE UNDERSIGNED MEMBERS OF THE COMMITTEE,
HAVE APPROVED THIS THESIS

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By

Lucas Allen Wukmer

COMMITTEE MEMBERS

Jen-Mei Chang, Ph.D. (Chair)

Mathematics and Statistics

James von Brecht, Ph.D.

Mathematics and Statistics

William Ziemer, Ph.D.

Mathematics and Statistics

ACCEPTED AND APPROVED ON BEHALF OF THE UNIVERSITY

Tangan Gao, Ph.D.
Department Chair, Mathematics and Statistics

California State University, Long Beach

December 2018

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Thank you for reading this.

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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] that there is some correlation between risk and placental health. Most ASD cases are not diagnosed until the child reaches three or four, so the benefit of any neonatal testing would be very beneficial, 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 labor for each trace. There has been work to automate this procedure [4] [2] [5]. 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. We continue the work of developing a procedure to automate extraction of the PCSVN.

Our basic goal of "vascular network extraction" is a frequent one in image processing. There have been many techniques adapted to extracting vascular networks. The placenta in particular presents a greater degree of difficulty due to the nature of the vascular network. It's a surface network, and the "background" has a great degree of topology itself, causing many naïve approaches that work with other image domains to fail completely.

Much work has been done 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] solved this problem by provided 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 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).

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

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 5.1), 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 section 3.2, 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. Seeing that f is one-to-one should make a lot of this futzing about complete overkill, but I've yet to find a way to distill it. That is, this development works for any parametrized surface element, not necessarily a graph. Whatever for now.

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*

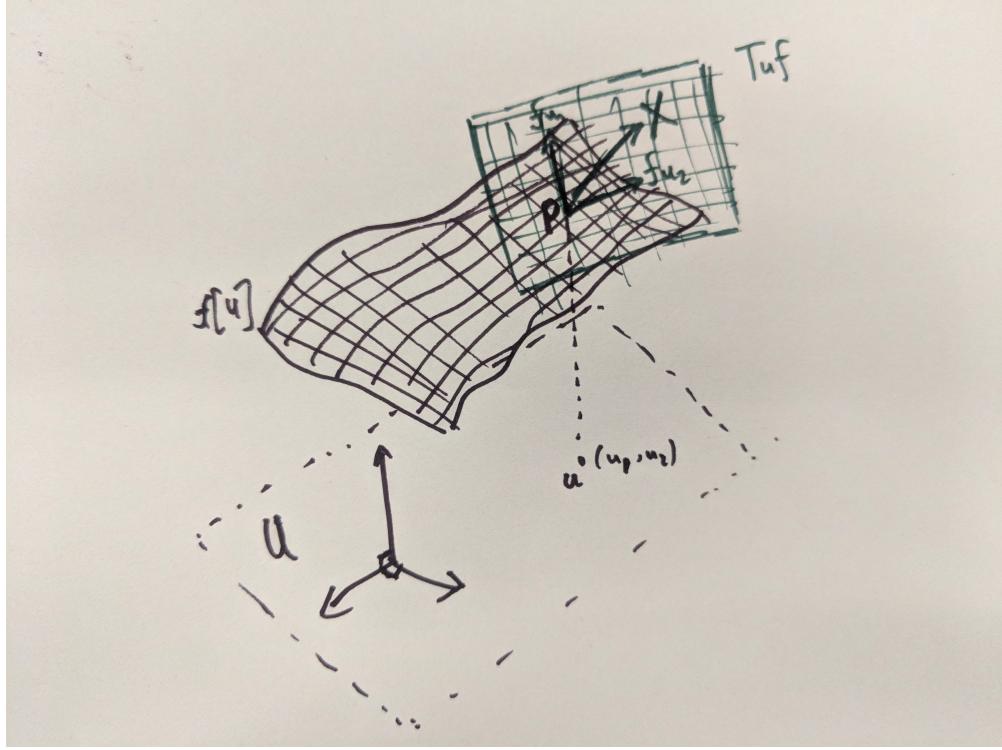


FIGURE 1: Tangent plane of a graph

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 simpler

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

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, which is certainly useful for surfaces f that are not graphs. We refer to [7] for the general proof. The situation is much less delicate if f is a graph—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

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

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

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

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

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 to 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 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 calculate 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 that, since 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

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 [9] 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

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

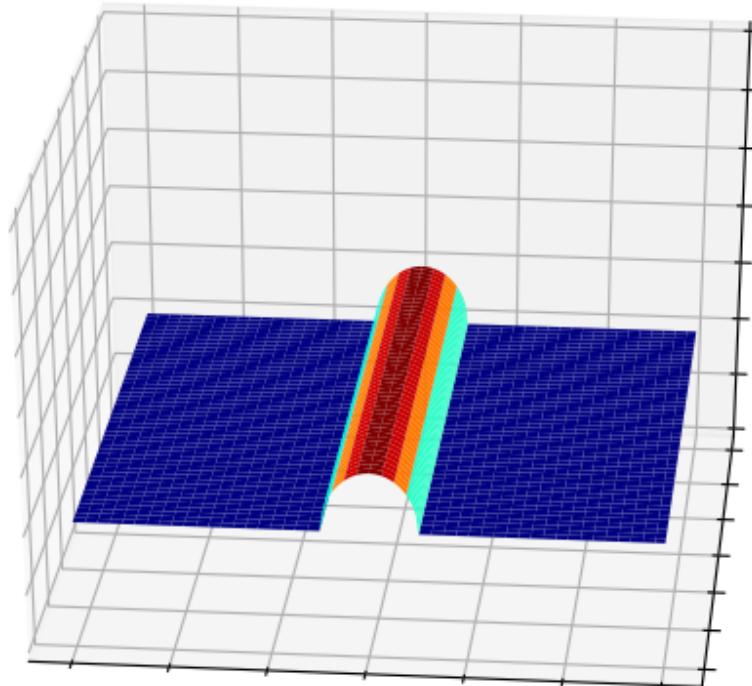


FIGURE 2: The graph of a cylindrical ridge of radius r

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

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

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

The gauss map is given by

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

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

We then calculate matrix elements of the Weingarten map's construction as given in eq. (2.41) and eq. (2.43) :

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

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

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

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 $\text{Hess}(x, y)$ 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, [10]:

Lemma 2.8 (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

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

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 $v_1, v_2 \neq 0$.¹

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

¹To simplify notation, we simplify our argument to consider two explicit eigenvectors only, since we're only concerned with the 2×2 matrix Hess anyway.

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 [11] is a widely used (cite) 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 [12] and [13], as well as a comparison given in [14]. 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:

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

where

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

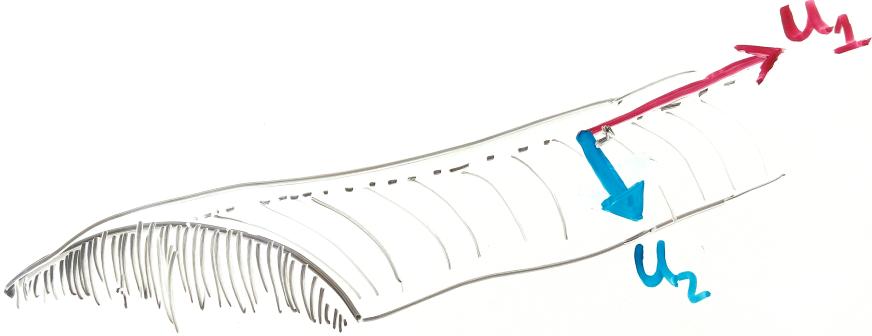


FIGURE 3: The principal eigenvectors at a ridge like structure

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 Note that the length of these vectors in this picture is not meant to represent their magnitudes, as u_2 should have a much larger relative magnitude by design!

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 5.1), 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.

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 some of these issues by casting this as a multiscale problem in chapter 4.

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 8.1.

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 still 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 $\lambda_2 < 0$.

The Frangi vesselness filter: 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,

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

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 is $\max\{V_\sigma\} \leq 1 - \exp\{-1\} \approx .8647$. 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 *gamma* that rescales V so that the structureness factor has a maximum output score of 1 regardless of choice of γ . Our final Frangi vesselness measure is thus

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

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 chose 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. If there is a lot of gain then β should be smaller. If this is not the case, a stronger filter can be created by requiring A to be much smaller.

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

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

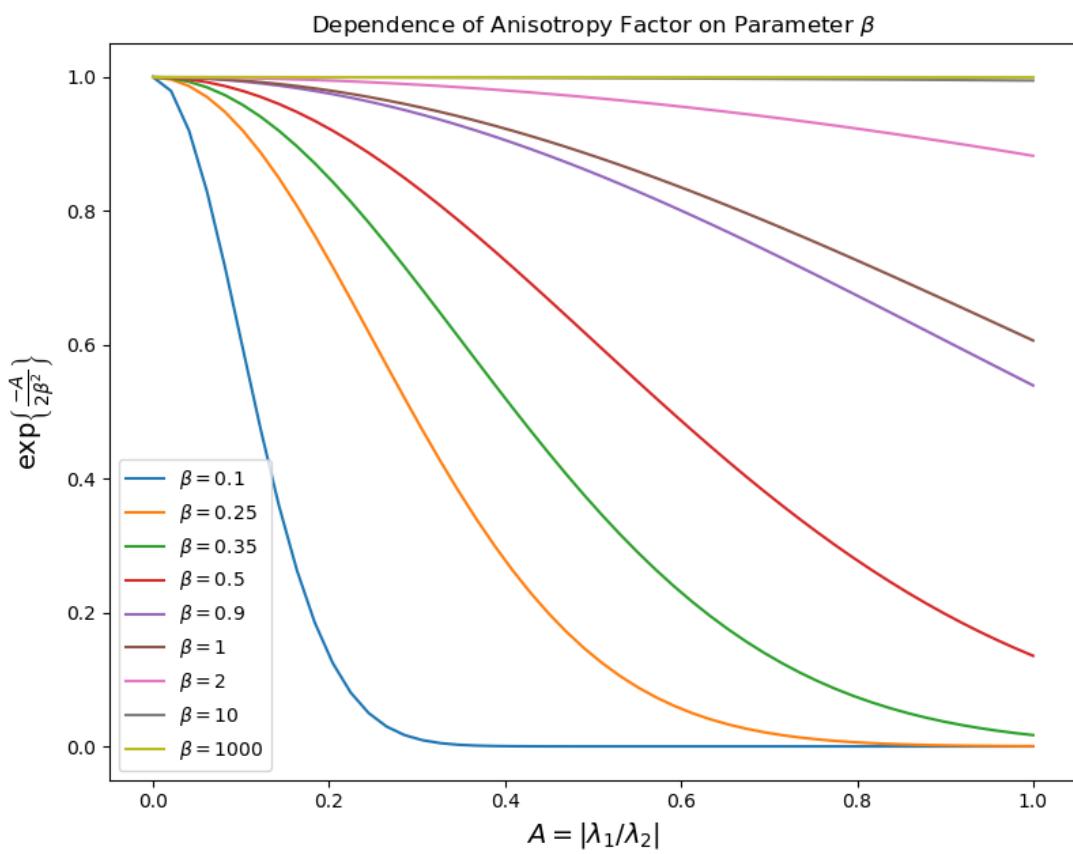


FIGURE 4: Dependence of the Anisotropy Factor on its Parameter

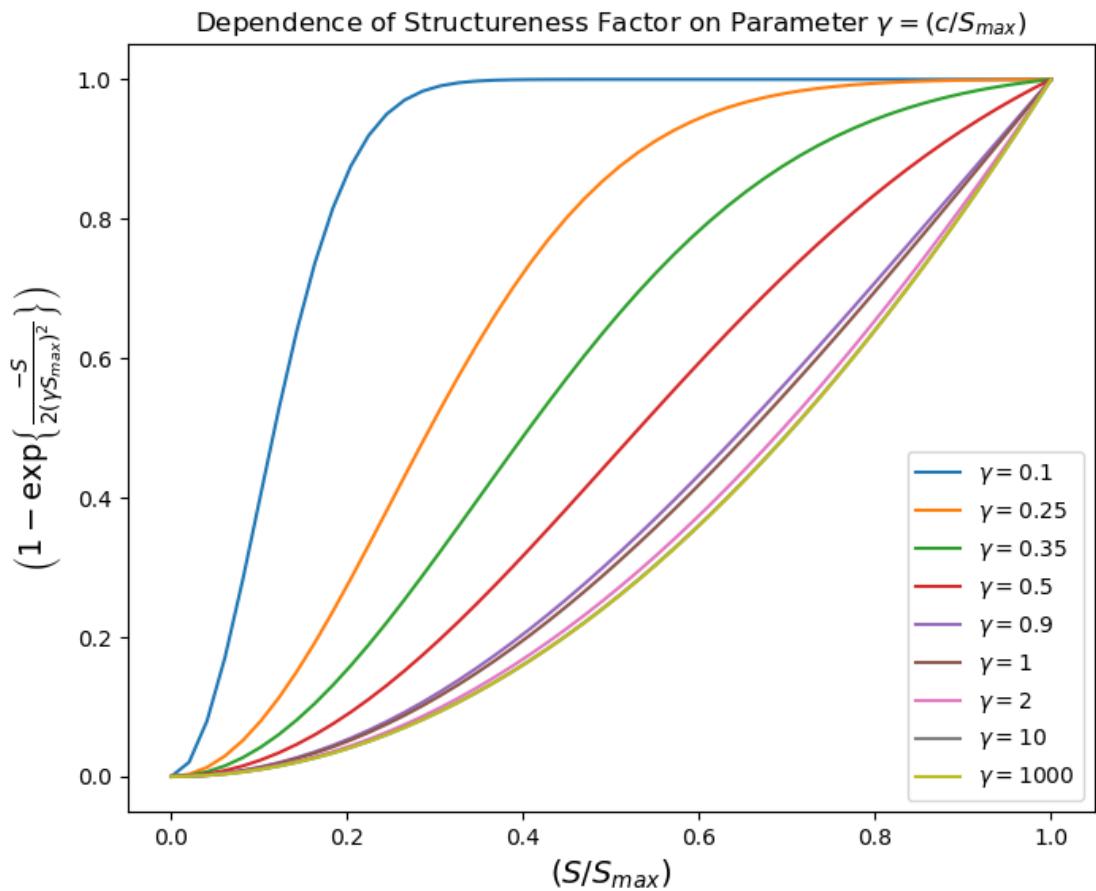


FIGURE 5: Dependence of the Structureness Factor on its Parameter

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

Linear Scale Space Theory

There is obviously a major disconnect in the ideas presented above. Although the ideas presented above require differentiation of continuous surfaces, our image is in fact a discrete pixel. 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. In particular, we seek to mitigate 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. Koenderink [15] 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 require that any such family of images must satisfy the heat equation

$$\Delta K(x, y, \sigma) = K_\sigma(x, y, \sigma) \text{ for } \sigma \geq 0 \text{ such that } K(x, y, 0) = u_0(x, y). \quad (3.5)$$

where $K : \mathbb{R}^3 \rightarrow \mathbb{R}$ and $u_0 : \mathbb{R}^2 \rightarrow \mathbb{R}$ is the original image (viewed as a continuous surface) and σ is a resolution parameter. Much work has been done to formalize this approach [16]. There is a long list of desired properties—we will try to identify a minimal subset of axioms and show that other desired properties follow.

Axioms

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

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

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

Axiom 3.1 (Linear-shift and Rotational Invariance). *Linear-shift (or translation) invariance means 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. Similarly, there should be not be favoritism toward any particular orientation of content within the image.*

Axiom 3.2 (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 a nonzero real number (as opposed to an integer). Moreover, we require that the operator behaves continuously with respect to the scale parameter.*

What happens as $\sigma \downarrow 0$ is not immediately clear though. An argument from functional analysis (see [17]) implies that there is a so-called “infinitesimal generator” A which is a limit case of our desired operator T ; that is

$$Au_0 = \lim_{\sigma \downarrow 0} \frac{T_\sigma u_0 - u_0}{\sigma} \tag{3.6}$$

and moreover that there is a resultant differential equation concerning the derivative of the family and A :

$$\partial_\sigma K(x, y; \sigma) = \lim_{\sigma \downarrow 0} \frac{K(\cdot; \sigma + h) - K(\cdot; \sigma)}{h} = A(T_\sigma u) = A(K(\cdot, \sigma)) \tag{3.7}$$

We shall return to this idea later and more concretely describe A once we actually characterize the generating operator T_σ .

Axiom 3.3 (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.*

$$T_\sigma u = T_{\sigma_1 + \sigma_2} u \quad (3.8)$$

Axiom 3.4 (Causality Condition). *The following requirement has great implication, and is also very successful in encoding our intuitive sense of “resolution”. 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.*

In other words, if $K(x_0, y_0; \sigma_0)$ is a local maximum (at the point (x_0, y_0) , at this fixed σ_0) i.e. then an increase in scale can only weaken this peak, i.e.

$$\begin{cases} \nabla K(x_0, y_0; \sigma_0) = 0 \\ \Delta K(x_0, y_0; \sigma_0) < 0 \end{cases} \implies K(x_0, y_0; \sigma_1) \leq K(x_0, y_0; \sigma_0) \forall \sigma_1 \geq \sigma_0 \quad (3.9)$$

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.

$$\begin{cases} \nabla K(x_0, y_0; \sigma_0) = 0 \\ \Delta K(x_0, y_0; \sigma_0) > 0 \end{cases} \implies K(x_0, y_0; \sigma_1) \geq K(x_0, y_0; \sigma_0) \forall \sigma_1 \geq \sigma_0 \quad (3.10)$$

This implies that no image feature is sharpened by an decrease and resolution—the only result is a monotonic blurring of the image as scale parameter σ tends to infinity.

Uniqueness of the Gaussian Kernel

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. (3.5) must hold. This has been shown in various ways, both by Koenderink [15], Babaud [18], as well as Lindeberg in [16]. In fact, it is shown that the Gaussian is the unique convolution kernel that works.

To this, show that:

- a kernel satisfying the above axioms must satisfy the heat equation
- the gaussian kernel satisfies that.
- gaussian kernel is the only kernel that works.

That is,

$$K(x, y; \sigma) = T_\sigma u_0 = G_\sigma \star u_0 \quad \text{where} \quad G_\sigma := \frac{1}{2\pi\sigma^2} e^{(-|x|^2/(2\sigma^2))} \quad (3.11)$$

We can show that this solution solves the heat equation. Given u_0 as a continuous image (unscaled), we construct PDE with this as a boundary condition.

$$u : \mathbb{R}^2 \supset \Omega \rightarrow \mathbb{R} \text{ with } u(\mathbf{x}, t) : \begin{cases} \frac{\partial u}{\partial t}(\mathbf{x}, t) = \Delta u(\mathbf{x}, t) & , t \geq 0 \\ u(\mathbf{x}, 0) = u_0(\mathbf{x}) \end{cases} \quad (3.12)$$

We show that

$$u(\mathbf{x}, t) = (G_{\sqrt{2t}} \star u_0)(\mathbf{x}) \quad (3.13)$$

solves (the above tagged equation), where

s

First, we need a quick lemma regarding differentiation a continuous convolution.

Lemma 3.1. *Derivative of a convolution is the way that it is (obviously rewrite this).*

Proof. For a single variable,

$$\frac{\partial}{\partial \alpha} [f(\alpha) \star g(\alpha)] = \frac{\partial}{\partial \alpha} \left[\int f(t)g(\alpha - t)dt \right] \quad (3.14)$$

$$= \int f(t) \frac{\partial}{\partial \alpha} [g(\alpha - t)] dt \quad (3.15)$$

$$= \int f(t) \left(\frac{\partial g}{\partial \alpha} \right) g(\alpha - t) dt \quad (3.16)$$

$$= f(\alpha) \star g'(\alpha) \quad (3.17)$$

By symmetry of convolution we can also conclude

$$\frac{\partial}{\partial \alpha} [f(\alpha) \star g(\alpha)] = f'(\alpha) \star g(\alpha)$$

If f and g are twice differentiable, we can compound this result to show a similar statement holds for second derivatives, and then, given the additivity of convolution, we may conclude

$$\Delta(f \star g) = \Delta(f) \star g = f \star \Delta(g) \quad (3.18)$$

□

Theorem 3.2. $u(\mathbf{x}, t) = (G_{\sqrt{2t}} \star u_0)(\mathbf{x})$ solves the heat equation.

Proof. We focus on the particular kernel

$$G_{\sqrt{2t}} = \frac{1}{4\pi t} e^{(-|\mathbf{x}|^2/(4t))}$$

Then

$$\frac{\partial u}{\partial t}(\mathbf{x}, t) = \frac{\partial}{\partial t} \left(G_{\sqrt{2t}}(\mathbf{x}, t) \star u_0(\mathbf{x}) \right) \quad (3.19)$$

$$= \frac{\partial}{\partial t} \left(G_{\sqrt{2t}}(\mathbf{x}, t) \right) \star u_0(\mathbf{x}) \quad (3.20)$$

$$= \frac{\partial}{\partial t} \left(\frac{1}{4\pi t} e^{(-|\mathbf{x}|^2/(4t))} \right) \star u_0(\mathbf{x}) \quad (3.21)$$

$$= \left[-\frac{1}{4\pi t^2} e^{(-|\mathbf{x}|^2/(4t))} + \frac{1}{4\pi t} \left(\frac{-|\mathbf{x}|^2}{4t^2} \right) e^{(-|\mathbf{x}|^2/(4t))} \right] \star u_0(\mathbf{x}) \quad (3.22)$$

$$= -\frac{1}{4t^2} \left(e^{(-|\mathbf{x}|^2/(4t))} + |\mathbf{x}|^2 G_{\sqrt{2t}}(\mathbf{x}, t) \right) \star u_0(\mathbf{x}) \quad (3.23)$$

and from the previous lemma,

$$\Delta u(\mathbf{x}, t) = \Delta \left(G_{\sqrt{2t}} \star u_0(\mathbf{x}) \right) = \Delta \left(G_{\sqrt{2t}} \right) \star u_0(\mathbf{x})$$

We explicitly calculate the Laplacian of $G_\sigma(x, y) = A \exp(-\frac{x^2+y^2}{2\sigma^2})$ as follows:

$$\begin{aligned} \frac{\partial}{\partial x} G_\sigma(x, y) &= A \left(\frac{-2x}{2\sigma^2} \right) \exp \left(-\frac{x^2+y^2}{2\sigma^2} \right) \\ \implies \frac{\partial^2}{\partial x^2} G_\sigma(x, y) &= A \cdot \frac{\partial}{\partial x} \left[-\frac{x}{\sigma^2} \exp \left(-\frac{x^2+y^2}{2\sigma^2} \right) \right] \\ &= A \left[-\frac{1}{\sigma^2} \exp \left(-\frac{x^2+y^2}{2\sigma^2} \right) + \frac{x}{\sigma^2} \cdot \frac{2x}{2\sigma^2} \exp \left(-\frac{x^2+y^2}{2\sigma^2} \right) \right] \\ &= A \exp \left(-\frac{x^2+y^2}{2\sigma^2} \right) \left[-\frac{1}{\sigma^2} + \frac{x^2}{\sigma^4} \right] \\ &= \frac{1}{\sigma^2} G_\sigma(x, y) \left[\frac{x^2}{\sigma^2} - 1 \right] \end{aligned}$$

By symmetry of argument we also may conclude

$$\frac{\partial^2}{\partial y^2} G_\sigma(x, y) = \frac{1}{\sigma^2} G_\sigma(x, y) \left[\frac{y^2}{\sigma^2} - 1 \right]$$

and so

$$\Delta G_\sigma(x, y) = \frac{\partial^2}{\partial x^2}(G_\sigma) + \frac{\partial^2}{\partial y^2}(G_\sigma) = \frac{1}{\sigma^2} G_\sigma(x, y) \left[\frac{x^2 + y^2}{\sigma^2} - 2 \right] \quad (3.24)$$

Then, given lemma 3.1, we conclude

$$\Delta [G_\sigma(x, y) \star u_0(x, y)] = \left(\frac{1}{\sigma^2} G_\sigma(x, y) \left[\frac{x^2 + y^2}{\sigma^2} - 2 \right] \right) \star u_0(x, y) \quad (3.25)$$

For particular choices of $\sigma(t) = \sqrt{2t}$ and $A = \frac{1}{4\pi t}$, we see

$$\Delta [G_{\sqrt{2t}}(x, y) \star u_0(x, y)] = \left(\frac{1}{2t} G_{\sqrt{2t}}(x, y) \left[\frac{x^2 + y^2}{2t} - 2 \right] \right) \star u_0(x, y) \quad (3.26)$$

$$= \left(G_{\sqrt{2t}}(x, y) \left[\frac{x^2 + y^2}{4t^2} - \frac{1}{t} \right] \right) \star u_0(x, y) \quad (3.27)$$

We then calculate the time derivative, using our particular choice of $\sigma(t) = \sqrt{2t}$ and

$A = \frac{1}{4\pi t}$ as:

$$\frac{\partial}{\partial t} [G_{\sigma(t)}(x, y) \star u_0(x, y)] = \frac{\partial}{\partial t} [G_{\sigma(t)}(x, y)] \star u_0(x, y) \quad (3.28)$$

$$= \frac{\partial}{\partial t} [G_{\sqrt{2t}}(x, y)] \star u_0(x, y) \quad (3.29)$$

$$= \frac{\partial}{\partial t} \left[\frac{1}{4\pi t} \exp \left(-\frac{x^2 + y^2}{4t} \right) \right] \star u_0(x, y) \quad (3.30)$$

$$= \left[-\frac{1}{4\pi t^2} \exp \left(-\frac{x^2 + y^2}{4t} \right) + \frac{1}{4\pi t} \left(\frac{x^2 + y^2}{4t^2} \exp \left(-\frac{x^2 + y^2}{4t} \right) \right) \right] \star u_0(x, y) \quad (3.31)$$

$$= \left(G_{\sqrt{2t}}(x, y) \left[\frac{x^2 + y^2}{4t^2} - \frac{1}{t} \right] \right) \star u_0(x, y) \quad (3.32)$$

Combining these results, we find that

$$\frac{\partial}{\partial t} [G_{\sqrt{2t}} \star u_0] = \Delta [G_{\sqrt{2t}} \star u_0] \quad (3.33)$$

as desired. \square

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 continuous surface definition 2.2, we might naively 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 3.1 (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

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

The reality of the matter is that a discretely sampled Gaussian is not an appropriate kernel for creating discrete scale space. In [19] and in particular [20], Lindeberg demonstrated that the sampled Gaussian kernel violates not only semigroup property (axiom 3.3), but—much less forgivably—the causality property (axiom 3.3). 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 3.4 and axiom 3.3:

Definition 3.2 (Discrete Gaussian Kernel). *The discrete Gaussian kernel, which can be shown to be a suitable generator for scale space, is given by*

$$T(n; \sigma) = e^{-\alpha\sigma} I_n(\alpha\sigma), \quad I_n(\sigma) = I_{-n}(\sigma) = (-1)^n J_n(i\sigma) \quad n \geq 0, \sigma, \alpha > 0 \quad (3.34)$$

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

$$K(x, \sigma) = \sum_{n=-\infty}^{\infty} T(n; \sigma) f(x-n) \quad \text{for } x \in \mathbb{Z}, t > 0 \quad (3.35)$$

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 central difference. Lastly, the 2D version of the family given in eq. (3.35) can be obtained by independent convolution of its dimensions (i.e. it is separable). We will make these ideas explicit in chapter 6 and the Appendix.

CHAPTER 4

THE FRANGI FILTER: A MULTISCALE APPROACH

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 our developments in section 3.1, we wish to probe at multiple scales regions that would receive a high vesselness score at any range, and consider them all together. Frangi [11] approached this problem by simply aggregating vesselness measure over all scales:

$$V(x_0, y_0) = \max_{\sigma \in \Sigma} V_\sigma(x_0, y_0) \quad (4.1)$$

where $\Sigma := \{\sigma_0, \sigma_1, \dots, \sigma_N\}$ is a range of parameters at which to probe. These should be chosen to be representative enough of all scales where meaningful content is expected to be found.

Thresholding

After this procedure, we are left with a matrix with as many samples/pixels as the original image, all with a vesselness measure between 0 and 1 for each pixel in the image:

$$V_\Sigma := [V(x, y)]_{0 \leq x < M, 0 \leq y < N} \quad (4.2)$$

Notably, Frangi [11] refrained from explicitly interpreting the probability assigned by eq. (4.1); that is—whether a particular point (x, y) in the image definitely a vessel or not. Instead, he cautioned that the result should not be used as a segmentation

method alone, and that the size of the vasculature cannot be determined rigorously from the filter alone.

However, for the purposes of obtaining an intermediate result, we wish to be final about the whole matter and ultimately say whether or not a pixel does in fact corresponds to a curvilinear structure. A straightforward enough approach is to simply threshold at some fixed value. The resulting matrix can be given in terms of either eq. (4.1) or eq. (4.2)

$$V_{\Sigma,\alpha}(x,y) = \begin{cases} 1 & \text{if } V(x,y) \geq \alpha \\ 0 & \text{else} \end{cases}, \quad \alpha > 0 \text{ for } \alpha \text{ fixed.} \quad (4.3)$$

We will discuss alternatives methods of aggregating results from our multiscale method, as well as optimal values for parameters and scales in chapter 6. As a final note, we admit that any future extensions of this work (as will be discussed in chapter 8) should not hold too much stock in this thresholded result, and analyzing the raw vesselness score eq. (4.2), or even the un-merged scale-wise scores, would be far more rewarding.

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.

Calculating the 2D Hessian

According to section 3.2.3, 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]. Specific implementation will be discussed in chapter 6.

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 chapter 6.

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:

$$f(t) = \sum_{-\infty}^{\infty} c_n e^{i \frac{2\pi n}{T} t}, \quad c_n = \frac{1}{T} \int_{-T/2}^{T/2} f(t) e^{-i \frac{2\pi n}{T} t} dt \quad (4.4)$$

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

$$F(\mu) := \mathcal{F}\{f(t)\} = \int_{-\infty}^{\infty} f(t) e^{i 2\pi \mu t} dt \quad (4.5)$$

An inverse transform will then recover our original signal:

$$f(t) = \mathcal{F}^{-1}\{F(\mu)\} = \int_{-\infty}^{\infty} F(\mu)e^{i2\pi\mu t}dt \quad (4.6)$$

Together, eq. (4.5) and eq. (4.6) 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 :

$$s_{\Delta T}(t) := \sum_{n=-\infty}^{\infty} \delta[t - n\Delta T], \quad \delta[t] = \begin{cases} 1, & t = 0 \\ 0, & t \neq 0 \end{cases} \quad (4.7)$$

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

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

$$\tilde{f}(t) = f(t)s_{\Delta T}(t) \quad (4.8)$$

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.

$$\tilde{F}(\mu) = \sum_{n=-\infty}^{\infty} f_n e^{-i2\pi\mu n\Delta T}, \quad f_n = \tilde{f}(n) = f(n\Delta T) \quad (4.9)$$

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

2D DFT Convolution Theorem .

Theorem 4.1 (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:

$$F(u, v) := \mathcal{D}\{f(x, y)\} = \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} f(x, y) e^{-2\pi i (\frac{ux}{M} + \frac{vy}{N})} \quad (4.10)$$

$$H(u, v) := \mathcal{D}\{h(x, y)\} = \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} h(x, y) e^{-2\pi i (\frac{ux}{M} + \frac{vy}{N})} \quad (4.11)$$

and given the convolution of the two functions

$$(f \star h)(x, y) = \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} f(m, n) h(x - m, y - n) \quad (4.12)$$

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

$$(f \star h)(x, y) = \mathcal{D}^{-1}\{MN \cdot F(u, v)H(u, v)\} \quad (4.13)$$

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

Proof.

$$(f \star h)(x, y) = \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} f(m, n)h(x-m, y-n) \quad (4.14)$$

$$= \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} \left(\sum_{p=0}^{M-1} \sum_{q=0}^{N-1} F(p, q) e^{2\pi i (\frac{mp}{M} + \frac{nq}{N})} \right) \left(\sum_{u=0}^{M-1} \sum_{v=0}^{N-1} H(u, v) e^{2\pi i (\frac{u(x-m)}{M} + \frac{v(y-n)}{N})} \right) \quad (4.15)$$

$$= \left(\sum_{u=0}^{M-1} \sum_{v=0}^{N-1} H(u, v) e^{2\pi i (\frac{ux}{M} + \frac{vy}{N})} \right) \left(\sum_{p=0}^{M-1} \sum_{q=0}^{N-1} F(p, q) \left(\sum_{m=0}^{M-1} e^{2\pi i (\frac{m(p-u)}{M})} \right) \left(\sum_{n=0}^{N-1} e^{2\pi i (\frac{n(q-v)}{N})} \right) \right) \quad (4.16)$$

$$= \left(\sum_{u=0}^{M-1} \sum_{v=0}^{N-1} H(u, v) e^{2\pi i (\frac{ux}{M} + \frac{vy}{N})} \right) \left(\sum_{p=0}^{M-1} \sum_{q=0}^{N-1} F(p, q) (M \cdot \hat{\delta}_M(p-u)) (N \cdot \hat{\delta}_M(q-v)) \right) \quad (4.17)$$

$$= \left(\sum_{u=0}^{M-1} \sum_{v=0}^{N-1} H(u, v) e^{2\pi i (\frac{ux}{M} + \frac{vy}{N})} \right) \cdot MNF(u, v) \quad (4.18)$$

$$= MN \cdot \sum_{u=0}^{M-1} \sum_{v=0}^{N-1} F(u, v) H(u, v) e^{2\pi i (\frac{ux}{M} + \frac{vy}{N})} \quad (4.19)$$

$$= MN \cdot \mathcal{D}^{-1} \{ FH \} \quad (4.20)$$

where

$$\hat{\delta}_N(k) = \begin{cases} 1 & \text{when } k = 0 \pmod{N} \\ 0 & \text{else} \end{cases} \quad (4.21)$$

□

Above, we make use of the following lemma

Lemma 4.2. Let j and k be integers and let N be a positive integer. Then

$$\sum_{n=0}^{N-1} e^{2\pi i \left(\frac{n(j-k)}{N} \right)} = N \cdot \hat{\delta}_N(j-k) \quad (4.22)$$

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

$$z^N - 1 = (z - 1)(z^{n-1} + \dots + z + 1) = (z - 1) \sum_{n=0}^{N-1} z^n. \quad (4.23)$$

thus giving us

$$0 = \left(e^{2\pi i(j-k)/N} - 1\right) \sum_{n=0}^{N-1} e^{2\pi i n(j-k)/N} \quad (4.24)$$

To prove the claim in eq. (4.22), 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. (4.22) 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. (4.24). 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. (4.21), 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:

$$F(\mu, \nu) = \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} f(x, y) e^{-i2\pi(\mu x/M + \nu y/N)} \quad (4.25)$$

$$= \sum_{x=0}^{M-1} e^{-i2\pi\mu x/M} \left[\sum_{y=0}^{N-1} f(x, y) e^{-i2\pi\nu y/N} \right] \quad (4.26)$$

$$= \sum_{x=0}^{M-1} e^{-i2\pi\mu x/M} \mathcal{F}_x\{f(x, y)\} \quad (4.27)$$

$$= \mathcal{F}_y\{\mathcal{F}_x\{f(x, y)\}\} \quad (4.28)$$

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

$$F(u) = \sum_{x=0}^{M-1} f(x) W_M^{ux}, \quad \text{where} \quad W_m := e^{-i2\pi/m} \quad (4.29)$$

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. (4.29) and split it into odd and even entries in the summation

$$F(u) = \sum_{x=0}^{2K-1} f(x) W_{2K}^{ux} \quad (4.30)$$

$$= \sum_{x=0}^{K-1} f(2x) W_{2K}^{u(2x)} + \sum_{x=0}^{K-1} f(2x+1) W_{2K}^{u(2x+1)} \quad (4.31)$$

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

$$W_{(2m)}^{(2n)} = e^{\frac{-i2\pi(2m)}{2m}} = e^{\frac{-i2\pi m}{n}} = W_m^n \quad (4.32)$$

$$W_m^{(u+m)x} = e^{\frac{-i2\pi(u+m)x}{m}} = e^{\frac{-i2\pi unx}{m}} e^{\frac{-i2\pi mx}{m}} = e^{\frac{-i2\pi ux}{m}} (1) = W_m^{ux} \quad (4.33)$$

$$W_{2m}^{(u+m)} = e^{\frac{-i2\pi(u+m)}{2m}} = e^{\frac{-i2\pi ux}{2m}} e^{-i\pi} = W_{2m}^u e^{-i\pi} = -W_{2m}^u \quad (4.34)$$

Thus we can rewrite eq. (4.31) as

$$F(u) = \sum_{x=0}^{K-1} f(2x) W_{2K}^{2ux} + \sum_{x=0}^{K-1} f(2x+1) W_{2K}^{2ux} W_{2K}^u \quad (4.35)$$

$$\implies F(u) = \left(\sum_{x=0}^{K-1} f(2x) W_K^{ux} \right) + \left(\sum_{x=0}^{K-1} f(2x+1) W_K^{ux} \right) W_{2K}^u \quad (4.36)$$

The major advance comes via using the identities eq. (4.32) to consider the

Fourier transform K frequencies later :

$$F(u+K) = \left(\sum_{x=0}^{K-1} f(2x) W_K^{(u+K)x} \right) + \left(\sum_{x=0}^{K-1} f(2x+1) W_K^{(u+K)x} \right) W_{2K}^{(u+K)} \quad (4.37)$$

$$\implies F(u+K) = \left(\sum_{x=0}^{K-1} f(2x) W_K^{ux} \right) - \left(\sum_{x=0}^{K-1} f(2x+1) W_K^{ux} \right) W_K^u \quad (4.38)$$

Comparing eq. (4.36) and eq. (4.38), 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:

$$\mathcal{D}_u\{f_{\text{even}}(t)\} := \sum_{x=0}^{K-1} f(2x) W_K^{ux} \quad (4.39)$$

$$\mathcal{D}_u\{f_{\text{odd}}(t)\} := \sum_{x=0}^{K-1} f(2x+1) W_K^{ux} \quad (4.40)$$

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. (4.39) 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. (4.39) 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. (4.25).

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.

CHAPTER 5

RESEARCH PROTOCOL

Samples / Image Domain

We ultimately perform a multiscale Frangi filter to estimate the PCSVN from a subset of 201 color placental images 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. 6.

Each layer is roughly 1954x1200 pixels (with some occasional variation). In fig. 6a, a cleaned, fixed placenta is placed on a table with a camera a fixed distance away, and a ruler and penny (presumably for redundancy) to aid registration and calibration of the resolution. fig. 6b 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. 6c and fig. 6d are both 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. 6e. The 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

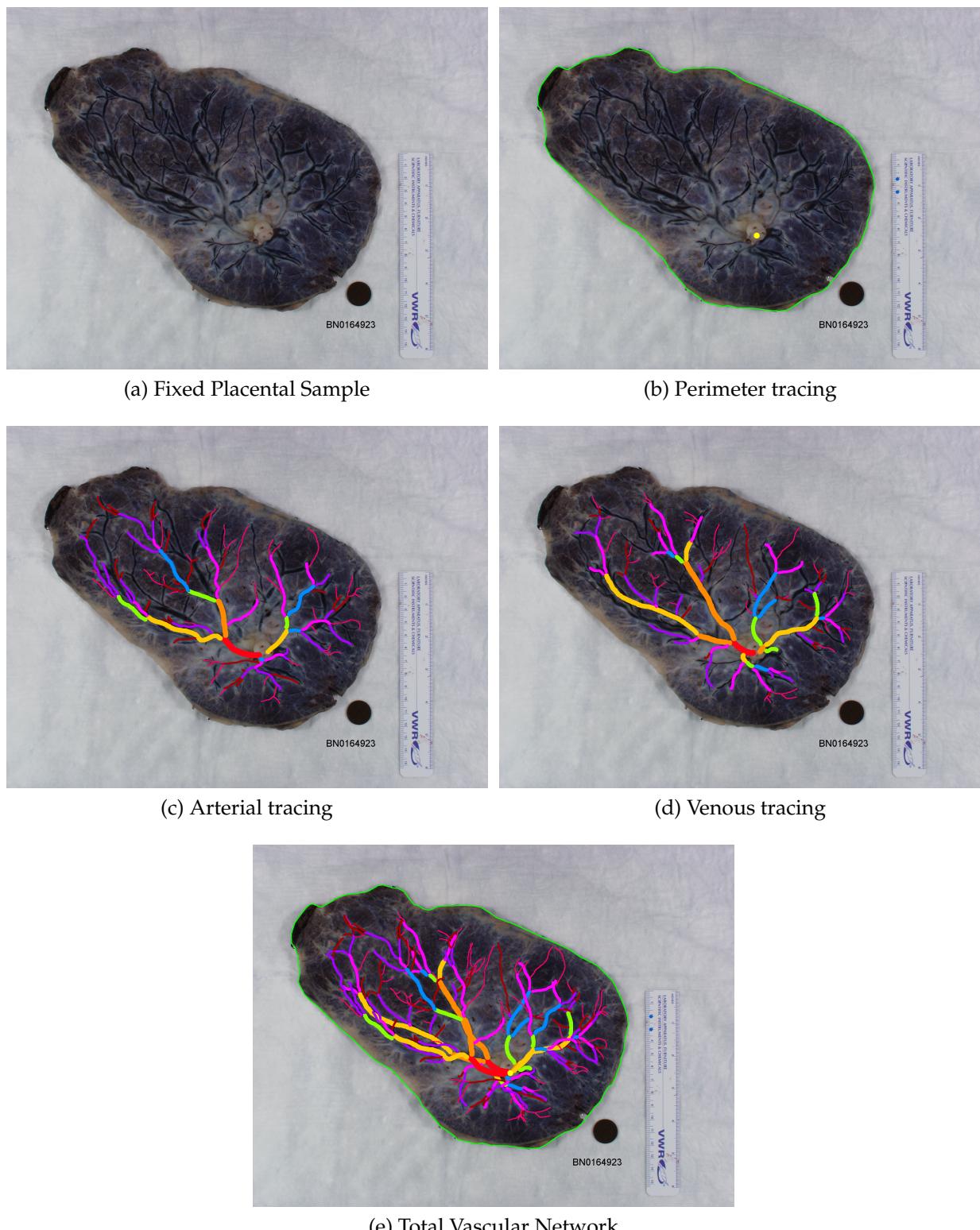


FIGURE 6: A representative placental sample and tracing

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 1: Vessel width color code

diameter are either binned to three or (quite frequently) left untraced. The correspondence between pencil color and (binned) vessel width is given in table 1.

All in all, these hand-traced and rather 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 our results section, where we will discuss methods to simulate the subjectivity of decision.

Knowns and Unknowns

Of course, 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. 6e or fig. 7d without any user intervention.

For our purposes however, we will use a limited amount of information from the tracings, namely the provided placental perimeter (shown in green in fig. 6). 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 as in [2]. We leave that for future work. We do use the traced placental perimeter at our own peril, however, since often there are tears in the side of the plate or large amounts of non-vascular content with large changes in height that are not adequately accounted for in the perimeter tracing.

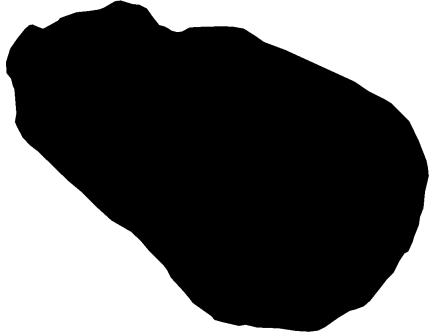
Finally, we will consider the location of the umbilical insertion point as a “known”, as the vessels around it are frequently impossible to see and we wish to exclude them from consideration. It is not unreasonable, however, to consider this to be a known—in future preparations of samples, we could simply 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. 6 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. Our preprocessed samples used by the algorithm are given in section 5.2.

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.

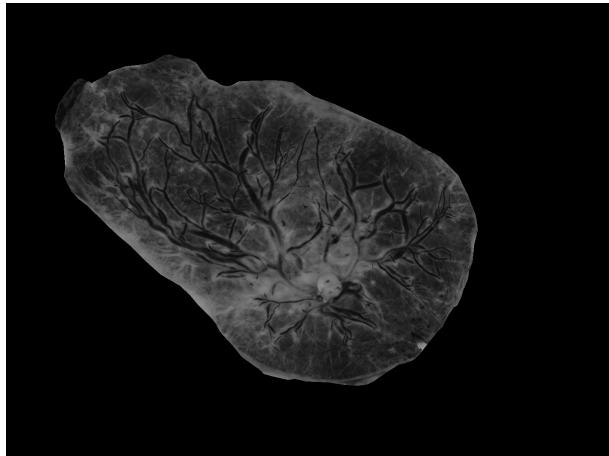
As a point of technicality, the grayscale image in fig. 7c is not actually produced directly by the extractor plug-in, but created when the 3 channel RGB image fig. 7b is



(a) Background Mask (in white)



(b) Sample with BG removed



(c) Grayscale



(d) Trace / “Ground Truth”

FIGURE 7: Preprocessed files from an NCS sample

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 [11], 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:

$$L = \frac{299}{1000} R + \frac{587}{1000} G + \frac{114}{1000} B \quad (5.1)$$

It should be noted that this choice is not automatic—several other attempts have used the green channel unmodified, as in [4] and [2].

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 performs 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 adjacent areas from consideration. This excluding function, `plate_morphology.dilate_plate`, ultimately relies on two functions provided by the Python library `scikit-image` [27]. The first, `skimage.segmentation.find_boundaries()`, takes the mask input (such as fig. 7a) and calculates where differences in a morphological erosion and dilation occur (which should have the same effect as using the perimeter labeled in fig. 6b directly, though we’ve chosen to not include that in our sample). That boundary itself is then dilated by the desired factor. The second is a much quicker implementation of binary dilation that is particularly efficient for our problem: we iterate through an array of

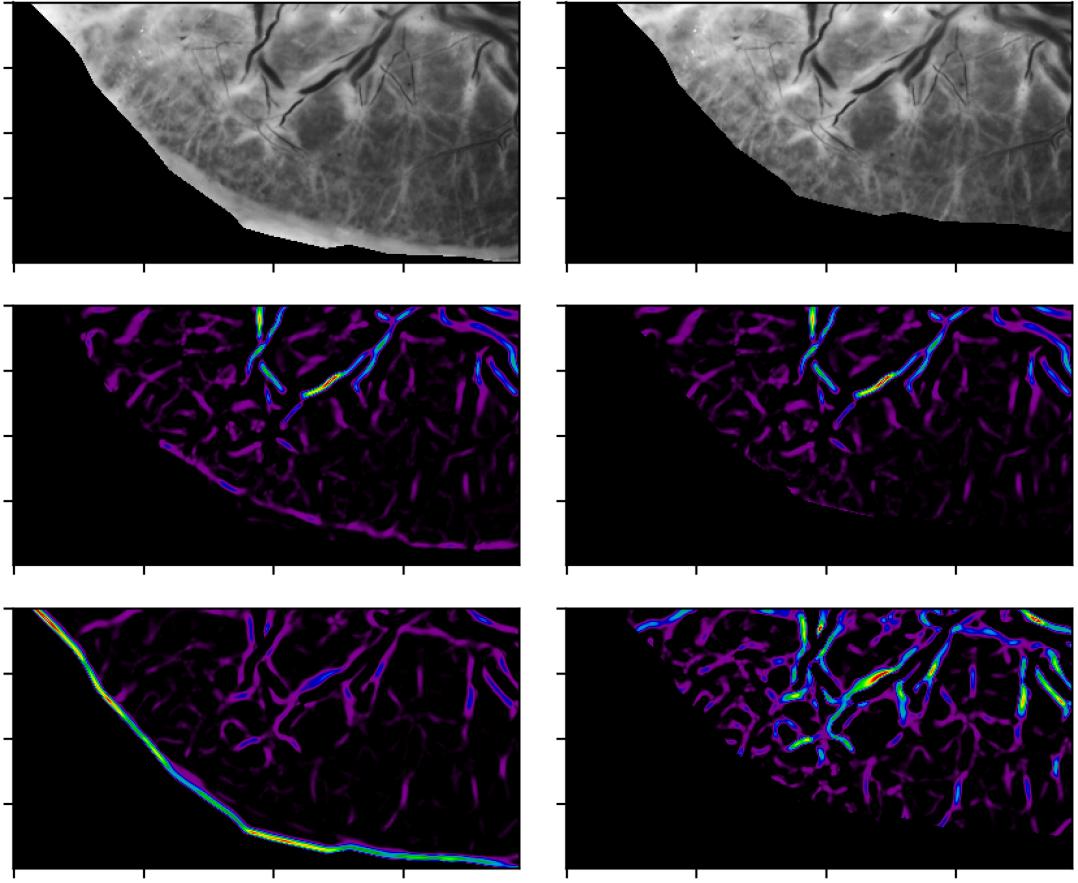


FIGURE 8: Effect of boundary dilation on Frangi responses

indices for the image where the boundary occurs and simply extend the mask R pixels in each direction (like a giant plus scale). Since these pixels are all connected, the effect is very similar to convolving with a disk of radius R , but is much faster.

fig. 8 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. 8 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 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.

The code for generating fig. 8 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.

Cut Removal

Sometimes there are small cuts that appear on the side of the placental plate, which can lead to large filter responses. We would like to filter these out to eliminate false positives in any way we can. These places are identified somewhat reliably by the tracing protocol with a blue dot. We perform a morphological watershedding in this area in an attempt to add this area to the mask. The threshold for the watershed is ultimately

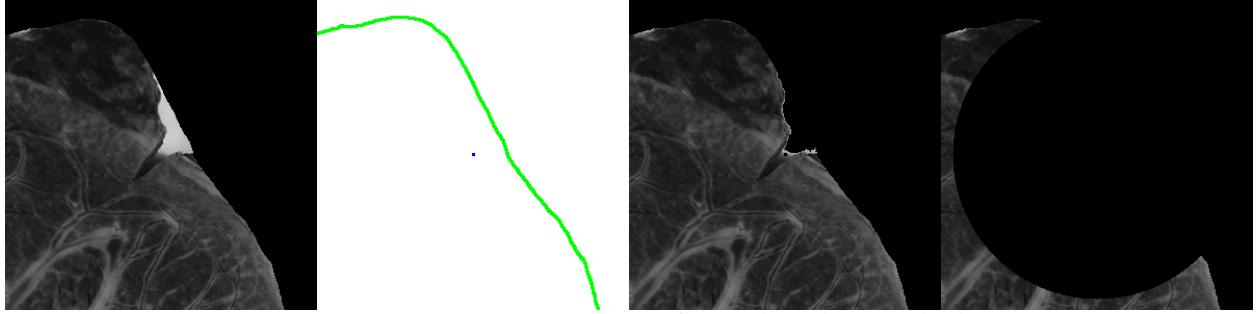


FIGURE 9: Removing a “cut” from the placental plate.

based on the background value of the blue dot; if this is incorrectly placed (or anything else weird happens), we can manually opt to simply remove a large area from consideration from the plate, as we do the umbilical cord insertion point. This is demonstrated in fig. 9. From left to right, we have the original masked placental sample, the cut mark noted on the perimeter layer, the improved mask after watershedding, and finally, the “scorched earth” approach in case the previous attempt failed. In few additional cases, neither approach is adequate. We again will stress that a fully automated algorithm would have no knowledge of our traced perimeter (as in fig. 6b or the second from left image in fig. 9), so we anticipate a fully automated method of handling that problem should also be able to correct for these “cuts” as well.

Deglaring

Despite best efforts when harvesting samples, some placental images have 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, at the expense of processing time.

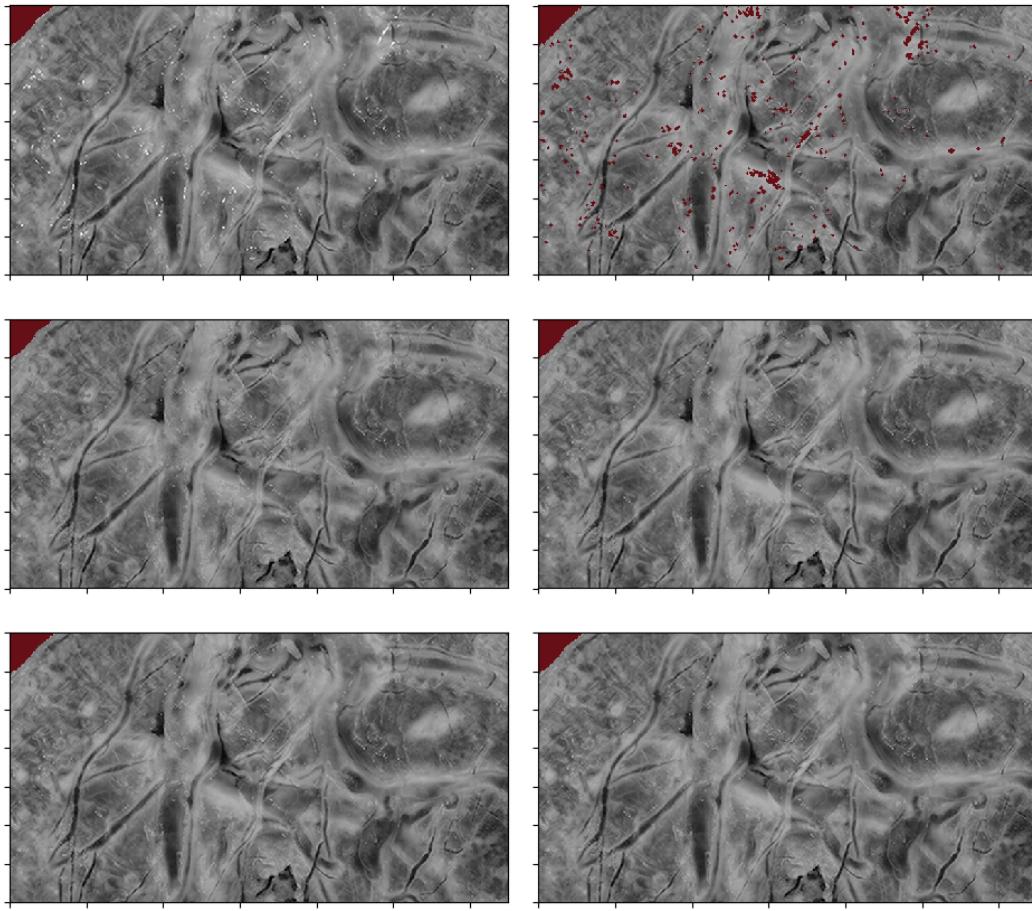


FIGURE 10: Deglaring a sample using a hybrid inpainting method

The function `inpaint_biharmonic` is based on [28], 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 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

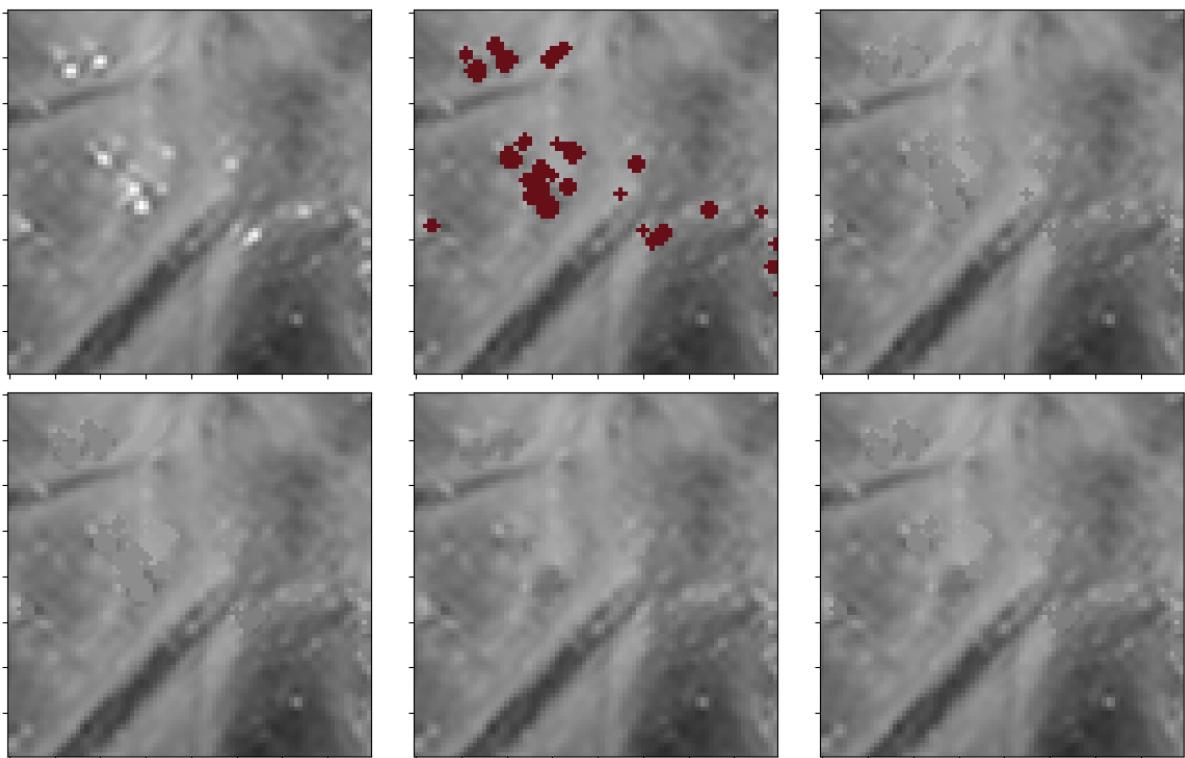


FIGURE 11: Comparison of glare inpainting methods (detail)

regions of glare. can be found in `preprocessing.py`. The first, called `inpaint_glare()` (change this name) 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. 10, and a zoomed in portion is shown in fig. 11. 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 [29] that is 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 list of scales is denoted as $\Sigma := \{\sigma_1, \sigma_2, \dots, \sigma_N\}$.

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 [11], 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 [15], it is reasonable and natural to select these logarithmically; that is, for some selected inputs $m < M$ we have

$$\sigma_1 = 2^m, \sigma_j = 2^{(m + \frac{M-m}{N-1}j)}, \sigma_N = 2^M \quad (5.2)$$

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 $\sigma = 2$, there will probably not be not be a substantial difference in response between, say, $\sigma = 46$ and $\sigma = 47$. Historically, there was another benefit of using a logarithmic scale spice: 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.

If there is no particular care taken in selecting a minimum and maximum range at which to probe, then we should assure that there is no noise being introduced at either ends, especially if the Frangi filter at which “throw out” bad ones somehow. We will approach this issue in our discussion of “variable thresholding.” Our final remark is that this choice of scale size is intuitively dependent on the resolution of the image.

Once we have this chosen set 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 take its eigenvalues and then compute the Frangi filter according to section 3.1 and chapter 4. 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.

```
% DECISION TREE
For each sample:
```

- A) Preprocessing
 - 1) RGB to single channel
 - + Luminance transform
 - . Isolate green channel only (Almoussa, Huynh)
 - 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, Hy
    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

```

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

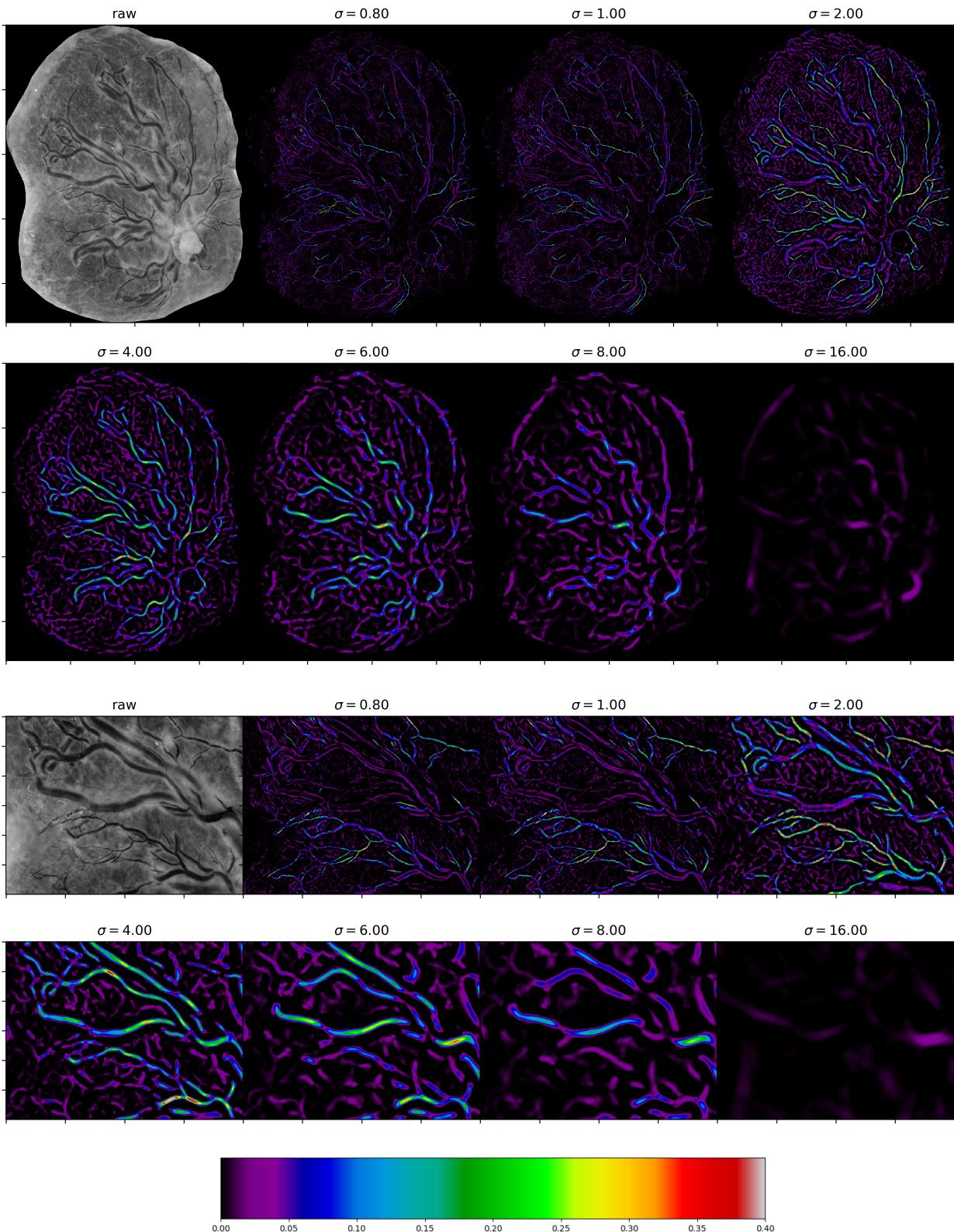


FIGURE 12: Signed Frangi output (plate and inset) (Example 1)

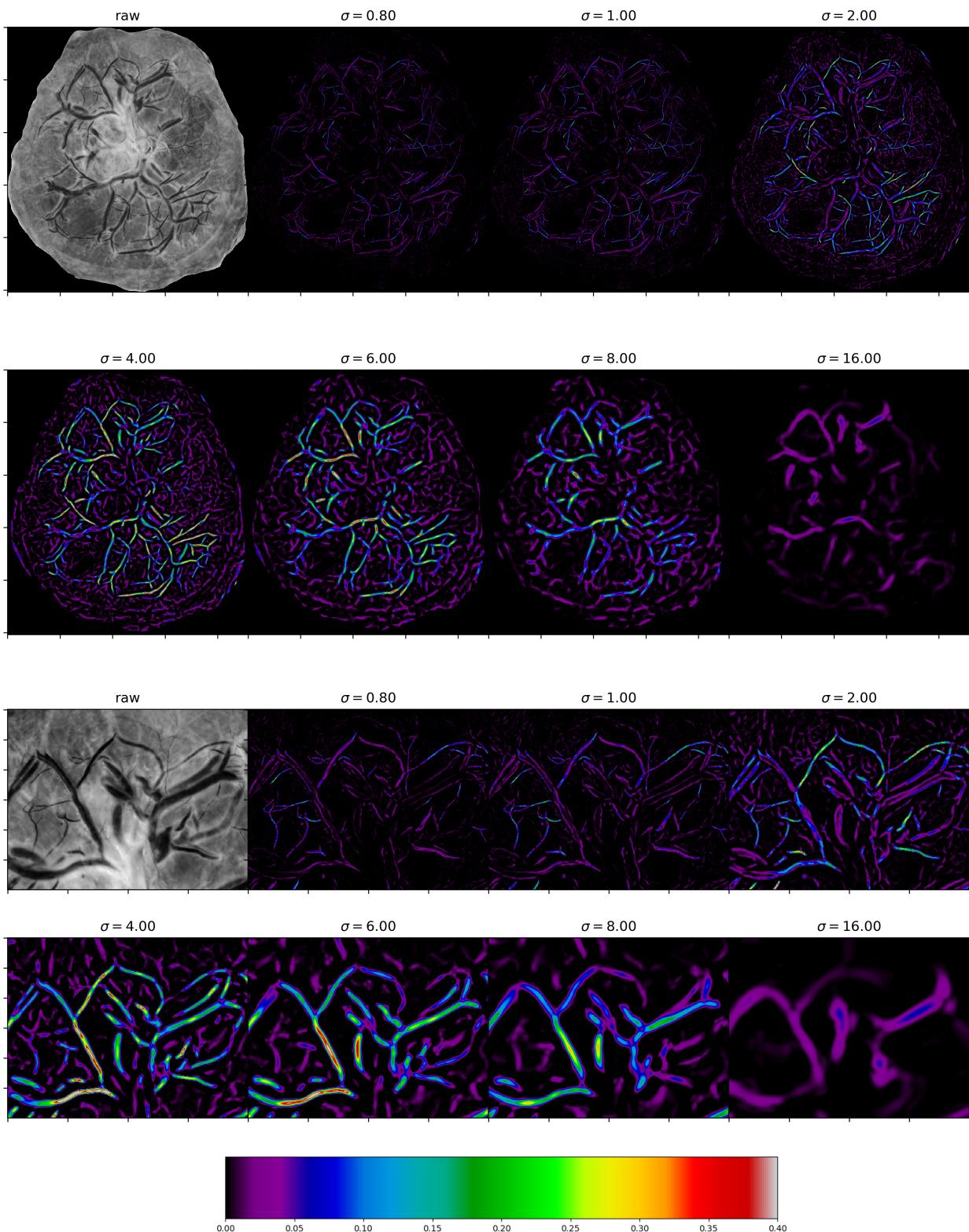


FIGURE 13: Signed Frangi output (plate and inset) (Example 1)

CHAPTER 6

IMPLEMENTATIONS

Calculating the Hessian via FFT

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. 14, 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. 15, 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 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

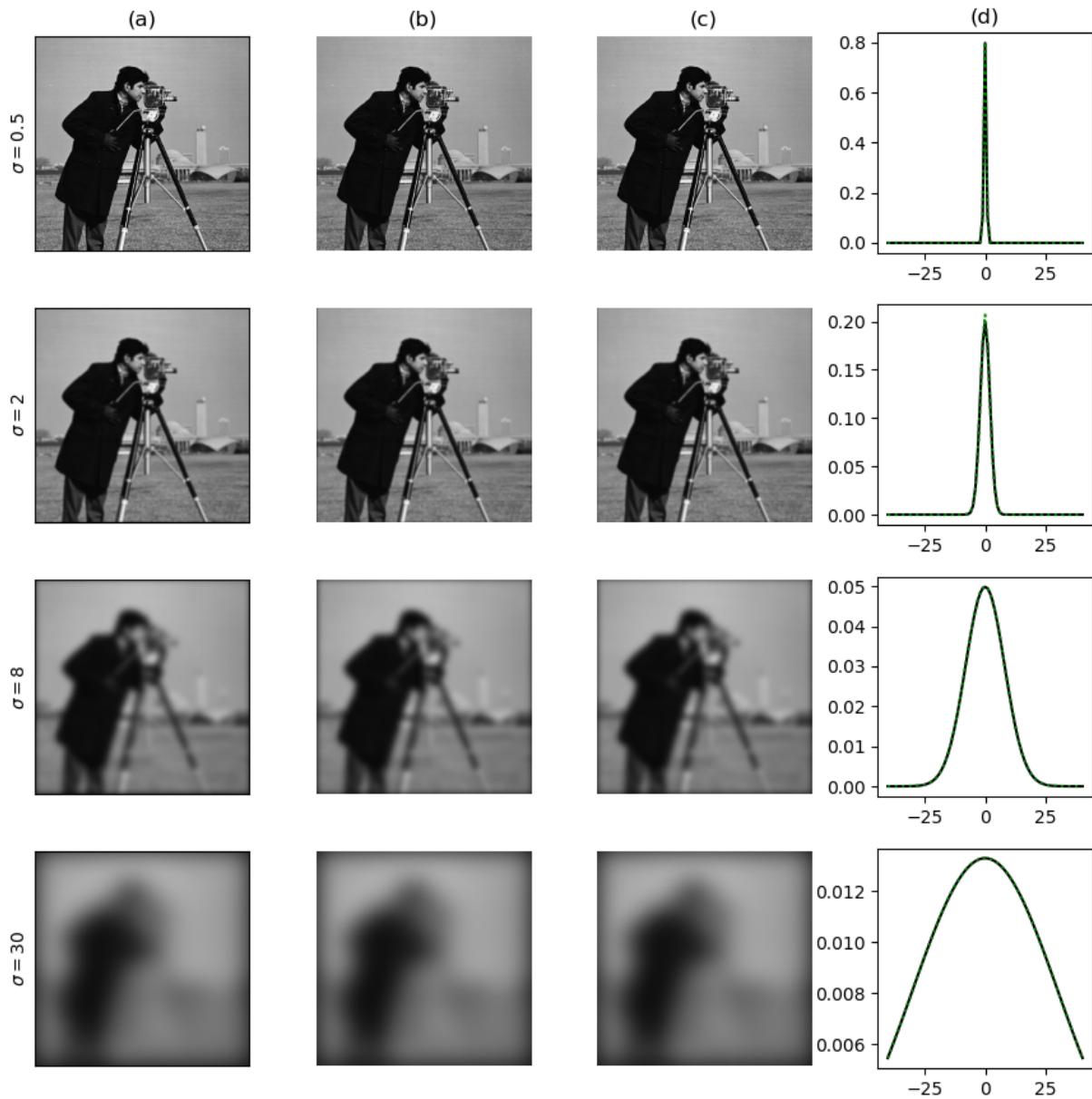


FIGURE 14: Compatibility of Gaussian convolution strategies

blurring method	MSE	MAE
spatial convolution, sampled kernel	0.00054426	0.02015643
FFT convolution, sampled kernel	0.00055205	0.02029916
FFT convolution, discrete kernel	0.00054406	0.02015336

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

TABLE 2: MSE of Gaussian blurs ($\sigma = 0.3$) **TABLE 3:** MSE of Frangi scores $\sigma = 0.3$

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

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).

We could show this again with a zero border or maybe even just a 1D signal.

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 2, table 3, table 4 and table 5 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. 16, fig. 17, fig. 18, fig. 19, 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.

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

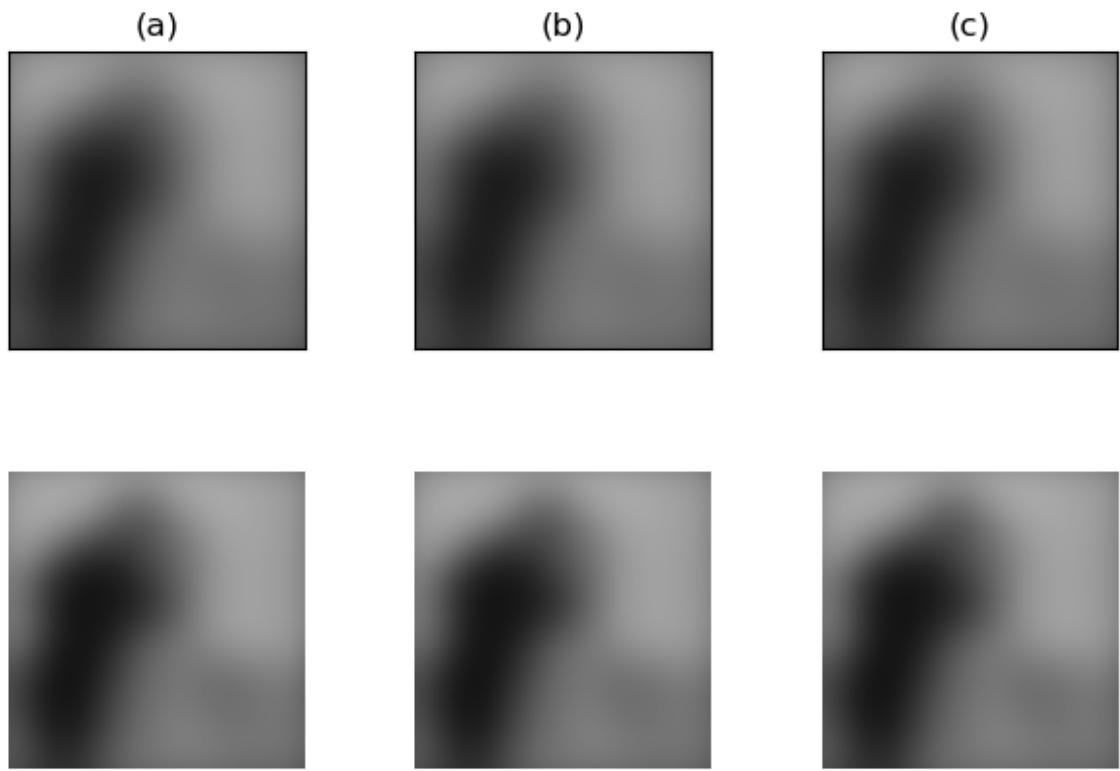


FIGURE 15: Iterative Gaussian blur

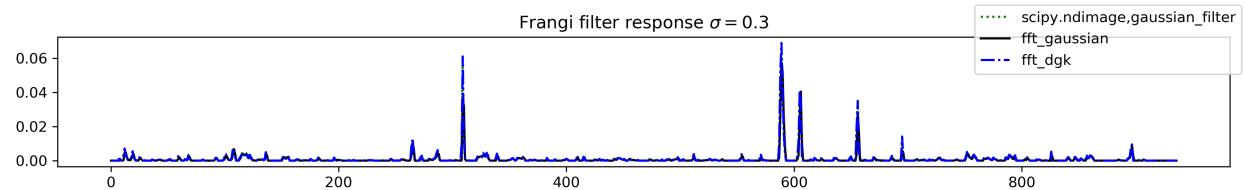


FIGURE 16: Image cross-section of Gaussian blurred images

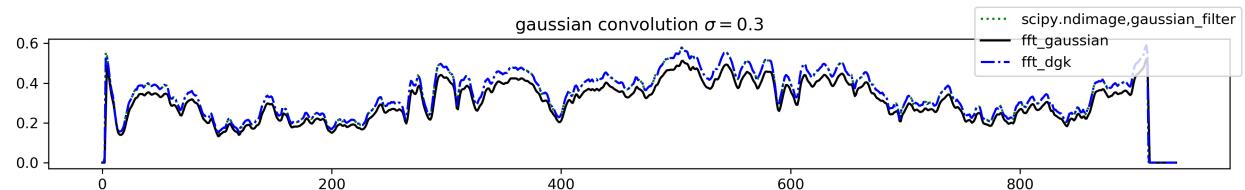


FIGURE 17: Image cross-section of Frangi targets images

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

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

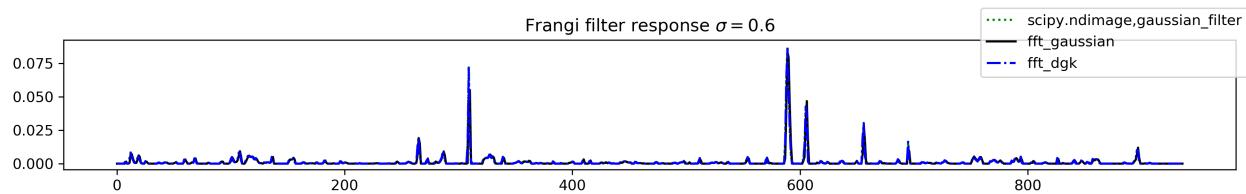


FIGURE 18: Image cross-section of Gaussian blurred images $\sigma = 5$

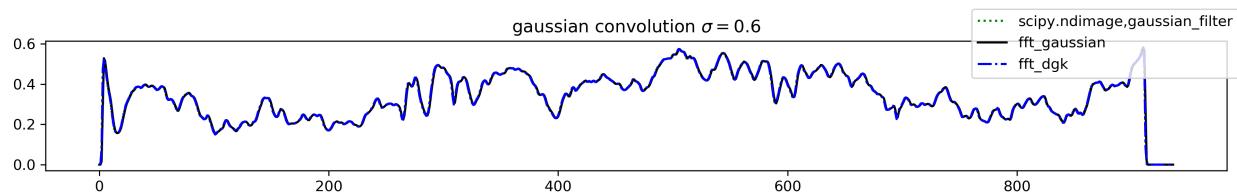


FIGURE 19: Image cross-section of Frangi targets images $\sigma = 5$

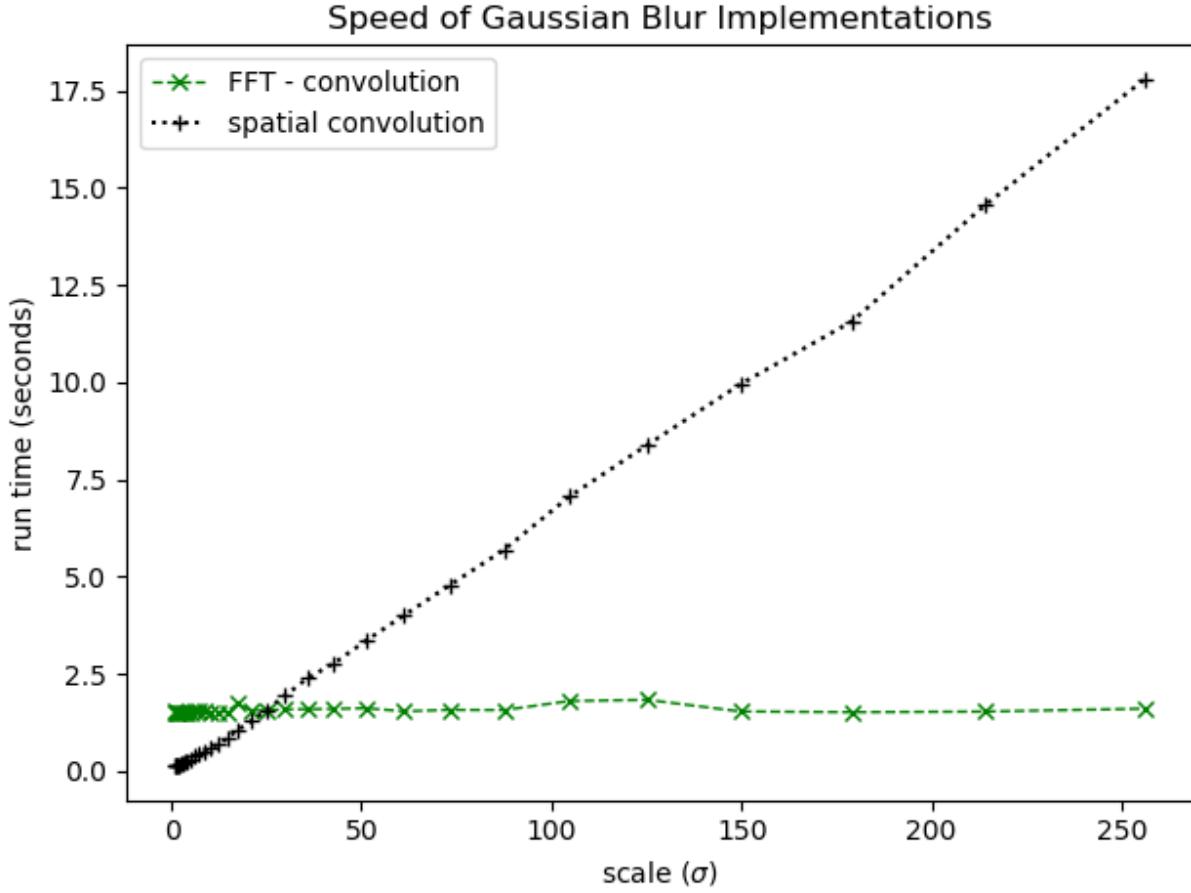


FIGURE 20: Time required

(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.

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 [11] refrained from any explicit

analysis of the Frangi score apart from taking the maximum across all scales, as in eq. (4.1). Still, we wish to demonstrate some several immediate methods of postprocessing these samples in order to illustrate the usefulness of this optimized Frangi filter.

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 bounds where structure is expected to be found. Ideally we could create a filter that would do that.

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.

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 bolster 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 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} .

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. 22. 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. 22 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 7, 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 coefficient (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.

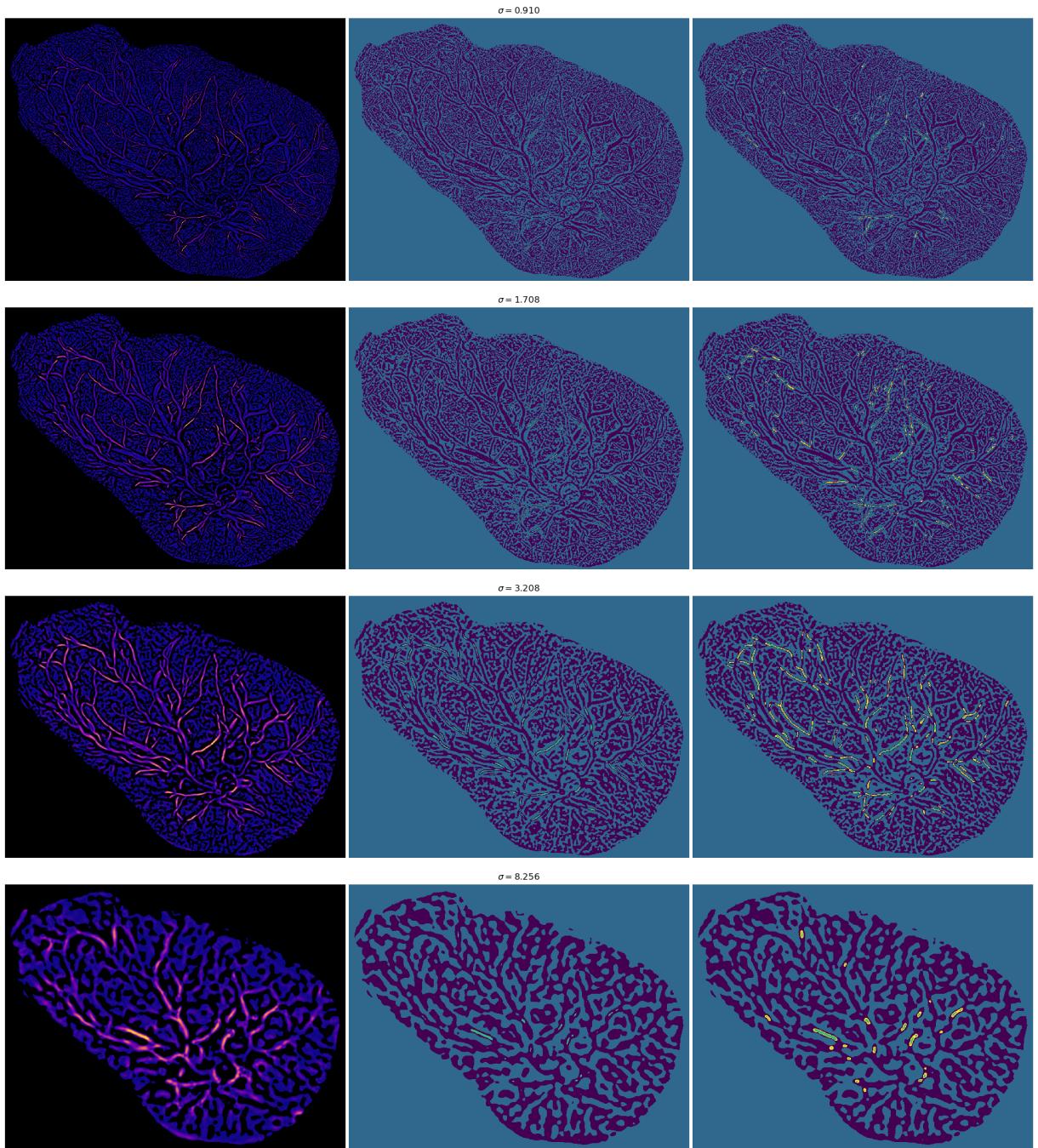


FIGURE 21: Scale-wise random walker segmentation (select scales)



FIGURE 22: Random walker segmentation (result and sample)

CHAPTER 7

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 $\beta = .35$ and $\gamma = 0.5$, 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.

Sample visual output

In fig. 23 and fig. 24 we take a partial look at the Frangi output for two particularly well-behaved samples. In the top-left, the preprocessed placenta is shown. In the top-right, the maximum of the Frangi output over N scales. The bottom left and right images are simple segmentation strategies of merging the result.

Binary Classifications and the confusion matrix

Here, we demonstrate the visual outputs produced by `extract_NCS_pcsvn.py`. This particular sample, BN4569506, is a relatively well-behaved sample, and segmentation was comparatively successful.

There are use MCC [31]

Variations in the Data Set and Imperfections of the Ground Truth

Sometimes the output doesn't agree with the trace, i.e. "the ground truth" is not 100% correct. sometimes either there's a false negative (reported) but something just wasn't traced in the original 1602443.

As seen in fig. 26, 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

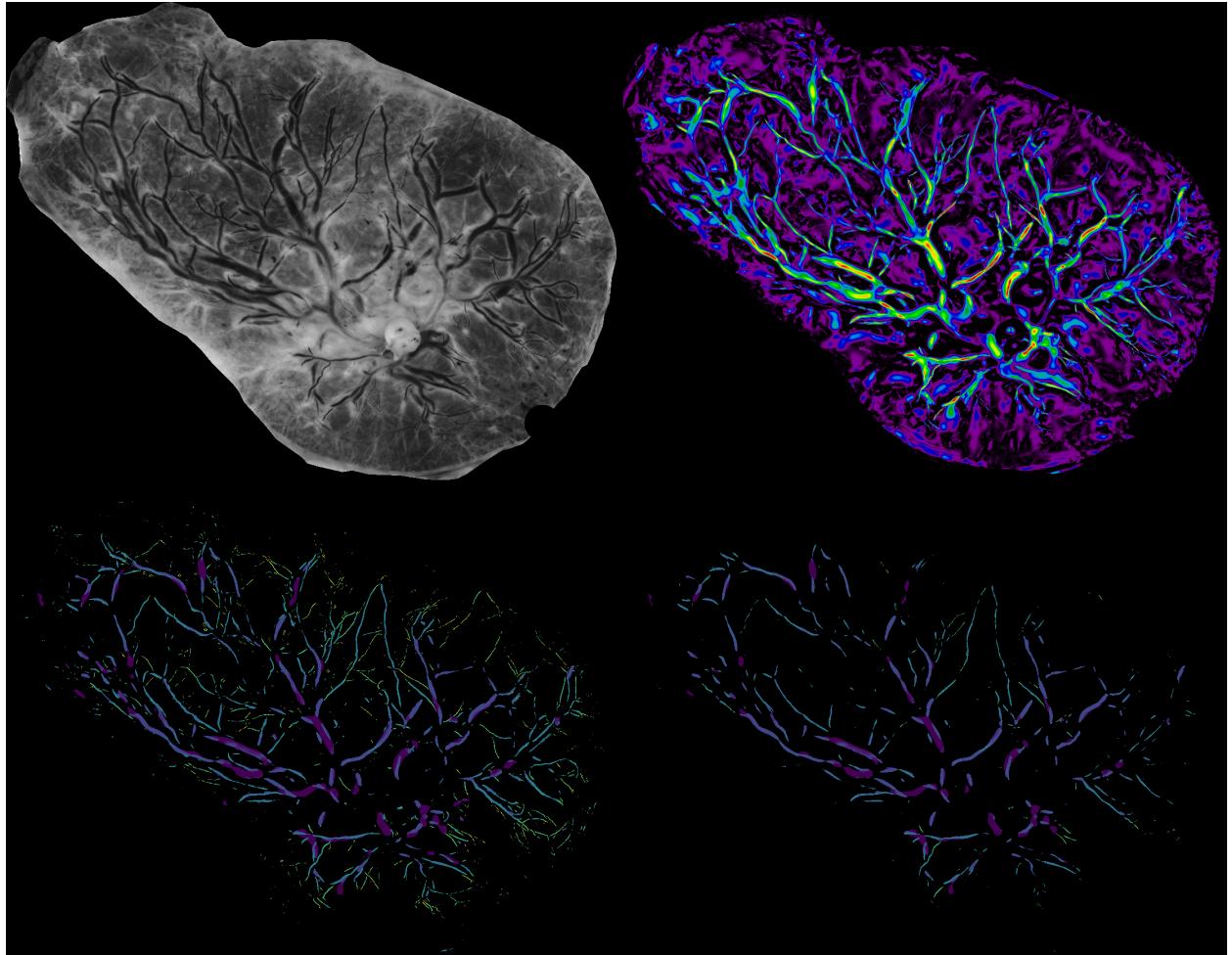


FIGURE 23: Sample Multiscale Frangi output ($\beta = 0.35$) with simple segmentation strate-
gies (Example 1)

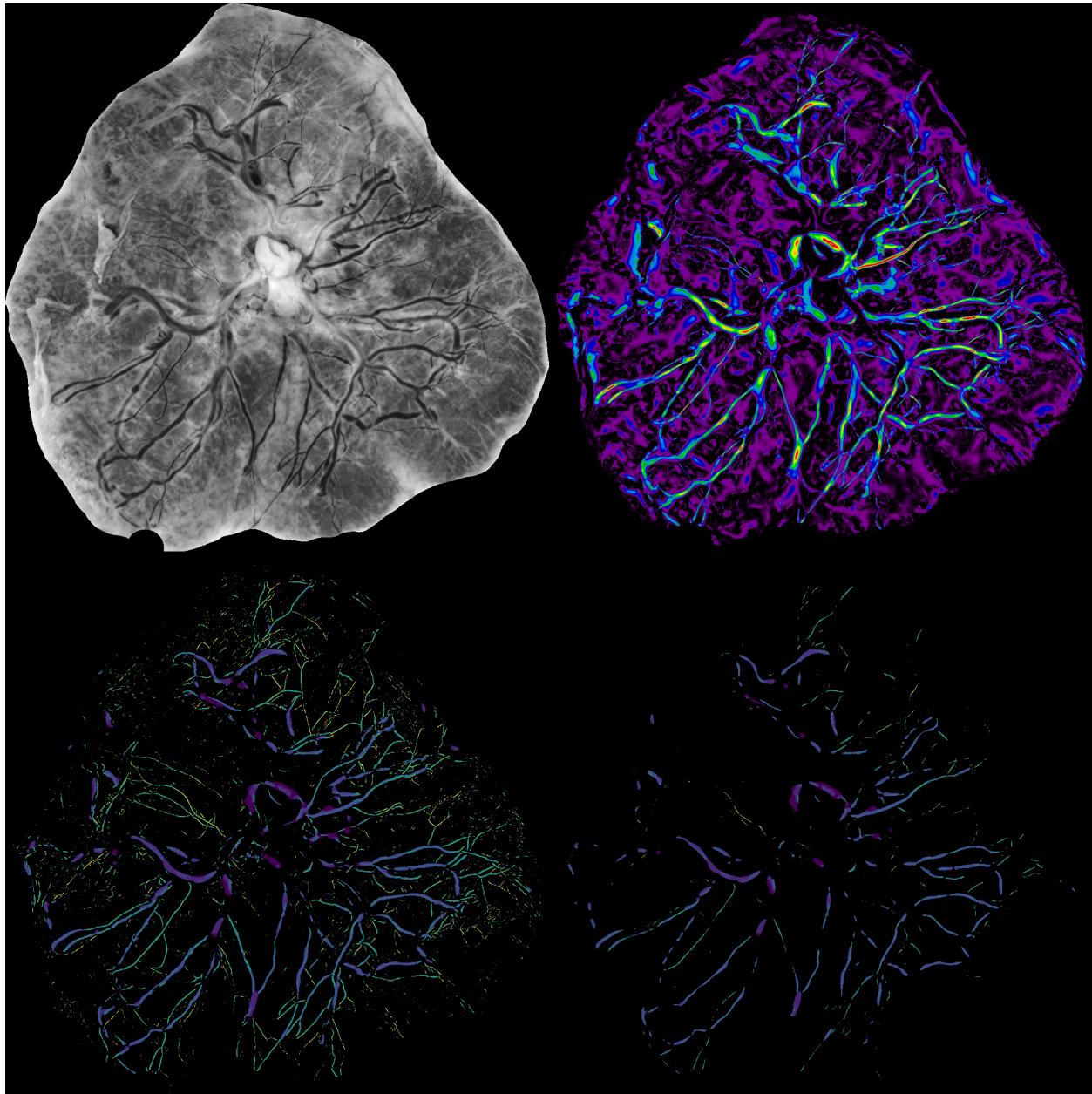


FIGURE 24: Sample Multiscale Frangi output ($\beta = 0.35$) with simple segmentation strategies (Example 2)

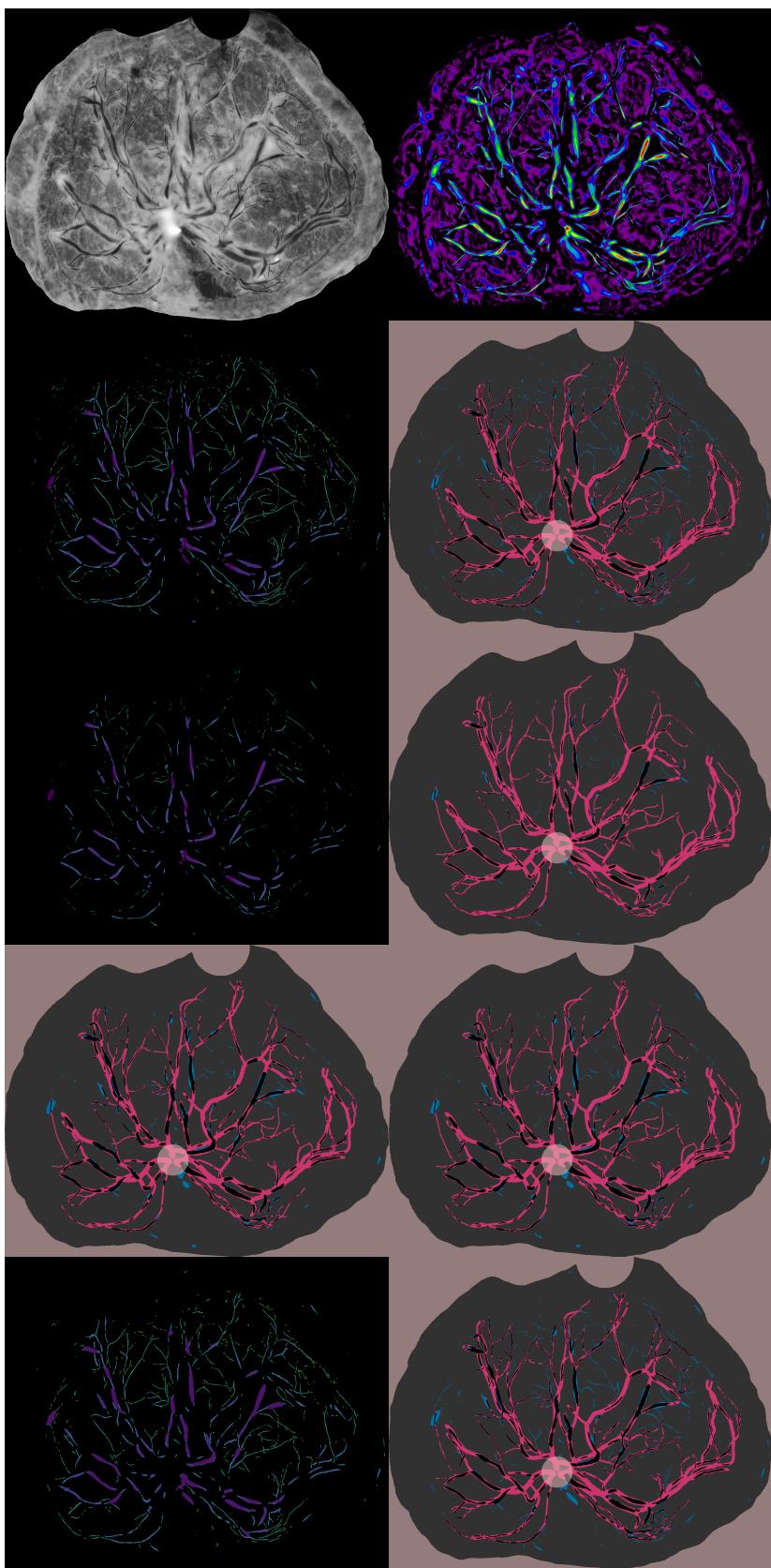


FIGURE 25: Demonstration of postprocessing techniques
85

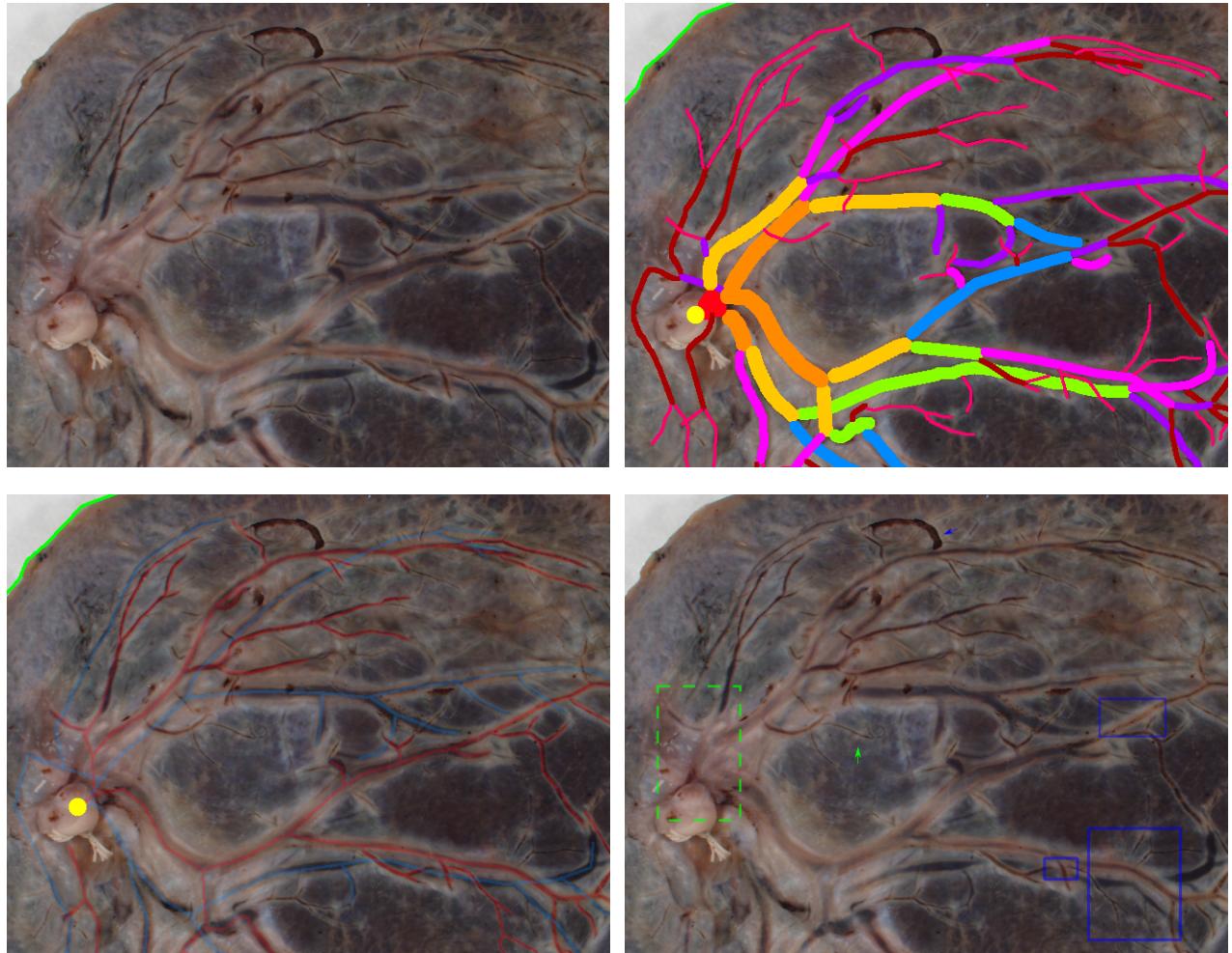


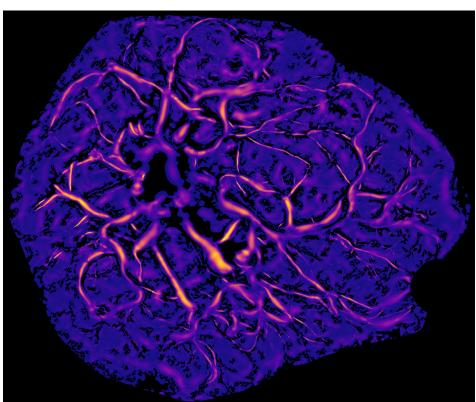
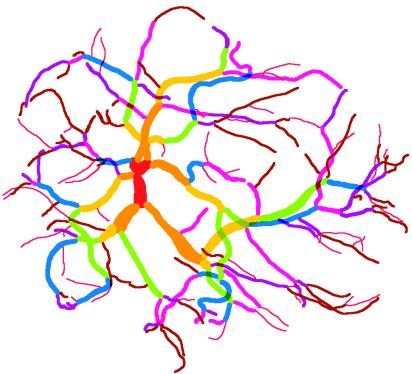
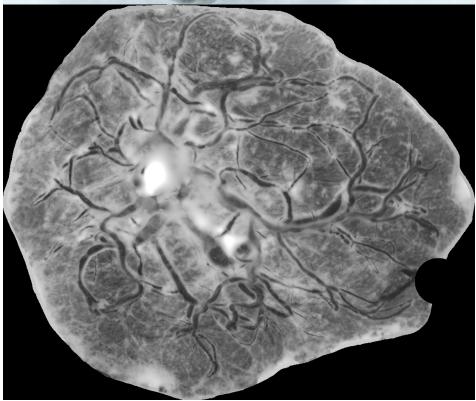
FIGURE 26: Issues with ground truth and sample quality

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.

Results



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 27: Vesselness scores and percentile thresholds

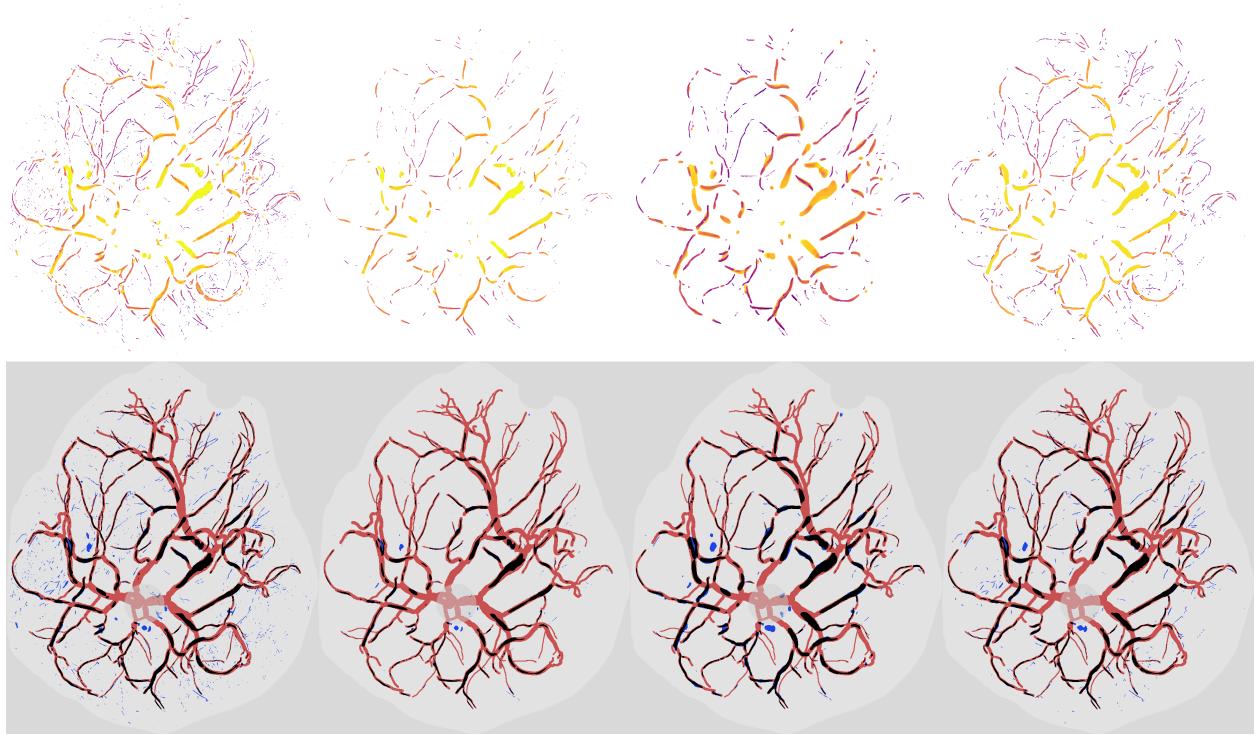


FIGURE 28: Sample of Frangi-based Segmentation Methods (pt. 2)

	PF	FA	RW	PS
MCC	0.4872	0.4208	0.5249	0.4877
skel coverage	0.5085	0.3245	0.4493	0.4650
precision	0.8044	0.9472	0.8858	0.8697

TABLE 6: Scores for merging techniques

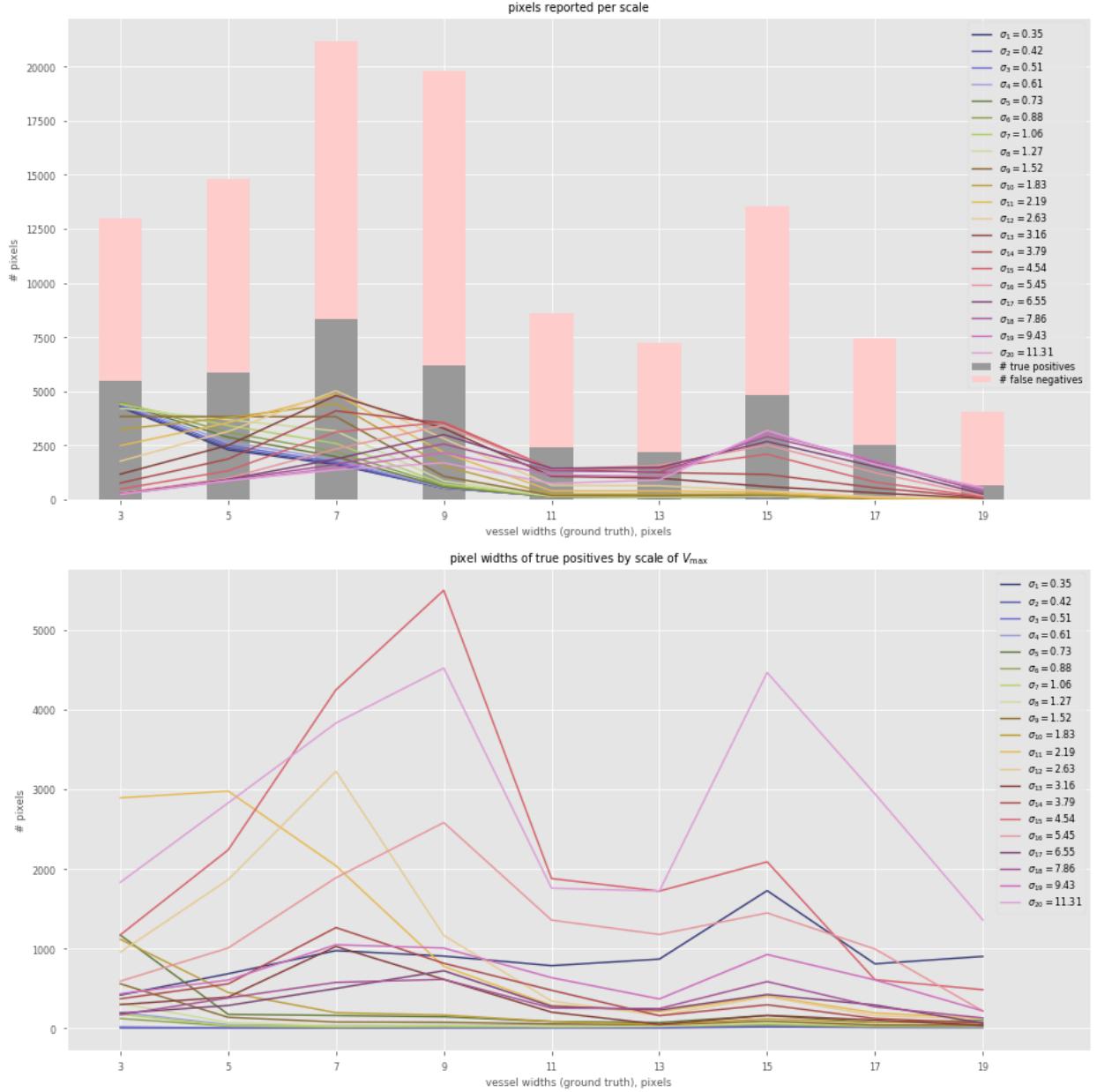


FIGURE 29: Pixel Width of Ground Truth vs. Scale Length for True Positives

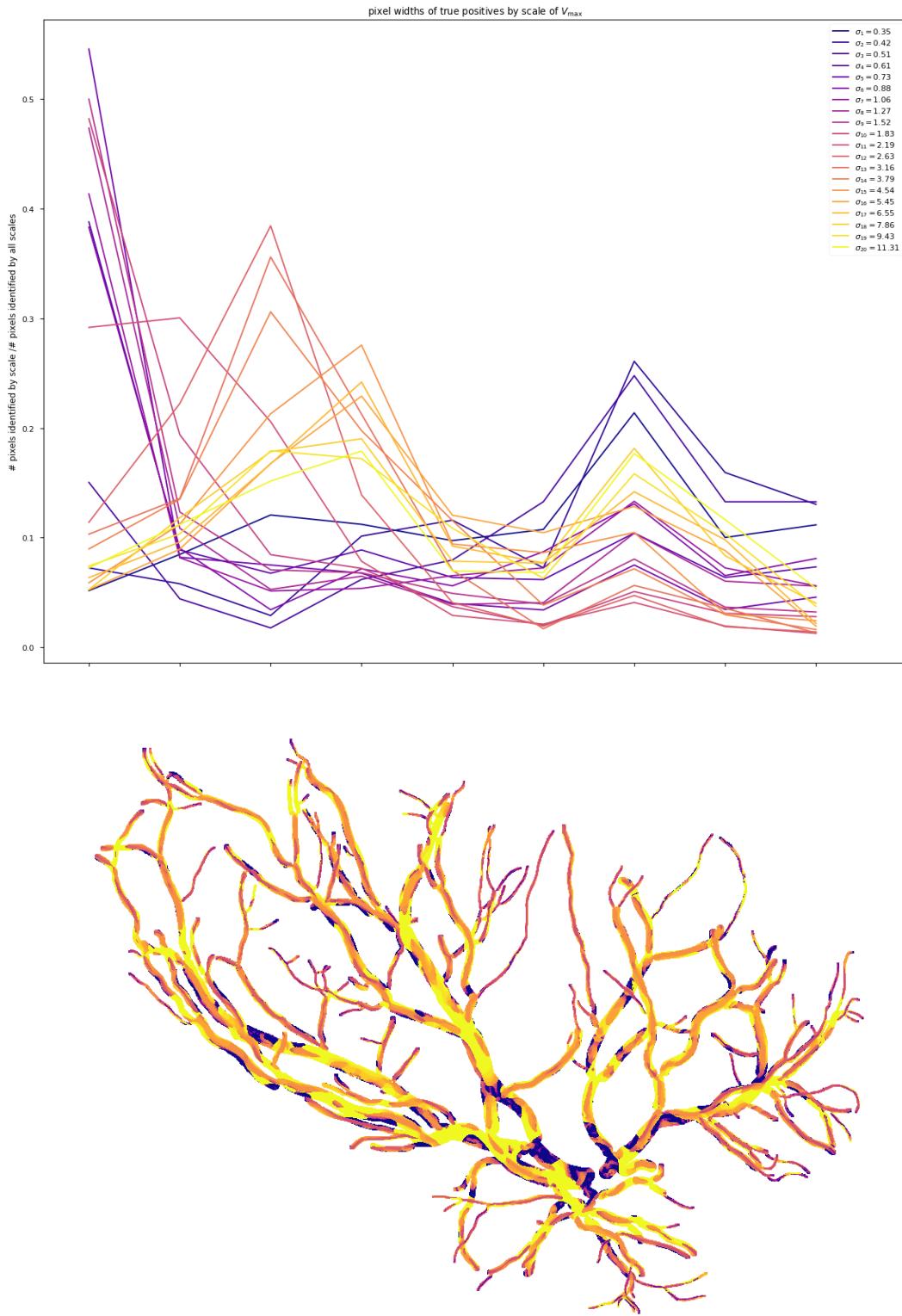


FIGURE 30: Scale of maximum Frangi score for true positives and false negatives

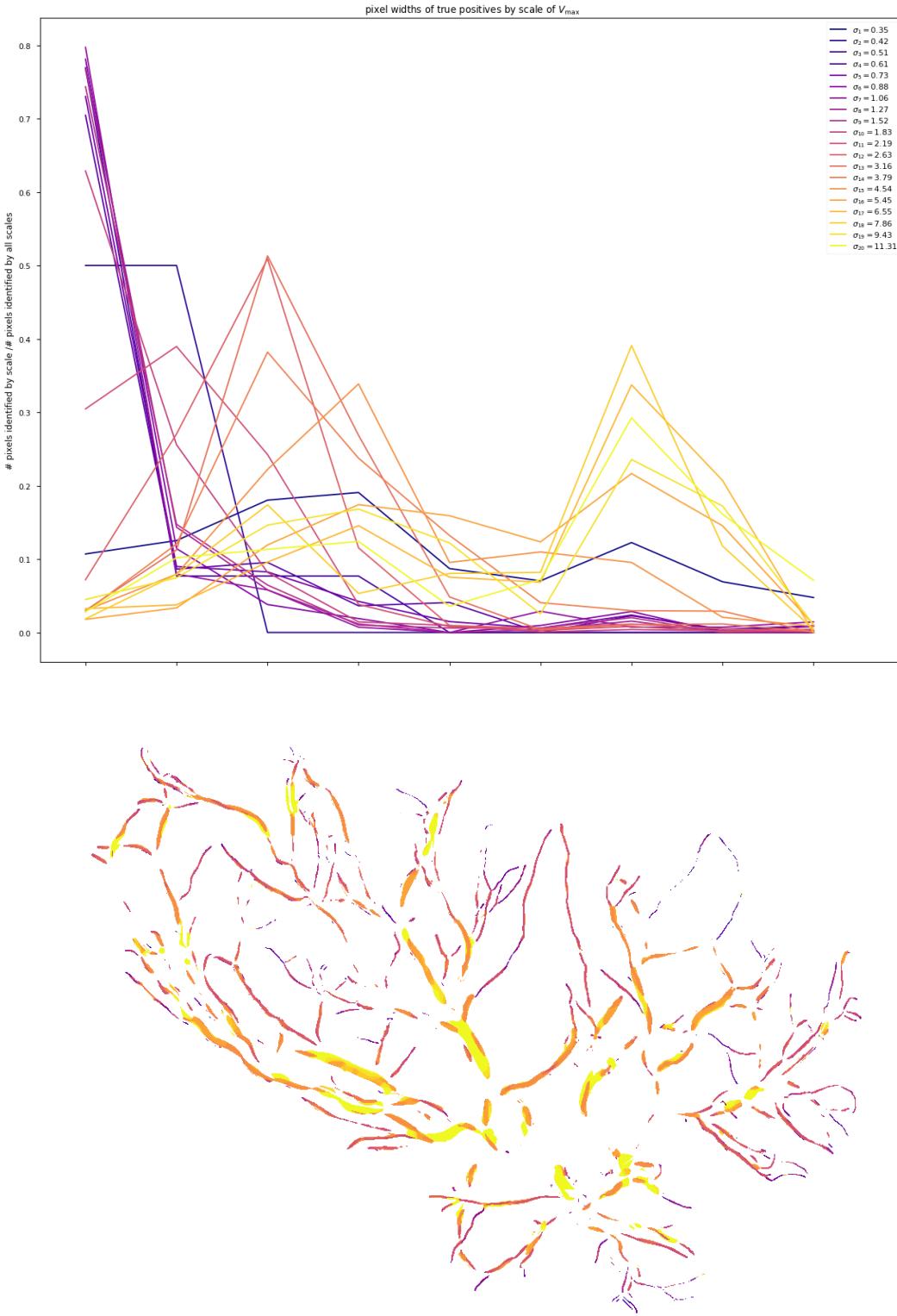


FIGURE 31: Scale of maximum Frangi score for true positives only (percentile filtering)

CHAPTER 8

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.

- Solve the Network Connection Problem (PICTURE OF GAPS) 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} .
- Look into gradient prefiltering more as well as varying γ more, especially in areas where we suspect the network could be completed.
- Look into using signed frangi arguments.
- Use this as preprocessing for a Neural Network. (cite kara's work, katalinas work)
- Apply to more image domains (STARE, other placental domains).

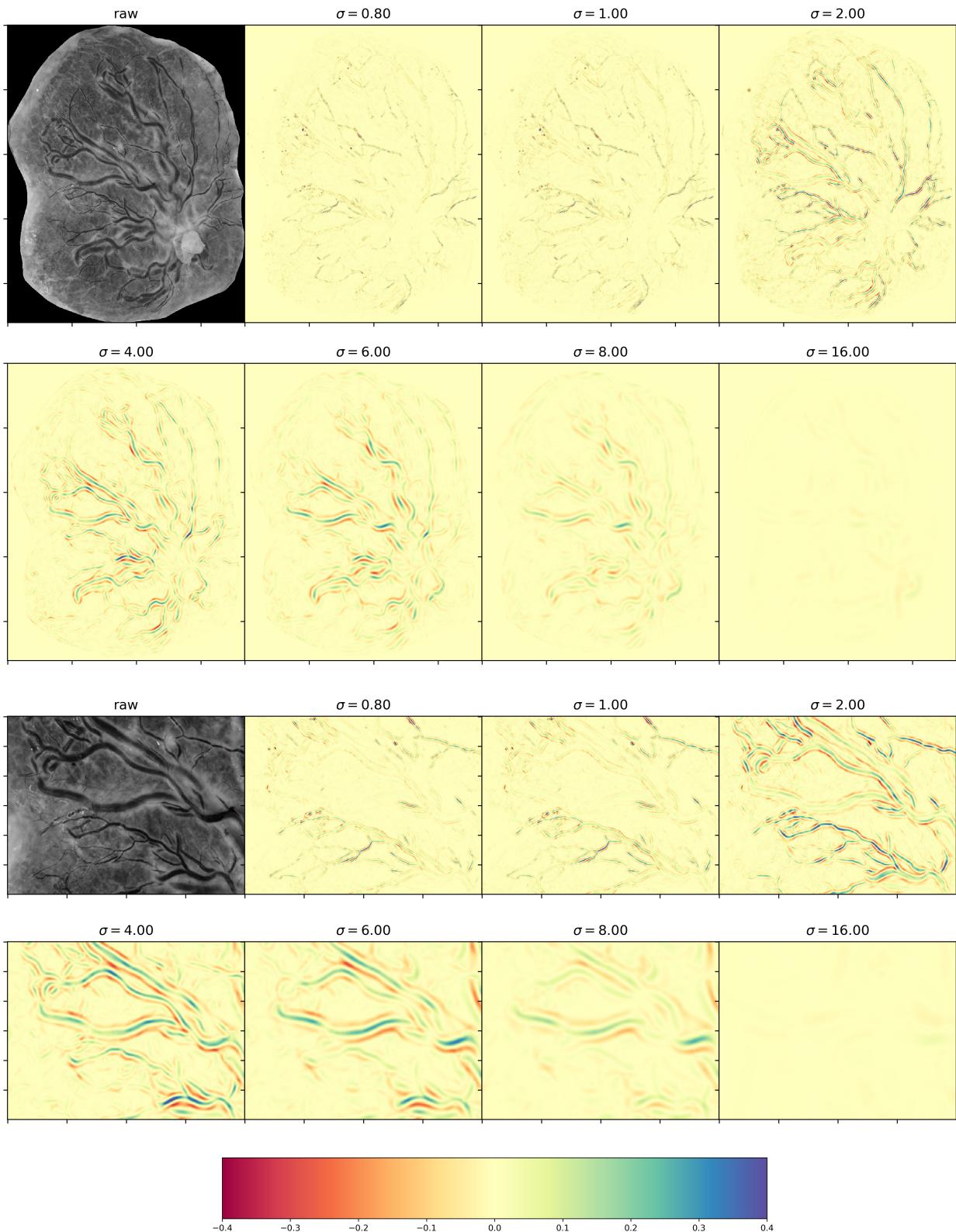


FIGURE 32: Signed Frangi output (plate and inset) (Example 1)

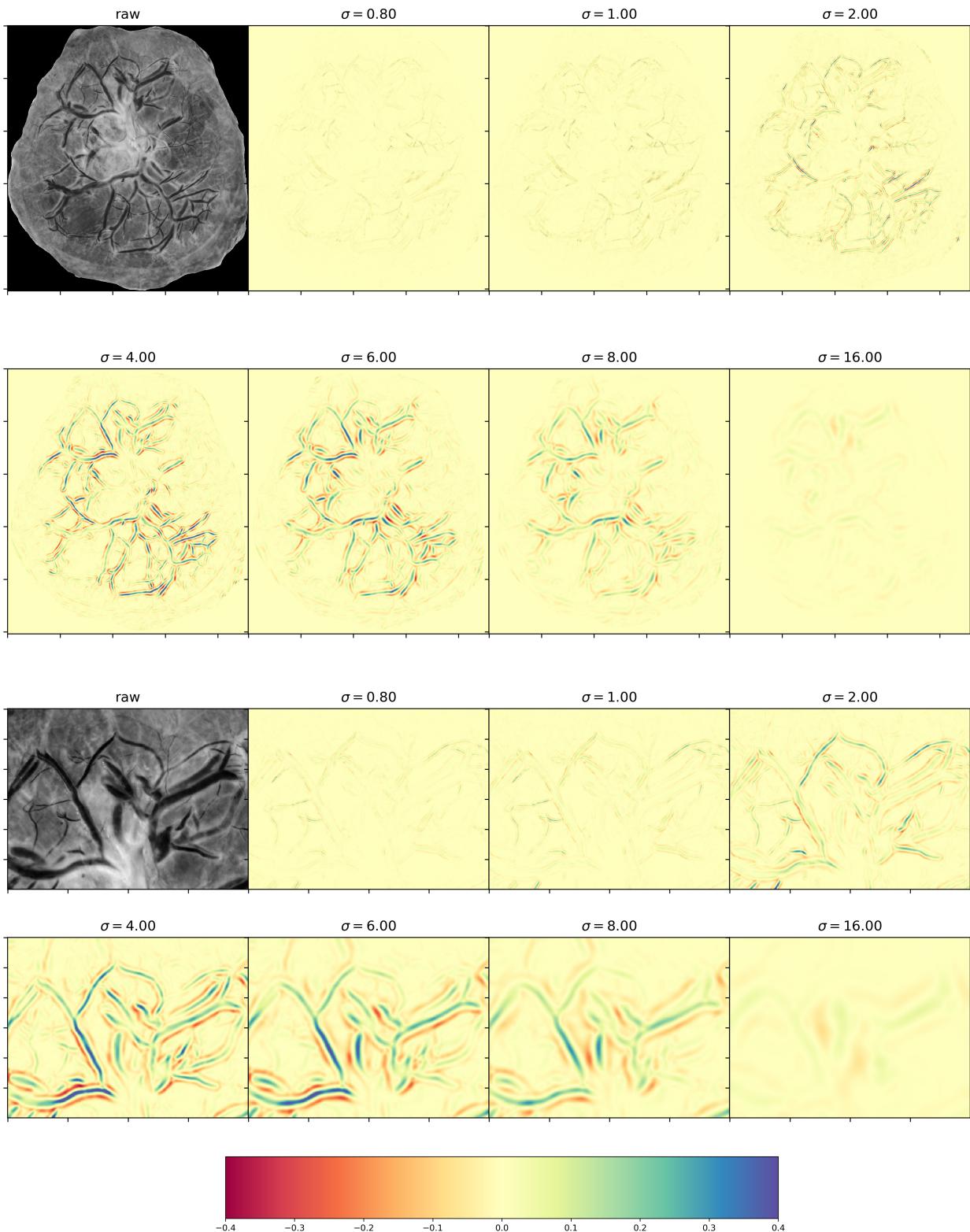


FIGURE 33: Signed Frangi output (plate and inset) (Example 1)

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 #!/usr/bin/env python3
2
3 from skimage.filters import sobel
4 from frangi import frangi_from_image
5 from plate_morphology import dilate_boundary
6 from skimage.morphology import remove_small_holes, remove_small_objects
7 from merging import nz_percentile
8
9 s = sobel(img)
10 s = dilate_boundary(s, mask=img.mask, radius=20)
11 finv = frangi_from_image(s, sigma=0.8, dark_bg=True)
12
13 finv_thresh = nz_percentile(finv, 80)
14
15 margins = remove_small_objects((finv > ft).filled(0), min_size=32)
16
17 margins_added = remove_small_holes(np.logical_or(margins, approx),
18                                     min_size=100, connectivity=2)
19
20 markers = np.zeros(img.shape, dtype=np.uint8)
21
22 markers[Fmax < .1] = 1
23 markers[margins_added] = 2
24
25 rw = random_walker(img, markers)
26 approx_rw = (rw==2)
27 confusion_rw = confusion(approx_rw, trace, bg_mask=ucip_mask)
28 mccs_rw = mccs(approx_rw, trace, bg_mask=ucip_mask)
29 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 { 1 , 2 } of an image,
14     that is, the eigenvalues of the Hessian at each point (x,y). The output
15     is arranged such that | 1 | <= | 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 (Hxx,Hxy,Hyy) 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 | 1 | <= | 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(' =', 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 ={}'.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  ={} (fast)'.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  ={}'.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  ={} (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  ={}'.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  ={} (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 # placentalas = list_placentas('T-BN')
46 # load placentalas 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 placentalas = list_by_quality(0, N=1)
52 # load from a file (sample names are keys of the json file)
53 # placentalas = list_by_quality(json_file='manual_batch.json')
54
55 # for a single named sample, use a 1 element list.
56 # placentalas = ['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_PCSVN 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 else:
160     img = raw_img.copy()
161
162 if REMOVE_GLARE:
163     img = inpaint_hybrid(img)
164
165 if USE_NPZ_FILES:
166     # find the first npz file with the sample name in it in the
167     # specified directory.
168     stub = filename.rstrip('.png')
169     for f in os.scandir(NPZ_DIR):
170         if f.name.endswith('npz') and f.name.startswith(stub):
171             npz_filename = os.path.join(NPZ_DIR, f.name)
172             print(f'using the npz file {npz_filename}')
173             break # we'll just use the first one we can find.
174     else:
175         print(f'no npz file found for {filename}.')
176         npz_filename = None
177     else:
178         npz_filename = None
179
180 # set a lambda function to make output file names
181 outname = get_outname_lambda(filename, output_dir=OUTPUT_DIR)
182
183 if npz_filename is not None:
184
185     F = np.load(npz_filename)['F']
186
187     # in case preprocessing happens inside extract_pcsvn, do it out here
188
189     print('successfully loaded the frangi targets!')
190
191 else:
192     print('finding multiscale frangi targets')
193
194     # F is an array of frangi scores of shape (*img.shape, N_SCALES)
195     F, jfile = extract_pcsvn(img, filename, dark_bg=DARK_BG, beta=BETAS,
196                               scales=scales, gamma=GAMMAS, c=CS,
197                               kernel='discrete', dilate_per_scale=True,
198                               verbose=False, signed_frangi=SIGNED_FRANGI,
199                               generate_json=True, output_dir=OUTPUT_DIR,
200                               rescale_frangi=RESCALE_FRANGI,
201                               gradient_filter=GRADIENT_FILTER)
202
203 if MAKE_NPZ_FILES:
204     npzfile = ".".join((outname("F").rsplit('.', maxsplit=1)[0], 'npz'))
205
206     print("saving frangi targets to ", npzfile)
207     np.savez_compressed(npzfile, F=F)
208
209

```

```

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

```

```

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

```

```

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

```

```

402 print('percentage of skeltrace covered (random_walker):',
403       f'{pnc_rw:.2%}')
404 print('percentage of skeltrace covered (sieving):',
405       f'{pnc_S:.2%}')
406
407 print(f'mcc score of {m_score:.3} for percentile filtering')
408 print(f'mcc score of {m_score_FA:.3} with fixed alpha {FIXED_ALPHA}')
409 print(f'mcc score of {m_score_rw:.3} after random walker')
410 print(f'mcc score of {m_score_S:.3} after sieving')
411
412
413 precision_score = lambda t: int(t[0]) / int(t[0] + t[2])
414
415 precision = precision_score(counts)
416 precision_FA = precision_score(counts_FA)
417 precision_rw = precision_score(counts_rw)
418 precision_S = precision_score(counts_S)
419
420 precisions[filename] = (precision, precision_FA, precision_rw, precision_S)
421
422 print(f'precision of {precision:.3} for percentile filtering')
423 print(f'precision of {precision_FA:.3} for fixed alpha')
424 print(f'precision of {precision_rw:.3} for random walker')
425 print(f'precision of {precision_S:.3} for sieving')
426
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 ### THIS IS ALL A HORRIBLE MESS. FIX IT
437 # why don't you just return the dict instead
438 with open(jfile, 'r') as f:
439     slog = json.load(f)
440
441 c2d = lambda t: dict(zip(('TP', 'TN', 'FP', 'FN'), [int(c) for c in t]))
442
443 slog['counts'] = c2d(counts)
444 slog['counts_FA'] = c2d(counts_FA)
445 slog['counts_rw'] = c2d(counts_rw)
446 slog['counts_S'] = c2d(counts_S)
447 slog['pnc'] = pncts[filename]
448 slog['mcc'] = mccs[filename]
449 slog['scale_maxes'] = list(scale_maxes)
450 slog['ALPHAS'] = list(ALPHAS)
451 slog['precision'] = precisions[filename]
452
453
454 with open(jfile, 'w') as f:
455     json.dump(slog, f)
456
457 plt.close('all')
458
459 # Post-run Meta-Output and Logging -----
460
461 timestamp = datetime.datetime.now()
462 timestamp = timestamp.strftime("%y%m%d_%H%M")
463
464 mccfile = os.path.join(OUTPUT_DIR, f"runlog_{timestamp}.json")
465
```

```

466 runlog = {
467     'time': timestring,
468     'DARK_BG': DARK_BG,
469     'DILATE_PER_SCALE': DILATE_PER_SCALE,
470     'SCALE_RANGE': SCALE_RANGE,
471     'SCALE_TYPE': SCALE_TYPE,
472     'N_SCALES': N_SCALES,
473     'scales': list(scales),
474     'ALPHAS': list(ALPHAS),
475     'BETAS': None,
476     'use_npz_files': False,
477     'remove_glare': REMOVE_GLARE,
478     'files': list(placentas),
479     'MCCS': mccs,
480     'PNC': pncts,
481     'precisions': precisions
482 }
483
484 # save to a json file
485 with open(mccfile, 'w') as f:
486     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
30 plt.close('all')
31
32 # show dependence of structureness factor on its parameter
33 for gamma in [0.1, 0.25, 0.35, 0.5, 0.9, 1, 2, 10, 1000]:
34     plt.plot(dom, s(dom, gamma), label=r'$\gamma=$' .format(gamma))
35
36 plt.ylabel(r'$\left(1-\exp\left(\frac{-S}{2\gamma^2}\right)\right)$',
37           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'$\beta=\{0\}$'.format(beta))
48
49 plt.ylabel(r'$\exp\left(-A\frac{\beta^2}{2}\right)$',
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
62     fig = plt.figure(figsize=(8,5))
63     ax = fig.gca(projection='3d')
64     X, Y = np.meshgrid(dom, dom)
65
66     Z = r(X,beta)*s(Y,gamma)
67
68     surf = ax.plot_surface(X,Y,Z, cmap='coolwarm', linewidth=0)
69
70     ax.set_xlabel(r'$\lambda_1 / \lambda_2$')
71     ax.set_ylabel(r'$S / S_{max}$')
72
73     ax.set_title(r'Rescaled Frangi filter, '
74                  r'$\beta=\{0\}, \gamma=\{1\}$'.format(beta, gamma))
75
76     #fig.colorbar(surf, shrink=0.5, aspect=5)
77     fig.tight_layout()
78
79     plt.savefig(f'demo_output/frangi3d/{n}.png', dpi=300)
80
81     plt.close()
82
83 imgs = [imread(f'demo_output/frangi3d/{n}.png') for n in range(36*1)]
84 imgs = np.stack(imgs)
85
86 for n in range(6):
87     plt.imsave(f'demo_output/frangi3d/frangi3dpart{n}.png',
88                montage(imgs[(n*6):((n+1)*6)], multichannel=True,
89                        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
70    result in a "looser" filter. For example, if gamma = .25, then the
71    maximum score is (1-exp{-8}) around .999 (it may be desirable that the
72    franginess score should be able to achieve a score of 1).

```

```

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:2f}')
109 #gamma0 = .5*hessian_norm(hesh).max()
110 #print(f'\t{gamma0:.5f} = frob-norm      pre-dilation')
111
112 #gamma1 = .5*hessian_norm(hesh, mask=collar).max()
113 #print(f'\t{gamma1:.5f} = frob-norm      post-collar dilation {dilation_radius}')
114 #l2gamma = .5*np.max(np.abs(k2))
115 #print(f'\t{l2gamma:.5f} =      from L2-norm      (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{gamma:.5f} =      post-hdilation (radius {hdilation}) (old )')
122
123 #print('changing      to L2-norm with collar')
124 #gamma = max(gamma1, l2gamma, 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))
133 #plt.show()
134 #print(hnorm[~collar].min(), hnorm[~collar].max())
135 #if hnorm[~collar].max() < 0.1:
136

```

```

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 structureness: ', S.max())
150     #c = gamma*S.max()
151
152 if verbose:
153     print(f'finding Frangi targets with   ={beta} and   ={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
197     -----
198         K1, K2 : ndarray (each)
199             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,  $\sqrt{K_1^{**2} + K_2^{**2}}$ . 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     hnrm = (hxx**2 + 2*hxy**2 + hyy**2)
314
315     if mask is not None:
316         hnrm[mask] = 0
317
318     hnrm = np.sqrt(hnrm)
319     return hnrm
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 (np.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}')
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
354     # is c is not provided, calculate it
355 if c is None:
356     c = gamma * np.sqrt(S).max() # the max Frob norm of the Hessian
357
358 #print(f'inside structureness,   ={gamma}, c={c}')
359
360 if c == 0:
361     return np.zeros_like(S)
362
363 elif c == 'inf' or np.isinf(c):
364     return np.ones_like(S)
365
366 elif c is None:
367     return S
368
369 else:
370     return S / (2*c**2)

```

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

```

115 # so that scipy.ndimage.gaussian_filter doesn't use uint8 precision (jesus)
116 img = ma.masked_array(img_as_float(img), mask=img.mask)
117
118 test_sigmas = [.3, .6, 1.0, 5.0, 15, 30, 60, 90]
119
120 for sigma in test_sigmas:
121
122     print("*"*80, '\n\n', f"  ={sigma}"))
123     #print('applying standard gauss blur')
124
125     # this is exactly how it's passed to skimage.feature.hessian_matrix(...)
126     A = gaussian_filter(img.filled(0), sigma, mode='constant', cval=0)
127
128     #print('applying fft gauss blur')
129     B = fft_gaussian(img, sigma, kernel='sampled')
130     C = fft_gaussian(img, sigma, kernel='discrete')
131
132     #print('calculating first derivatives')
133     # zero the masks before calculating derivates if they're masked
134     Agrad = np.gradient(A)
135     Bgrad = np.gradient(B)
136     Cgrad = np.gradient(C)
137
138     axes = range(img.ndim)
139
140     #print('calculating second derivatives')
141     # this is the same way it's done in skimage.feature.hessian_matrix(...)
142     H_A = [np.gradient(Agrad[ax0], axis=ax1)
143            for ax0, ax1 in combinations_with_replacement(axes, 2)]
144     H_B = [np.gradient(Bgrad[ax0], axis=ax1)
145            for ax0, ax1 in combinations_with_replacement(axes, 2)]
146     H_C = [np.gradient(Cgrad[ax0], axis=ax1)
147            for ax0, ax1 in combinations_with_replacement(axes, 2)]
148
149     #print('calculating eigenvalues of hessian')
150     ak1, ak2 = principal_curvatures(img, sigma=sigma, H=H_A)
151     bk1, bk2 = principal_curvatures(img, sigma=sigma, H=H_B)
152     ck1, ck2 = principal_curvatures(img, sigma=sigma, H=H_C)
153
154
155     #RA = anisotropy(ak1,ak2)
156     #RB = anisotropy(bk1,bk2)
157     #RC = anisotropy(ck1,ck2)
158
159     #SA = structureness(ak1, ak2)
160     #SB = structureness(bk1, bk2)
161     #SC = structureness(ck1, ck2)
162
163     ## ugh, apply masks here. too large to be conservative?
164     ## otherwise structureness only shows up for small sizes
165     new_mask = dilate_boundary(None, radius=int(3*sigma), mask=img.mask)
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=\{\}$$'.format(sigma))
191 plt.tight_layout()
192 plt.savefig('Gslice_sigma={:d}.png'.format(int(sigma*10)), dpi=300)
193 plot_image_slices((FA,FB,FC), labels=labels, formats=formats,
194                     title=r'Frangi filter response $\sigma=\{\}$$'.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
19 image based in frequency space (rather than direct convolution with a gaussian
20 as is standard in scipy, for example).
21
22 TODO: PROVIDE MAIN USAGE NOTES
23 """
24
25 def fft_gaussian(img, sigma, kernel=None):
26     """
27     https://docs.scipy.org/doc/scipy/reference/generated/scipy.signal.fftconvolve.html
28
29     in particular the example in which a gaussian blur is implemented.
30
31     along with the comment:
32     "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 by using scipy.special.iv instead we prevent blowups
71 """
72 dom = np.arange(-(n_samples//2), (n_samples//2) + 1)
73 #there should be a scaling parameter alpha but whatever
74 #return np.exp(-t) * iv(dom,t)
75 return iv(dom, sigma**2)
76
77 def fft_dgk(img, sigma, order=0, A=None):
78 """
79 This is the discrete gaussian kernel which is supposedly less crappy
80 than using a sampled gaussian.
81 """
82 m, n = img.shape
83 # i don't know if this will suck if there are odd dimensions
84 kernel = np.outer(discrete_gaussian_kernel(m, sigma**2),
85                   discrete_gaussian_kernel(n, sigma**2))
86
87 return signal.fftconvolve(img, kernel, mode='same')
88
89 def fft_fdgk(img, sigma):
90 """
91 convolve with discrete gaussian kernel in freq. space
92 """
93 # this would be a lot better since you wouldn't have to deal
94 # with an arbitrary cutoff of size of the discrete kernel
95 # since the freq. space version is just
96 # 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     e 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]] ]
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
151     if img is None:
152         img = img_as_float(camera())
153     else:
154         img = img_as_float(img)
155
156     sample_sigmas = (.5, 2, 8, 30)
157     #sample_sigmas = (.2, 2)
158
159     # 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}')
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}')
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}')
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}')
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     else:
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])]


```

```

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(' ', 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'$\sigma={:.2f}$'.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 the contents of this file should be split up between frangi (multiscale)
4 and scoring/output
5 """
6 from placenta import get_named_placenta
7 from diffgeo import principal_directions
8 from frangi import frangi_from_image
9 from skimage.util import img_as_float
10 import numpy as np
11 from preprocessing import inpaint_hybrid
12
13 from merging import nz_percentile
14
15 from plate_morphology import dilate_boundary
16
17 import matplotlib.pyplot as plt
18 import matplotlib as mpl
19 import numpy.ma as ma
20
21 import os.path
22 import json
23 import datetime
24
25
26 def make_multiscale(img, scales, beta=0.5, gamma=0.5, c=None, dark_bg=True,
27                     find_principal_directions=False, dilate_per_scale=True,
28                     signed_frangi=False, kernel=None, verbose=True,
29                     rescale_frangi=False, gradient_filter=False):
30     """Returns an ordered list of dictionaries for each scale of Frangi info.
31
32     beta, gamma, and c can all be vectors as long as scales or constants
33     if c is None it will be set.
34
35     Each element in the output contains the following info:
36     {'sigma': sigma,
37      'beta': beta,
38      'gamma': gamma,
39      'H': hesh,
40      'F': targets,
41      'k1': k1,
42      'k2': k2,
43      't1': t1, # if find_principal_directions
44      't2': t2 # if find_principal_directions
45      }
46
47     is it necessary to lug all this shit around?
48 """
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([x])
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(' ', 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
98             t1, t2 = principal_directions(img, sigma=sigma, H=this_scale['H'],
99                                           mask=pd_mask)
100
101            # add them to this scale's output
102            this_scale['t1'] = t1
103            this_scale['t2'] = t2
104
105        else:
106            if verbose:
107                print('skipping principal direction calculation')
108
109            # store results as a list of dictionaries
110            multiscale.append(this_scale)
111
112    print()
113    return multiscale
114
115
116 def extract_pcsvn(img, filename, scales, beta=0.5, gamma=0.5, c=None,

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

308         placentas.append(f)
309
310     return sorted(placentas)
311
312
313 def show_mask(img, mask=None, interactive=False, mask_color=None):
314     """
315     rename this color_mask since showing the mask is just a secondary feature
316     show a masked grayscale image with a dark blue masked region
317
318     custom version of imshow that shows grayscale images with the right
319     colormap and, if they're masked arrays, sets makes the mask a dark blue) a
320     better function might make the grayscale value dark blue (so there's no
321     confusion)
322
323     if interactive, this operates like "plt.imshow"
324     if interactive==False, return the RGB matrix
325
326     if mask provided, add it to the image. (pass img.data instead if you don't
327     want to use the original mask)
328     """
329
330     if mask_color is None:
331         mask_color = (0, 0, 60)
332
333     # if there's no mask at all
334     if (mask is None) and (not is_masked(img)):
335         if interactive:
336             plt.imshow(img, cmap=plt.cm.gray)
337             return # we're done
338         else:
339             # return as an rgb image so output is uniform
340             return gray2rgb(img)
341
342     elif not is_masked(img):
343         # add mask to the image / add to existing mask
344         # if i just rewrite img will it change outside this function?
345         new_img = ma.masked_array(img, mask=mask)
346     else:
347         new_img = img.copy()
348
349     # otherwise, get an RGB array, black where the mask is
350     mimg = gray2rgb(new_img.filled(0))
351
352     # fill masked regions with the mask color
353     mimg[new_img.mask, :] = mask_color
354
355     if interactive:
356         plt.imshow(mimg)
357     else:
358         return mimg
359
360
361 def _cropped_bounds(img, mask=None):
362
363     if mask is not None:
364
365         img = ma.masked_array(img, mask=mask)
366
367         X, Y = (np.argwhere(np.invert(img.mask)).any(axis=k)).squeeze()
368             for k in (0, 1)
369             )
370
371     if X.size == 0:

```

```

372     X = [None, None] # these will slice correctly
373     if Y.size == 0:
374         Y = [None, None]
375
376     return Y[0], Y[-1], X[0], X[-1]
377
378
379 def cropped_args(img, mask=None):
380     """
381     get a slice that would crop image
382     i.e. img[cropped_args(img)] would be a cropped view
383     """
384
385     x0, x1, y0, y1 = _cropped_bounds(img, mask=None)
386
387     return np.s_[x0:x1, y0:y1]
388
389
390 def cropped_view(img, mask=None):
391     """
392     removes entire masked rows and columns from the borders of a masked array.
393     will return a masked array of smaller size
394
395     don't ask me about data
396
397     the name sucks too
398     """
399
400     # find first and last row with content
401     x0, x1, y0, y1 = _cropped_bounds(img, mask=mask)
402
403     return img[x0:x1, y0:y1]
404
405
406 CYAN = [0, 255, 255]
407 YELLOW = [255, 255, 0]
408
409
410 def measure_ncs_markings(ucip_img=None, filename=None, verbose=True):
411     """
412     find location of ucip and resolution of image based on input
413     (similar to perimeter layer in original NCS data set
414
415     Parameters
416     -----
417
418     ucip_img: an RGB ndarray or None
419         The perimeter layer of an NCS sample (colorations according to the
420         tracing protocol). if None, filename must be included. Default is None.
421     filename:
422         the filename of the SAMPLE (not the ucip image file itself)
423
424     Returns
425     -----
426     m : tuple of ints
427         the coordinates of (the center of) of the umbilical cord point
428         (depicted as a yellow dot) in the original image.
429     resolution: a float
430         measured distance between the two cyan dots
431     """
432
433     if ucip_img is None:
434         ucip_img = open_typefile(filename, 'ucip')
435

```

```

436 if ucip_img is None:
437     # if it's still none (no file), return None
438     return None, None
439
440 # just in case it's got an alpha channel, remove it
441 img = ucip_img[:, :, 0:3]
442
443 # given the image img (make sure no alpha channel)
444 # find all cyan pixels (there are two boxes of 3 pixels each and we
445 # just want to extract the middle of each
446 if verbose:
447     print('the image size is {}x{}'.format(img.shape[0], img.shape[1]))
448
449 rulemarks = np.all(img == CYAN, axis=-1)
450
451 # turn into two pixels (these should each be shape (18,))
452 X, Y = np.where(rulemarks)
453
454 assert X.shape == Y.shape
455
456 # if they followed the protocol correctly...
457 if X.size == 18:
458     # get the two pixels at the center of each box
459     A, B = (X[4], Y[4]), (X[13], Y[13])
460 else:
461     # dots are a nonstandard size for some reason. this works too.
462     thinned = morphology.thin(rulemarks)
463     X, Y = np.where(thinned)
464     assert(thinned.sum() == 2) # there should be just two pixels now.
465     A, B = (X[0], Y[0]), (X[1], Y[1])
466
467 ruler_distance = np.sqrt((A[0] - B[0])**2 + (A[1] - B[1])**2)
468 if verbose:
469     print(f'one cm equals {ruler_distance} pixels')
470
471 # the umbilical cord insertion point (UCIP) is a yellow circle, radius 19
472 ucipmarks = np.all(img == YELLOW, axis=-1)
473 X, Y = np.where(ucipmarks)
474
475 # find midpoint of the x & y coordinates
476 assert X.max() - X.min() == Y.max() - Y.min()
477 radius = (X.max() - X.min()) // 2
478
479 mid = (X.min() + radius, Y.min() + radius)
480
481 if verbose:
482     print('the middle of the UCIP location is', mid)
483     print('the radius outward is', radius)
484     print('the total measurable diameter is', radius*2 + 1)
485
486 return mid, ruler_distance
487
488 def add_ucip_to_mask(m, radius=100, mask=None, size_like=None):
489 """
490 - m is a tuple (2x1) representing the (coordinate) midpoint of the UCIP
491 - radius around which to dilate the UCIP is the dilation radius as it
492 works in morphology--this is passed directly to skimage.morphology.disk.
493 thus a circle centered at point m with diameter 2*radius + 1
494 - if no mask is supplied, dilate the point in an array of zeros the shape
495 of 'size_like' (would be the same as passing mask=np.zeros_like(size_like))
496
497 Note: this behaves much faster than binary dilation on the point
498 """

```

```

500 if mask is None:
501     if size_like is not None:
502         mask = np.zeros_like(size_like)
503     else:
504         raise ValueError("No mask info supplied!")
505
506 # an empty mask (since we need to merge--we don't want to copy the
507 # zeros of the dilated UCIP -- just the ones!)
508 to_add = np.zeros_like(mask)
509
510 # this is way faster than dilating the point in the matrix,
511 # just set this at the centered point
512
513 # doesn't check for out of bounds stuff. use at your own peril
514 D = morphology.disk(radius)
515 to_add[m[0]-radius:m[0]+radius+1, m[1]-radius:m[1]+radius+1] = D
516
517 # merge with supplied mask
518 return mask | to_add
519
520
521 if __name__ == "__main__":
522     """test that this works on an easy image."""
523
524     test_filename = 'barium1.png'
525
526     img = get_named_placenta(test_filename, maskfile=None)
527
528     print('showing the mask of', test_filename)
529     print('run plt.show() to see masked output')
530
531     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
112        if pinds:
113            break #otherwise increase the size of the window
114
115    if pinds:
116
117        # max distance to boundary point in the window
118        # we really only need to keep the largest; deque?
119        dists = sorted([(pp, 12_dist(P,pp)) for pp in pinds],
120                      key=lambda t: t[1])
121        r = 2*int(dists[0][1]) + 1 # get largest radius but closest point
122        P = dists[0][0]
123        B = np.zeros_like(img.mask)
124
125        B[cutmarks] = True
126
127        # center a disk of found radius there
128        D = disk(r)
129        winx = max(P[0]-r,0), min(P[0]+r+1,B.shape[0])
130        winy = max(P[1]-r,0), min(P[1]+r+1,B.shape[1])
131        try:
132            B[winx[0]:winx[1], winy[0]:winy[1]] = D
133        except ValueError:
134            # they're out of bounds so it's a size mismatch. fix it
135            # by starting/ending D index with opposite sign of the initial
136            # p +/- radius that was out of bounds
137            # for example P[0]-r was -9 and everything else was fine
138            # so you just need to set left side to D[9:,:]
139            # but you should wrap this up in a function so the three times
140            # you do it here and the one time in ucip all gets the same
141            # code
142            print("too close to the boundary or size mismatch?")
143            success = False
144        else:
145            dilcut[B] = ma.masked
146            success = True
147
148    else:
149        print("we completely failed to mask the cut. too close to the",
150              "boundary to fit an unmodified disk in. fix this")
151        success = False
152
153 return dilcut, success
154
155 def mask_cuts_watershed(img, ucip, mask_only=False, in_place=False,
156                         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     If in_place, this changes the mask of the image directly (but still returns
169     a masked array. If mask_only is True, in_place will automatically be set to
170     False to prevent hideous side effects
171
172     if return_success, this function returns True if there was a cutmark found,
173     otherwise False as a second output
174     """
175
176     # get indices where the blue square indicating center of a cut appears
177     cutmarks = np.all(ucip==(0,0,255), axis=-1)
178
179     if not np.any(cutmarks):
180
181         #print("no cutmarks found on image")
182
183         if return_success:
184             return img, False
185         else:
186             return img
187     else:
188         #print("found a cutmark!")
189         pass
190
191     cutmarks = np.nonzero(cutmarks)
192     # get the first pixel of it (we don't need to be too precise here)
193     X, Y = cutmarks[0][0], cutmarks[1][0]
194
195     # get a value somewhat lower than the value of bg in the cut
196     # (this should be a high number before we take 85%)
197     # sometimes this is in a shadowy region which fucks everything up though
198     #threshold = max(img[cutmarks].mean() * .85, 175)
199     # get the brightest value in a smallish window around the cut * .85
200     threshold = np.max(img[X-10:X+10,Y-10:Y+10])
201
202     rmin, rmax = max(0, X-100), min(img.shape[0], X+100)
203     cmin, cmax = max(0, Y-100), min(img.shape[1], Y+100)
204     cutregion = np.s_[rmin:rmax, cmin:cmax] # get a window around the mark
205
206     # mark inside of the placenta with label 2, original mask and cutmarks with
207     # label 1, and the rest with 0 (i dunno)
208     markers = np.zeros(img.shape, dtype='int32')
209     markers[img.filled(255) < threshold] = 2
210     markers[img.mask] = 1
211     markers[cutmarks] = 1
212
213     # perform watershedding on the thresholded image to fill in the cut with
214     # label 1
215     cutfix = watershed(img.filled(255) < threshold, markers=markers)
216
217     # this is a waste considering the in_place, but eh

```

```

219 new_mask = img.mask.copy()
220 new_mask[cutregion] = (cutfix[cutregion] == 1)
221
222 if mask_only:
223     out = new_mask
224
225 elif not in_place:
226     out = ma.masked_array(img, mask=new_mask)
227
228 else:
229     # will this work?
230     img[new_mask] = ma.masked
231
232     out = img
233
234 # now return succeed if asked to
235 if return_success:
236     return out, True
237
238 else:
239     return out
240
241
242 if __name__ == "__main__":
243
244     # DEMO FOR SHOWING OFF DILATE_BOUNDARY EFFECT
245
246     from placenta import get_named_placenta
247     from frangi import frangi_from_image
248     import matplotlib.pyplot as plt
249
250     import os.path
251
252     dest_dir = 'demo_output'
253     img = get_named_placenta('T-BN0164923.png')
254
255     sigma = 3
256     radius = 25
257
258     inset = np.s_[800:1000, 500:890]
259
260     D = dilate_boundary(img, radius=radius)
261
262     Fimg = frangi_from_image(img, sigma, dark_bg=False, dilation_radius=None)
263     FD = frangi_from_image(D, sigma, dark_bg=False)
264     FDinv = frangi_from_image(D, sigma, dark_bg=True)
265     Finv = frangi_from_image(img, sigma, dark_bg=True, dilation_radius=None)
266
267     fig, axes = plt.subplots(ncols=2, nrows=3)
268
269     axes[0,0].imshow(img[inset].filled(0), cmap=plt.cm.gray)
270     axes[0,1].imshow(D[inset].filled(0), cmap=plt.cm.gray)
271     axes[1,0].imshow(Fimg[inset].filled(0), cmap=plt.cm.nipy_spectral)
272     axes[1,1].imshow(FD[inset].filled(0), cmap=plt.cm.nipy_spectral)
273     axes[2,0].imshow(Finv[inset].filled(0), cmap=plt.cm.nipy_spectral)
274     axes[2,1].imshow(FDinv[inset].filled(0), cmap=plt.cm.nipy_spectral)
275
276     for a in axes.ravel():
277         # get rid of all the labels
278         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
7 from skimage.filters import sobel
8 from skimage.morphology import remove_small_holes, remove_small_objects, thin
9 from frangi import frangi_from_image
10 from 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, return_labels=False):
47     """Random walker on each a multiscale Frangi result"""
48     print('doing scalewise random walk', end=' ')
49     V = np.transpose(F, axes=(2, 0, 1))
50     W = np.zeros(V.shape, np.bool)
51     for n, v in enumerate(V):
52         print(' ', end=' ', flush=True)

```

```

53     markers = np.zeros(v.shape, np.int32)
54     markers[v == 0] = 1
55     # this could be a vector too
56     markers[v > high_thresh] = 2
57     # or 1-v
58     W[n] = (random_walker(v, markers) == 2)
59     print()
60     if not return_labels:
61         return W.any(axis=0)
62     else:
63         # argmax grabs the first scale where it was satisfied
64         # so this will grab the lowest scale that matches
65         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 from skimage.restoration import inpaint_biharmonic
13 import numpy as np
14 import numpy.ma as ma
15 from scipy.ndimage import label
16 from skimage.util import img_as_float
17 from skimage.segmentation import find_boundaries
18 from plate_morphology import dilate_boundary
19
20
21 def inpaint_glare(img, threshold=175, window_size=15, mask=None):
22     """
23     img is a masked array type uint [0,255]
24     """
25
26     # bool array, true where glare
27     if mask is None:
28         glared = mask_glare(img, threshold=threshold, mask_only=True)
29     else:
30         glared = mask
31
32     B = ma.masked_array(img, mask=glared) # masked background *and* glare
33     new_img = img.copy() # copy values of original image (will rewrite)
34     d = int(window_size)
35
36     for j, k in zip(*np.where(glared)):
37         # rewrite all glared pixels with the mean of nonmasked elements
38         # in a window_size window. (this doesn't check OoB, be careful!)
39         new_img[j, k] = B[j-d:j+d, k-d:k+d].compressed().mean()
40
41     return new_img
42
43
44 def inpaint_with_boundary_median(img, threshold=175, mask=None):
45     mask glare pixels, then replace by the median value on the mask's boundary

```

```

47 """
48     if mask is None:
49         glared = mask_glare(img, threshold=threshold, mask_only=True)
50     else:
51         glared = mask
52
53     B = ma.masked_array(img, mask=glared)
54
55     new_img = img.copy() # copy values of original image (will rewrite)
56     bounds = find_boundaries(glared)
57     lb, _ = label(bounds)
58     fill_vals = np.zeros_like(img.data)
59
60     # for each boundary of masked region, find the median value of the img
61     for lab in range(1, lb.max()+1):
62         inds = np.where(lb == lab)
63         fill_vals[inds] = nz_median(B[inds])
64
65     # label masked regions together with their boundaries (they'll be
66     # connected)
67     lm, _ = label(np.logical_or(glared, lb != 0))
68
69     # fill the masked areas with the corresponding fill value
70     for lab in range(1, lm.max()+1):
71         inds = np.where(lm == lab)
72         # find locations of filled values corresponding to this label
73         # median in case there's overlapped regions? (sloppy)
74         replace_value = nz_median(fill_vals[inds])
75
76         if replace_value == 0:
77             raise
78
79         fill_vals[inds] = replace_value
80
81     # now fill in the values
82     new_img[glared] = fill_vals[glared]
83
84     return new_img
85
86 def nz_median(A):
87
88     if ma.is_masked(A):
89         relevant = A[A > 0].compressed()
90     else:
91         relevant = A[A > 0]
92
93     return np.median(relevant)
94
95
96 def inpaint_hybrid(img, threshold=175, min_size=64, boundary_radius=10):
97 """
98     use biharmonic inpainting in larger, inner areas (important stuff)
99     and median inpainting in smaller areas and along boundary
100 """
101
102     glare = mask_glare(img, threshold=threshold, mask_only=True)
103
104     glare_inside = dilate_boundary(glare, mask=img.mask,
105                                     radius=boundary_radius).filled(0)
106
107     large_glare = remove_small_objects(glare_inside, min_size=min_size,
108                                         connectivity=2)
109     small_glare = np.logical_and(glare, np.invert(large_glare))
110

```

```

111 # inpaint smaller and less important values with less expensive method
112 inpainted = inpaint_with_boundary_median(img, mask=small_glare)
113 hybrid = img_as_float(inpainted) # scale 0 to 1
114
115 # inpaint larger regions with biharmonic inpainting
116 large_inpainted = inpaint_biharmonic(img.filled(0), mask=large_glare)
117
118 # now overwrite with these values
119 hybrid[large_glare] = large_inpainted[large_glare]
120
121 # put on old image mask
122 return ma.masked_array(hybrid, mask=img.mask)
123
124 def inpaint_with_biharmonic(img, threshold=175):
125     """
126     use biharmonic inpainting *all* glare
127     """
128     glare = mask_glare(img, threshold=threshold, mask_only=True)
129     inpainted = inpaint_biharmonic(img_as_float(img.filled(0)), mask=glare)
130
131     if ma.is_masked(img):
132         return ma.masked_array(inpainted, mask=img.mask)
133     else:
134         return inpainted
135
136 def mask_glare(img, threshold=175, mask_only=False):
137     """
138     for demoing purposes, with placenta.show_mask
139
140     if mask_only, just return the mask. Otherwise return a copy of img with
141     that added to the mask. If you want the original mask to be ignored,
142     just pass img.filled(0) ya doofus
143
144     threshold is expected to be of the same dtype as img *unless# it assumes
145     its default value, in which case the threshold will be converted to a float
146
147     """
148     # if img.dtype is floating but threshold value is still the default
149     # this could be generalized
150     if np.issubdtype(img.dtype, np.floating) and (threshold == 175):
151         threshold = 175 / 255
152     # region to inpaint
153     inp = (img > threshold)
154
155     # get a larger area around the specks
156     inp = binary_dilation(inp, selem=disk(2))
157
158     # remove anything large
159     #inp = white_tophat(inp, selem=disk(3))
160
161     if mask_only:
162         return inp
163     else:
164         # both the original background *and* these new glared regions
165         # are masked
166         return ma.masked_array(img, mask=inp)
167
168
169 DARK_RED = np.array([103, 15, 23]) / 255.
170
171 # test it on a particularly bad sample
172 if __name__ == "__main__":
173
174     from placenta import get_named_placenta, show_mask

```

```

175 import matplotlib.pyplot as plt
176
177 filename = 'T-BN0204423.png' # a particularly glary sample
178 img = get_named_placenta(filename)
179
180 img = ma.masked_array(img_as_float(img), mask=img.mask)
181 crop = np.s_[150:500, 150:800] # indices to zoom in on the region
182 zoom = np.s_[300:380, 300:380] # even smaller region
183
184 inset = zoom # which view to use
185
186 masked = mask_glare(img) # for viewing
187 inpainted = inpaint_glare(img)
188 minpainted = inpaint_with_boundary_median(img)
189 hinpainted = inpaint_hybrid(img)
190 binpainted = inpaint_with_biharmonic(img)
191
192 # view the closeup like this
193 minpainted_view = show_mask(minpainted, interactive=False,
194                             mask_color=DARK_RED)
195 inpainted_view = show_mask(inpainted, interactive=False,
196                            mask_color=DARK_RED)
197 masked_view = show_mask(masked, interactive=False,
198                          mask_color=DARK_RED)
199 img_view = show_mask(img, interactive=False,
200                      mask_color=DARK_RED)
201 hinpainted_view = show_mask(hinpainted, interactive=False,
202                           mask_color=DARK_RED)
203 binpainted_view = show_mask(binpainted, interactive=False,
204                           mask_color=DARK_RED)
205
206 # view them all next to each other
207
208 fig, axes = plt.subplots(ncols=3, nrows=2)
209
210 axes[0,0].imshow(img_view[inset])
211 axes[0,1].imshow(masked_view[inset])
212 axes[0,2].imshow(inpainted_view[inset])
213 axes[1,0].imshow(minpainted_view[inset])
214 axes[1,1].imshow(binpainted_view[inset])
215 axes[1,2].imshow(hinpainted_view[inset])
216
217 for a in axes.ravel():
218     # get rid of all the labels
219     plt.setp(a.get_xticklabels(), visible=False)
220     plt.setp(a.get_yticklabels(), visible=False)
221
222 # lol matlab
223 for i in range(5):
224     fig.tight_layout()
225
226 IMGS = np.vstack((
227     np.hstack((img_view, masked_view, inpainted_view)),
228     np.hstack((minpainted_view, binpainted_view, hinpainted_view))))
229
230 # THEN IMSAVE
231
232 # plt.imsave('preprocessing_comparison_cropped.png', IMGS)
233 # plt.imsave('preprocessing_comparison_zoomed.png', IMGS)
234
235 # if it's zoomed, then rescale the output in GIMP to 4x

```

listings/process_NCS_xcfs.py

```
1 #!/usr/bin/env python
2 """
3 This should be a plugin to take images from the folder NCS_vessel_GIMP_xcf
4 and create trace, mask, and backgrounded images from each xcf file.
5
6 to use:
7 chmod +x and then copy or link to ~/gimp-2.x/plug-ins/
8 """
9
10
11 from gimpfu import *
12 import os.path
13 from functools import partial
14
15 #basefile, ext = os.path.splitext(xcffile)
16
17 def _outname(base, s=None):
18
19     #base = base.split("_", maxsplit=1)[0]
20     if s is None:
21         stubs = (base, 'png')
22     else:
23         stubs = (base, s, 'png')
24     file
25     filename = '.'.join(stubs)
26
27     return os.path.join(os.getcwd(), filename)
28
29 # get active image
30 def process_NCS_xcf(timg, tdrawable):
31     img = timg
32     basename, _ = os.path.splitext(img.name) # split off extension .xcf
33     basename = basename.split("_")[0] # only get T-BN-kjlksf part
34     print "*" * 80
35     print '\n\n'
36
37     print "Processing " , img.name
38     # generate output names easier
39     outname = partial(_outname, base=basename)
40
41     # get coordinates of the center
42     cx, cy = img.height // 2 , img.width // 2
43
44     # disable the undo buffer
45     img.disable_undo()
46
47     #perimeter = pdb.gimp_image_get_layer_by_name(img, 'perimeter')
48
49     for layer in img.layers:
50         if layer.name.lower() in ('perimeter', 'perimeters'):
51             # .copy() has optional arg of "add_alpha_channel"
52             mask = layer.copy()
53             break
54     else:
55         print "Could not find a perimeter layer."
56         print "Layers of this image are:"
57         for n,layer in enumerate(img.layers):
58             print "\t", n, ":", layer.name
59         print "Skipping this file."
60
61     return
```

```

62
63     for layer in img.layers:
64         layer.visible = False
65
66     mask.name = "mask" # name the new layer
67     img.add_layer(mask,0) # add in position 0 (top)
68
69     pdb.gimp_layer_flatten(mask) # Remove Alpha Channel.
70
71     # save the annotated perimeter file (for calculations later)
72     pdb.gimp_file_save(img,mask, outname(s="ucip"), '')
73
74     # remove unneeded annotations from mask layer
75     # color exchange yellow & blue to black
76     pdb.plug_in_exchange(img,mask,255,255,0,0,0,0,1,1,1)
77     pdb.plug_in_exchange(img,mask,0,0,255,0,0,0,0,1,1,1)
78
79     # set FG color to black (for tools, not of image)
80     gimp.set_foreground(0,0,0)
81
82     # Bucket Fill Inside black (center pixel is hopefully fine,
83     # do rest manually
84     pdb.gimp_edit_bucket_fill(mask,0,0,100,0,0,cx,cy)
85
86     # Color Exchange Green to White.
87     pdb.plug_in_exchange(img,mask,0,255,0,255,255,255,1,1,1)
88
89     # Color Exchange Cyan (00ffff) to White.
90     pdb.plug_in_exchange(img,mask,0,255,255,255,255,255,1,1,1)
91
92     # Export Layer as Image called "f".mask.png
93     pdb.gimp_file_save(img,mask, outname(s="mask"), '')
94
95     # invert (so exterior is now black)
96     pdb.gimp_invert(mask)
97     mask.mode = DARKEN_ONLY_MODE # the constant 9
98
99     # set bottom layer (placenta) to visible
100    raw = img.layers[-1]
101    raw.visible = True
102
103    # now make a new layer called 'raw_img' from visible
104    base = pdb.gimp_layer_new_from_visible(img,img,'base')
105    img.add_layer(base,0)
106    pdb.gimp_file_save(img , base, outname(s=None) , '')
107
108    # now get rid of mask and save the raw image
109    mask.visible = False
110    pdb.gimp_file_save(img, base, outname(s='raw') , '')
111
112
113    # now make the other one visible (this is dumb)
114    for layer in img.layers:
115        if layer.name.lower() in ("arteries", "veins"):
116            layer.visible = True
117        else:
118            layer.visible = False
119
120    # now with these two visible, merge them and add layer
121    trace = pdb.gimp_layer_new_from_visible(img,img,'trace')
122    img.add_layer(trace,0)
123
124    pdb.gimp_layer_flatten(trace) # remove alpha channel
125
126    # don't turn binary anymore

```

```

126 #pdb.gimp_desaturate(trace) # turn to grayscale
127 #pdb.gimp_threshold(trace,255,255) # anything not 255 turns black
128
129 pdb.gimp_file_save(img, trace, outname(s='ctrace'), '')
130
131 # now extract an each type individually.
132 found = 0
133 for subtype in ("arteries", "veins"):
134     for layer in img.layers:
135         if layer.name.lower() == subtype:
136             layer.visible = True
137             pdb.gimp_layer_flatten(layer) # remove alpha channel
138             pdb.gimp_file_save(img, layer, outname(s=subtype), '')
139             layer.mode = 9 # set to darken only (for merging)
140             found += 1
141         else:
142             layer.visible = False
143 if found < 2:
144     print "WARNING! Could not find appropriate artery/vein layers."
145
146
147 print "Saved. "
148
149
150 register(
151     "process_NCS_xcf",
152     "Create base image + trace + mask from an NCS xcf file",
153     "Create base image + trace + mask from an NCS xcf file",
154     "Luke Wukmer",
155     "Luke Wukmer",
156     "2018",
157     "<Image>/Image/Process_NCS_xcf...",
158     "RGB*, GRAY*",
159     [],
160     [],
161     process_NCS_xcf)
162
163 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[0]*g[0]))
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', 'r')
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
179 for sigma in np.logspace(-4, 8, base=2, num=50):
180     D = fft_gaussian(img, sigma, 'discrete')
181     gD = np.gradient(D)
182     Daa, Dbb = aa(gD), bb(gD)
183     Dcc = Daa / Dbb
184     aas = Daa[~dil].min(), Daa[~dil].max()
185     bbs = Dbb[~dil].min(), Dbb[~dil].max()
186     ccs = Dcc[~dil].min(), Dcc[~dil].max()
187     print(f"sigma={sigma:.3f}",
188           "\tmin: {:.6f},\tmax:{:.6f}".format(*aas),
189           "\tmin: {:.6f},\tmax:{:.6f}".format(*bbs),
190           "\tmin: {:.6f},\tmax:{:.6f}".format(*ccs), sep='\n')
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)

```

```

213 Dcc = Dbb / Daa
214 aas = Daa[~dil].min(), Daa[~dil].max()
215 bbs = Dbb[~dil].min(), Dbb[~dil].max()
216 ccs = Dcc[~dil].min(), Dcc[~dil].max()
217 print(f"sigma={sigma:.3f}",
218     "\tmin: {:.6f},\tmax:{:.6f}" .format(*aas),
219     "\tmin: {:.6f},\tmax:{:.6f}" .format(*bbs),
220     "\tmin: {:.6f},\tmax:{:.6f}" .format(*ccs), sep='\n')
221 data.append(
222     [sigma, *aas, *bbs, *ccs])
223
224 import pandas
225 table = pandas.DataFrame(data)
226 print(table)
227 from hfft import fft_hessian
228 get_ipython().run_line_magic('pinfo', 'fft_hessian')
229 helems = fft_hessian(img, sigma=1, kernel='discrete')
230 np.sqrt(helems[0]**2 + 2*helems[1]**2 + helems[2]**2)
231 _.shape
232 plt.imshow(np.sqrt(helems[0]**2 + 2*helems[1]**2 + helems[2]**2))
233 plt.show()
234 data = list()
235 for sigma in np.logspace(-4, 8, base=2, num=50):
236     D = fft_gaussian(img, sigma, 'discrete')
237     gD = np.gradient(D)
238     Daa, Dbb = aa(gD), bb(gD)
239     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 $\sigma={:.3f}$'.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[...,-1]
377 T[...,-1] / np.sqrt(T[...,-1])
378 T[...,-1] * np.sqrt(T[...,-1])
379 T[...,-1] * T[...,-1]
380 T[...,-1] * T[...,-1]**2
381 table
382 T[...,-3] * T[...,-3]**2
383 T[...,-3] * T[...,-3]
384 T[...,-4] * T[...,-4]
385 T[...,-4] / T[...,-4]
386 T[...,-4] / T[...,-4] > .01
387 which =
388 T[...,-1][which]
389 (T[...,-4] / T[...,-4]) > .001
390 scales
391 scales = np.logspace(-4,8, num=50, base=2)
392 scales
393 (T[...,-3] / T[...,-3]) > .001
394 (T[...,-3] / T[...,-3]) > .005
395 scales[_]
396 (T[...,-3] / T[...,-3]) > .001
397 scales
398 scales
399 (T[...,-3] / T[...,-3]) > .001
400 scales[_]
401 (T[...,-3] / T[...,-3]) > .05
402 T[...,-3]
403 (T[...,-3] / T[...,-3])

```

```

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
51     else:
52         printable = plate
53
54         plt.imshow(printable, cmap=CMAP)
55         plt.title(r'$\sigma={:.2f}$'.format(sigma))
56         plt.tight_layout()
57         c = plt.colorbar()
58         c.set_ticks = np.linspace(cmin, cmax, num=len(scales)+1)
59         plt.clim(cmin, cmax)
60         plt.axis('off')
61         outname = f'demo_output/scalesweep_{sample_name}_{label}_{n}.png'
62         plt.savefig(outname, dpi=300, bbox_inches='tight')
63         print('saved', outname)
64         plt.close()
65
66 # now make a stitched together version
67 for label in ['plate', 'inset']:
68     if label == 'inset':
69         L = fi
70         imgview = img[inset_slice].filled(0)
71         figsize = (12, 6)
72
73     else:
74         L = F
75         imgview = img[crop].filled(0)
76         figsize = (12, 9)
77 #adjust this manually depending on how many scales you end up using!
78
79 nrows, ncols = 2, 4
80 fig, axes = plt.subplots(nrows=nrows, ncols=ncols, figsize=figsize)
81
82 for n, (i, j) in enumerate(product(range(nrows), range(ncols))):
83
84     if n == 0:
85         axes[i,j].imshow(imgview, cmap=plt.cm.gray)
86         axes[i,j].set_title('raw')
87     else:
88         im = axes[i,j].imshow(L[n], cmap=CMAP, vmin=cmin, vmax=cmax)
89         axes[i,j].set_title(r'$\sigma={:.2f}$'.format(scales[n]))
90
91     plt.setp(axes[i,j].get_xticklabels(), visible=False)
92     plt.setp(axes[i,j].get_yticklabels(), visible=False)
93
94 fig.subplots_adjust(top=0.954, bottom=0.025, left=0.010,
95                     right=0.989, hspace=0.0, wspace=0.0)
96
97 plt.savefig(f'demo_output/scalesweep_stitch_{sample_name}_{label}.png',
98             dpi=300)
99
100 cfile = 'demo_output/scalesweep_colorbar.png'
101 if os.path.isfile(cfile):
102     continue # no need to make another
103
104 fig = plt.figure(figsize=(figsize[0],2))
105 ax1 = fig.add_axes([0.15, 0.25, 0.75, 0.5])
106 cbar = mpl.colorbar.ColorbarBase(ax1, cmap=CMAP,
107                                 norm=matplotlib.colors.Normalize(cmin,cmax),
108                                 orientation='horizontal')
109
110 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 import numpy as np
10
11 import itertools
12 from collections import deque
13
14 def rgb_to_widths(T):
15     """
16         this will take an RGB trace image (MxNx3) and return a 2D (MxN)
17         "labeled" trace corresponding to the traced pixel length.
18         there is no distinguishing between arteries and vessels
19
20         it's preferable to do this in real-time so only one tracefile
21         needs to be stored (making the sample folder less cluttered)
22         although obviously at the expense of storing a larger image
23         which is only needed for visualization purposes.
24
25     Input:
26         T: a MxNx3 RGB (uint8) array, where the colorations are
27             assumed as described in NOTES below.
28
29     Output:
30         widthtrace: a MxN array whose inputs describe the width of the
31             vessel (in pixels), see NOTES.
32
33     Notes:
34
35         The correspondence is as follows:
36         3 pixels: "#ff006f", # magenta
37         5 pixels: "#a80000", # dark red
38         7 pixels: "#a800ff", # purple
39         9 pixels: "#ff00ff", # light pink
40         11 pixels: "#008aff", # blue
41         13 pixels: "#8aff00", # green
42         15 pixels: "#ffc800", # dark yellow
43         17 pixels: "#ff8a00", # orange
44         19 pixels: "#ff0015" # bright red
45
46         According to the original tracing protocol, the traced vessels are
47         binned into these 9 sizes. Vessels with a diameter smaller than 3px
48         are not traced (unless they're binned into 3px).
49
50         Note: this does *not* deal with collisions. If you pass anything
51         with addition (blended colors) as the ctraces are, you will have
52         trouble, as those will not be registered as any of the colors above
53         and will thus be ignored. If you want to handle data from both
54         arterial *and* venous layers, you should do so outside of this
55         function.
56     """
57
58     # a 2D picture to fix in with the pixel widths
59     W = np.zeros_like(T[:, :, 0])
60
61     for pix, color in TRACE_COLORS.items():
62
63         #ignore pixelwidths outside the specified range
64         # get the 2D indices that are that color
65         idx = np.where(np.all(T == color, axis=-1))

```

```

66     W[idx] = pix
67
68
69     return W
70
71 def merge_widths_from_traces(A_trace, V_trace, strategy='minimum'):
72     """
73     combine the widths from two RGB-traces A_trace and V_trace
74     and return one width matrix according to 'strategy'
75
76     Parameters
77     -----
78     A_trace: ndarray
79         an MxNx3 matrix, where each pixel (along the
80         last dimension) is an RGB triplet (i.e. each entry
81         is an integer between [0,256]). The colors each
82         correspond to those in TRACE_COLORS, and (255,255,255)
83         signifies "no vessel". This will normally correspond to
84         the sample's arterial trace.
85     V_trace: ndarray
86         an MxNx3 matrix the same shape and other
87         requirements as A_trace (see above). This will normally
88         correspond to the sample's venous trace.
89     strategy: keyword string
90         when A_trace and V_trace coincide at some entry,
91         this is the merging strategy. It should be a keyword
92         of one of the following choices:
93
94         "minimum": take the minimum width of the two traces
95             (default). this is the sensible option if you
96             are filtering out larger widths.
97         "maximum": take the maximum width of the two traces
98         "artery" or "A" or "top": take the width from A_trace
99         "vein" or "V" or "bottom": take the width from V_trace
100
101    Returns
102    -----
103        W : ndarray
104        a width-matrix where each entry is a number 0 (no vessel), 3,5,7,...19
105
106    Notes
107    -----
108    Since arteries grow over the veins on the PCSVN and are generally easier
109    to extract, it might be preferable to indicate "arteries". In reality,
110    each strategy is a compromise, and only by keeping track of both would
111    you get the complete picture.
112
113    No filtering out widths is done here.
114    """
115    assert A_trace.shape == V_trace.shape
116
117    A = rgb_to_widths(A_trace)
118    V = rgb_to_widths(V_trace)
119
120    # collisions (where are widths both reported)
121    c = (A!=0)& (V!=0)
122
123    W = np.maximum(A,V) # get the nonzero value
124    if strategy == 'maximum':
125        pass # already done, else rewrite the collisions
126    elif strategy in ('arteries', 'A', 'top'):
127        W[c] = A[c]
128    elif strategy in ('veins', 'V', 'bottom'):
129        W[c] = V[c]

```

```

130     else:
131         if strategy != 'minimum':
132             print(f"Warning: unknown merge strategy: {strategy}")
133             print("Defaulting to minimum strategy")
134
135     W[c] = np.minimum(A[c], V[c])
136
137     return W
138
139 def filter_widths(W, widths=None, min_width=3, max_width=19):
140     """
141     Filter a width matrix, removing widths according to rules.
142
143     This function will take a 2D matrix of vessel widths and
144     remove any widths outside a particular range (or alternatively,
145     that are not included in a particular list)
146
147     Should be roughly as easy as doing it by hand, except that you
148     won't have to rewrite the code each time.
149
150     Inputs:
151
152     W: a width matrix (2D matrix with elements 0,3,5,7,...19
153
154     min_width: widths below this will be excluded (default is
155                 3, the min recorded width). assuming these
156                 are ints
157
158     max_width: widths above this will be excluded (default is
159                 19, the max recorded width)
160
161     widths: an explicit list of widths that should be returned.
162                 in this case the above min & max are ignored.
163                 this way you could include widths = [3, 17, 19] only
164                 """
165
166     Wout = W.copy()
167     if widths is None:
168         Wout[W < min_width] = 0
169         Wout[W > max_width] = 0
170
171     else:
172         # use numpy.isin(T, widths) but that's only in version 1.13 and up
173         # of numpy this is basically the code for that though
174         to_keep = np.in1d(W, widths, assume_unique=True).reshape(W.shape)
175         Wout[~to_keep] = 0
176
177     return Wout
178
179 TRACE_COLORS = {
180     3: (255, 0, 111),
181     5: (168, 0, 0),
182     7: (168, 0, 255),
183     9: (255, 0, 255),
184     11: (0, 138, 255),
185     13: (138, 255, 0),
186     15: (255, 200, 0),
187     17: (255, 138, 0),
188     19: (255, 0, 21)
189 }
190
191
192 def widths_to_rgb(w, show_non_matches=False):
193     """Convert width matrix back to RGB values.

```

```

194
195 For display purposes/convenience. Return an RGB matrix
196 converting back from [3,5,7, ... , 19] -> TRACE_COLORS
197
198 this doesn't do any rounding (i.e. it ignores anything outside of
199 the default widths), but maybe you'd want to?
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
218 def _hex_to_rgb(hexstring):
219 """
220 there's a function that does this in matplotlib.colors
221 but its scaled between 0 and 1 but not even as an
222 array so this is just as much work
223
224 ##TODO rewrite everything so this is useful if it's not been
225 rewritten already.
226 """
227 triple = hexstring.strip("#")
228 return tuple(int(x, 16) for x in (triple[:2], triple[2:4], triple[4:]))
229
230
231 def skeletonize_trace(T, T2=None):
232 """
233 if T is a boolean matrix representing a trace, then thin it
234
235 if T is an RGB trace, then register it according to the
236 tracing protocol then thin it
237
238 if T2 is provided, do the same thing to T2 and then merge the two
239 """
240 if T.ndim == 3:
241     trace = (rgb_to_widths(T) > 0) # booleanize it
242 else:
243     trace = T.astype('bool')
244
245 thinned = thin(trace)
246
247 if T2 is None:
248     return thinned
249
250 else:
251     # do the same thing to second trace and merge it
252     if T2.ndim == 3:
253         trace_2 = (rgb_to_widths(T2) > 0) # booleanize it
254         thinned_2 = thin(trace_2)
255
256     return np.logical_or(thinned, thinned_2)
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         #
291         #colordict = {
292             # 'TN': (49,49,49), # true negative# 'f7f7f7'
293             # 'TP': (0, 0, 0), # true positive # '000000'
294             # 'FN': (201,53,108), # false negative # 'f1a340' orange
295             # 'FP': (0,112,163), # false positive # '998ec4' purple
296             # 'mask': (247, 200, 200) # mask color (not used in MCC calculation)
297             #
298         colordict = {
299             'TP': (0,0,0),
300             'TN': (226,226,226),
301             'FN': (201,80,80),
302             'FP': (30,69,230),
303             'mask': (209,209,209)
304         }
305
306     #TODO: else check if mask is specified and add it as color of TN otherwise
307
308     true_neg_color = np.array(colordict['TN'], dtype='f')/255
309     true_pos_color = np.array(colordict['TP'], dtype='f')/255
310     false_neg_color = np.array(colordict['FN'], dtype='f') /255
311     false_pos_color = np.array(colordict['FP'], dtype='f')/255
312     mask_color = np.array(colordict['mask'], dtype='f') /255
313
314     assert test.shape == truth.shape
315
316     # convert to bool
317     test, truth = test.astype('bool'), truth.astype('bool')
318
319     # RGB array size of test and truth for output
320     output = np.zeros((test.shape[0], test.shape[1], 3), dtype='f')
321

```

```

322 # truth conditions
323 true_pos = (test==truth & truth)
324 true_neg = (test==truth & ~truth)
325 false_neg = (truth & ~test)
326 false_pos = (test & ~truth)
327
328 output[true_pos,:] = true_pos_color
329 output[true_neg,:] = true_neg_color
330 output[false_pos,:] = false_pos_color
331 output[false_neg,:] = false_neg_color
332
333 # try to find a mask
334 if bg_mask is None:
335     try:
336         bg_mask = test.mask
337     except AttributeError:
338         # no mask is specified, we're done.
339         return output
340
341 # color the mask
342 if tint_mask:
343     output[bg_mask,:] += mask_color
344     output[bg_mask,:] /= 2
345 else:
346     output[bg_mask,:] = mask_color
347
348 return output
349
350
351 def compare_trace(approx, trace=None, filename=None,
352                   sample_dir=None, colordict=None):
353     """
354     compare approx matrix to trace matrix and output a confusion matrix.
355     if trace is not supplied, open the image from the tracefile.
356     if tracefile is not supplied, filename must be supplied, and
357     tracefile will be opened according to the standard pattern
358
359     colordict are parameters to pass to confusion()
360
361     returns a matrix
362     """
363
364     # load the tracefile if not supplied
365     if trace is None:
366         if filename is not None:
367             try:
368                 trace = open_typefile(filename, 'trace')
369             except FileNotFoundError:
370                 print("No trace file found matching ", filename)
371                 print("no trace found. generating dummy trace.")
372                 trace = np.zeros_like(approx)
373         else:
374             print("no trace supplied/found. generating dummy trace.")
375             trace = np.zeros_like(approx)
376
377     C = confusion(approx, trace, colordict=colordict)
378
379     return C
380
381
382 def mcc(test, truth, bg_mask=None, score_bg=False, return_counts=False):
383     """
384     Matthews correlation coefficient
385     returns a float between -1 and 1

```

```

386 -1 is total disagreement between test & truth
387 0 is "no better than random guessing"
388 1 is perfect prediction
389
390 bg_mask is a mask of pixels to ignore from the statistics
391 for example, things outside the placental plate will be counted
392 as "TRUE NEGATIVES" when there wasn't any chance of them not being
393 scored as negative. therefore, it's not really a measure of the
394 test's accuracy, but instead artificially pads the score higher.
395
396 setting bg_mask to None when test and truth are not masked
397 arrays should give you this artificially inflated score.
398 Passing score_bg=True makes this decision explicit, i.e.
399 any masks (even if supplied) will be ignored, and your count of
400 false positives will be inflated.
401
402 """
403
404 true_pos = ((test == truth) & truth)
405 true_neg = ((test == truth) & ~truth)
406 false_neg = (truth & ~test)
407 false_pos = (test & ~truth)
408
409 if score_bg:
410     # take the classifications above as they are (nothing is masked)
411     pass
412 else:
413     # if no specified mask, check the test array itself?
414     if bg_mask is None:
415         try:
416             bg_mask = test.mask
417         except AttributeError:
418             # no mask is specified, we're done.
419             bg_mask = np.zeros_like(test)
420
421     # only get stats in the plate
422     true_pos[bg_mask] = 0
423     true_neg[bg_mask] = 0
424     false_pos[bg_mask] = 0
425     false_neg[bg_mask] = 0
426
427     # now tally
428     TP = true_pos.sum()
429     TN = true_neg.sum()
430     FP = false_pos.sum()
431     FN = false_neg.sum()
432
433 if not score_bg:
434     total = np.sum(~bg_mask)
435 else:
436     total = test.size
437
438 #print('TP: {}\\t TN: {}\\tFP: {}\\tFN: {}'.format(TP,TN,FP,FN))
439 #print('TP+TN+FN+FP={}\\ntotal pixels={}'.format(TP+TN+FP+TN,total))
440 # prevent potential overflow
441 denom = np.sqrt(TP+FP)*np.sqrt(TP+FN)*np.sqrt(TN+FP)*np.sqrt(TN+FN)
442
443 if denom == 0:
444     # set MCC to zero if any are zero
445     m_score = 0
446 else:
447     m_score = ((TP*TN) - (FP*FN)) / denom
448
449 if return_counts:

```

```

450         return m_score, (TP,TN,FP,FN)
451     else:
452         return m_score
453
454 def mean_squared_error(A,B):
455     """
456     get mean squared error between two matrices of the same size
457
458     input:
459         A, B : two ndarrays of the same size.
460
461     output:
462
463         mse: a single number.
464     """
465
466
467     try:
468         mse = ((A-B)**2).sum() / A.size
469
470     except ValueError:
471         print("inputs must be of the same size")
472         raise
473
474     return mse
475
476 def chain_lengths(iterable):
477
478     pos, s = 0, 0
479
480     for b, g in itertools.groupby(iterable):
481
482         if not b:
483             # alternative if the bottom doesn't work or something
484             #d = deque(enumerate(g,1), maxlen=1)
485             #pos += d[0][0] if d else 0
486
487             pos += sum((1 for i in g if not i))
488
489         else:
490
491             s = sum(g)
492
493             yield pos, s
494
495             pos += s
496
497         if not s:
498             # so it will return something even if iterable is empty
499             yield 0, 0
500
501
502 def _longest_chain_1d(iterable):
503     """
504     will return a tuple of ind, length
505     where ind is the position in the iterable the chain starts and length is the
506     length of the chain
507     """
508
509     return max(chain_lengths(iterable), key=lambda x: x[1])
510
511
512 def longest_chain(arr, axis):
513     """
514     Find where the longest chain of boolean values and occurs across an array
515     and also return its length
516     """

```

```

514
515     C = np.apply_along_axis(_longest_chain_1d, axis, arr.astype('bool'))
516
517     start_inds, chain_lens = np.split(C, 2, axis)
518
519     return np.squeeze(start_inds), np.squeeze(chain_lens)
520
521
522 def _bunch_hists(H, bunches):
523
524     return np.stack((np.sum(np.atleast_2d(H[b,:]), axis=0) for b in bunches))
525
526
527 def scale_to_width_plots(multiscale_approx, max_labels, widths, scales,
528                           bunches=None, cmap=None, approx_method=None,
529                           figsize=(13,14), style='seaborn', bunch_until=None):
530     """
531     multiscale_approx is a 3d boolean array whose first dimension is scale
532     max_labels is a 2d array of integers that say where the max value of
533     F occured. you can get max_labels by running V.argmax(axis=0)
534
535     in widths, each pixel has a unique width
536
537     bunches.flatten() should be the same as arange(scales)
538     but can be something like
539     ( (0,1,2,3), (4,5), 6, 7, 8, (9,10,11) )
540
541     or even
542
543     (2,3,4,5,(0,1,6,7))
544
545     this is to prevent similar scales from clogging, you can just bin them
546     all together.
547
548     approx method is a label to use in the fig titles
549     """
550
551     if bunches is None:
552         if bunch_until is not None:
553             indices = list(range(len(scales)))
554             bunches = [indices[:bunch_until],] + indices[bunch_until:]
555
556     plt.style.use(style)
557
558     fig, ax = plt.subplots(nrows=2, ncols=1, figsize=figsize)
559
560     A = multiscale_approx # easier to work with
561
562     wbins = np.arange(3,20,2) # bins of widths in ground truth
563
564     max_hists = [[np.sum((max_labels == s) & (widths==w)) for w in wbins]
565                  for s in range(len(scales))]
566
567     hists = np.array([[np.sum((widths==w) & A[n]) for w in wbins]
568                      for n in range(len(scales))])
569
570
571     if cmap is None:
572         # this will just use the default cycle of colors
573         colors = np.repeat(None, len(scales))
574     else:
575         if not isinstance(cmap, mpl.colors.LinearSegmentedColormap):
576             # try this

```

```

578     cmap = plt.get_cmap(cmap)
579
580     colors = cmap(np.linspace(0,1,len(scales)))
581
582     labels = [rf'$\sigma_{\{{k}\}}$={sigma:.2f}$'
583               for k, sigma in enumerate(scales,1)]
584
585     # number of true positives, false negatives for each width
586     tp_hists = [np.sum((widths==w) & A.any(axis=0)) for w in wbins]
587     fn_hists = [np.sum((widths==w) & ~A.any(axis=0)) for w in wbins]
588
589     if bunches is not None:
590         hists = _bunch_hists(hists, bunches)
591
592         # just return \sigma_{1,2,3} or something rather than listing
593         bunch_label = lambda b: r"$\sigma_{\{{\}}}$".format(', '.join([
594             str(x+1)
595             for x in b
596             ]))
597
598     labels = [labels[b] if np.isscalar(b) else bunch_label(b)
599               for b in bunches]
600
601     if cmap is None:
602         # just make it the appropriate length
603         cmap = np.repeat(None, len(bunches))
604     else:
605         colors = [colors[b] if np.isscalar(b) else colors[b[0]]
606                   for b in bunches]
607
608     ax[0].bar(wbins, tp_hists, color=(0.6,0.6,0.6),
609               label='# true positives')
610     ax[0].bar(wbins, fn_hists, bottom=tp_hists, color=(1,.8,.8),
611               label='# false negatives')
612
613     for h, mh, label, color in zip(hists, max_hists, labels, colors):
614         ax[0].plot(wbins, h, label=label, color=color)
615         ax[1].plot(wbins, mh, label=label, color=color)
616
617     ax[0].set_xticks(wbins)
618     ax[0].set_xlabel('vessel widths (ground truth), pixels')
619     ax[0].set_ylabel('# pixels')
620     ax[0].set_xlim(2,21)
621
622     ax[1].set_xticks(wbins)
623     ax[1].set_xlabel('vessel widths (ground truth), pixels')
624     ax[1].set_ylabel('# pixels')
625     ax[1].set_xlim(2,21)
626
627     title = 'pixels reported per scale'
628     max_title = r'pixel widths of true positives by scale of $V_{\max}$'
629     if approx_method is not None:
630         title += f'({approx_method})'
631         max_title += f'({approx_method})'
632
633     ax[0].set_title(title)
634     ax[1].set_title(max_title)
635     ax[0].legend(loc='best', labelspacing=0.2)
636     ax[1].legend(loc='best', labelspacing=0.2)
637
638     fig.tight_layout()
639     return fig, ax
640
641

```

```

642 def scale_to_argmax_plot(max_labels, widths, scales, normalize=False,
643                             bunches=None, cmap=None, figsize=(13,10),
644                             style='seaborn-paper', bunch_until=None):
645     """
646     if normalize, normalize each scale over columns (i.e. all widths)
647     multiscale_approx is a 3d boolean array whose first dimension is scale
648     max_labels is a 2d array of integers that say where the max value of
649     F occurred. you can get max_labels by running V.argmax(axis=0)
650
651     in widths, each pixel has a unique width
652
653     bunches.flatten() should be the same as arange(scales)
654     but can be something like
655     ( (0,1,2,3), (4,5), 6, 7, 8, (9,10,11) )
656
657     or even
658
659     (2,3,4,5,(0,1,6,7))
660
661     this is to prevent similar scales from clogging, you can just bin them
662     all together.
663
664     approx method is a label to use in the fig titles
665     """
666
667     if bunches is None:
668         if bunch_until is not None:
669             indices = list(range(len(scales)))
670             bunches = [indices[:bunch_until],] + indices[bunch_until:]
671
672     plt.style.use(style)
673
674     fig, ax = plt.subplots(figsize=figsize)
675
676     wbins = np.arange(3,20,2) # bins of widths in ground truth
677
678     max_hists = np.array([[np.sum((max_labels == s) & (widths==w)) for w in wbins]
679                           for s in range(len(scales))])
680
681     if normalize:
682         max_hists = max_hists / max_hists.sum(axis=1, keepdims=True)
683
684     if cmap is None:
685         # this will just use the default cycle of colors
686         colors = np.repeat(None, len(scales))
687     else:
688         if not isinstance(cmap, mpl.colors.LinearSegmentedColormap):
689             # try this
690             cmap = plt.get_cmap(cmap)
691
692         colors = cmap(np.linspace(0,1,len(scales)))
693
694     labels = [rf'$\sigma_{\{{k}\}}$={sigma:.2f}$'
695               for k, sigma in enumerate(scales,1)]
696
697     # number of true positives, false negatives for each width
698
699     if bunches is not None:
700
701         # just return \sigma_{1,2,3} or something rather than listing
702         bunch_label = lambda b: r"$\sigma_{\{{\}}}$".format(', '.join([
703             str(x+1)
704             for x in b
705         ]))
706
707     labels = [labels[b] if np.isscalar(b) else bunch_label(b)

```

```

706         for b in bunches]
707
708     if cmap is None:
709         # just make it the appropriate length
710         cmap = np.repeat(None, len(bunches))
711     else:
712         colors = [colors[b] if np.isscalar(b) else colors[b[0]]
713                   for b in bunches]
714
715     #ax.bar(wbins, tp_hists, color=(0.6,0.6,0.6),
716     #        label='# true positives')
717     #ax.bar(wbins, fn_hists, bottom=tp_hists, color=(1,.8,.8),
718     #        label='# false negatives')
719
720     for mh, label, color in zip(max_hists, labels, colors):
721         ax.plot(wbins, mh, label=label, color=color)
722
723
724
725     ax.set_xticks(wbins)
726     ax.set_xlabel('vessel widths (ground truth), pixels')
727     if normalize:
728         ax.set_ylabel('# pixels identified by scale /'
729                     '# pixels identified by all scales')
730     else:
731         ax.set_ylabel('# pixels')
732
733     ax.set_xlim(2,21)
734
735     max_title = r'pixel widths of true positives by scale of $V_{\max}$'
736
737     ax.set_title(max_title)
738     ax.legend(loc='best', labelspacing=0.2)
739
740     fig.tight_layout()
741     return fig, ax
742
743
744 if __name__ == "__main__":
745
746     import matplotlib.pyplot as plt
747     from skimage.data import binary_blobs
748
749     A = binary_blobs()
750     B = binary_blobs()
751
752     true_neg_color = np.array([247,247,247], dtype='f') # 'f7f7f7'
753     true_pos_color = np.array([0, 0, 0], dtype='f') # '000000'
754     false_neg_color = np.array([241,163,64], dtype='f')# 'f1a340'
755     false_pos_color = np.array([153,142,195], dtype='f') # '998ec4'
756
757     C = confusion(A,B)
758
759     fig, (ax0, ax1, ax2) = plt.subplots(nrows=1,
760                                         ncols=3,
761                                         figsize=(8, 2.5),
762                                         sharex=True,
763                                         sharey=True)
764
765     ax0.imshow(A, cmap='gray')
766     ax0.set_title('A')
767     ax0.axis('off')
768     ax0.set_adjustable('box-forced')
769

```

```

770 ax1.imshow(B, cmap='gray')
771 ax1.set_title('B')
772 ax1.axis('off')
773 ax1.set_adjustable('box-forced')
774
775 ax2.imshow(C)
776 ax2.set_title('confusion matrix of A and B')
777 ax2.axis('off')
778 ax2.set_adjustable('box-forced')
779
780 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         else:
81             im = axes[i,j].imshow(L[n], cmap=CMAP, vmin=cmin, vmax=cmax)
82             axes[i,j].set_title(r'$\sigma={:.2f}$'.format(scales[n]))
83
84         plt.setp(axes[i,j].get_xticklabels(), visible=False)
85         plt.setp(axes[i,j].get_yticklabels(), visible=False)
86
87         #for i in range(5):
88         #    fig.tight_layout()
89
90         #fig.subplots_adjust(right=0.8)
91         #cax = fig.add_axes([.85,.15,.05,.7])
92         #c = fig.colorbar(im, ax=cax)
93
94         fig.subplots_adjust(top=0.954, bottom=0.025, left=0.010,
95                             right=0.989, hspace=0.0, wspace=0.0)
96
97         plt.savefig(f'demo_output/signsweep_stitch_{sample_name}_{label}.png',
98                     dpi=300)
99
100        cfile = 'demo_output/signsweep_colorbar.png'
101        if os.path.isfile(cfile):
102            continue # no need to make another
103
104        fig = plt.figure(figsize=(figsize[0],2))
105        ax1 = fig.add_axes([0.15, 0.25, 0.75, 0.5])
106        cbar = mpl.colorbar.ColorbarBase(ax1, cmap=CMAP,
107                                         norm=mpl.colors.Normalize(cmin,cmax),
108                                         orientation='horizontal')
109
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)

```

```
113 #imga = plt.imshow(stitched, cmap=CMAP)
114 #plt.imsave(f'demo_output/signsweep_stitch_{sample_name}_{label}.png',
115 #            stitched, cmap=CMAP, vmin=cmin, vmax=cmax)
116
117 # also save the original pic
118 #plt.imsave(f'demo_output/signsweep_{sample_name}_{label}_raw',
119 #            imgview, cmap=plt.cm.gray)
```

APPENDIX B
3D VISUALIZATION OF THE FRANGI FILTER

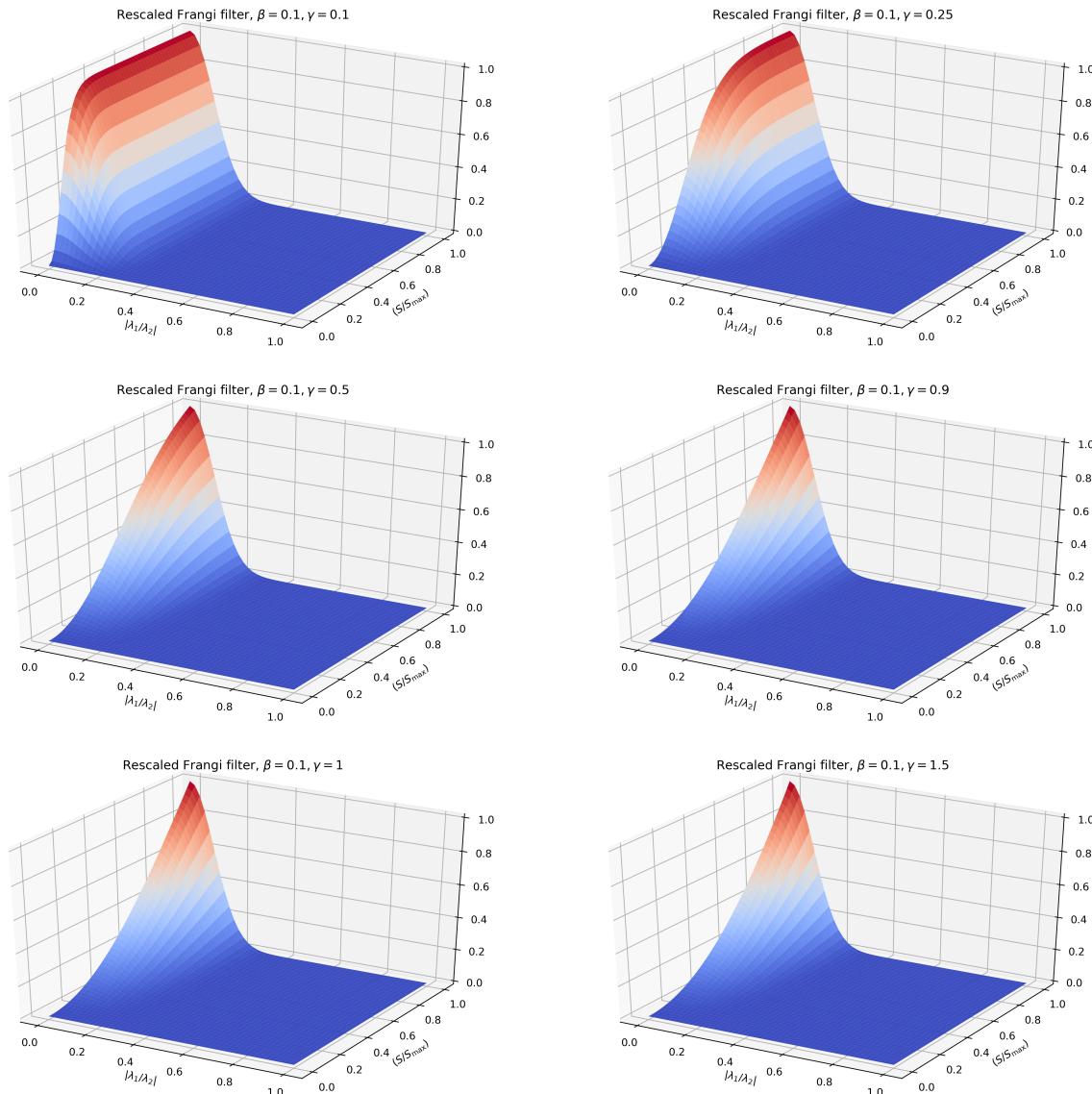


FIGURE 34: 3D graph of the Frangi Vesselness Measure, variable γ , $\beta = 0.1$

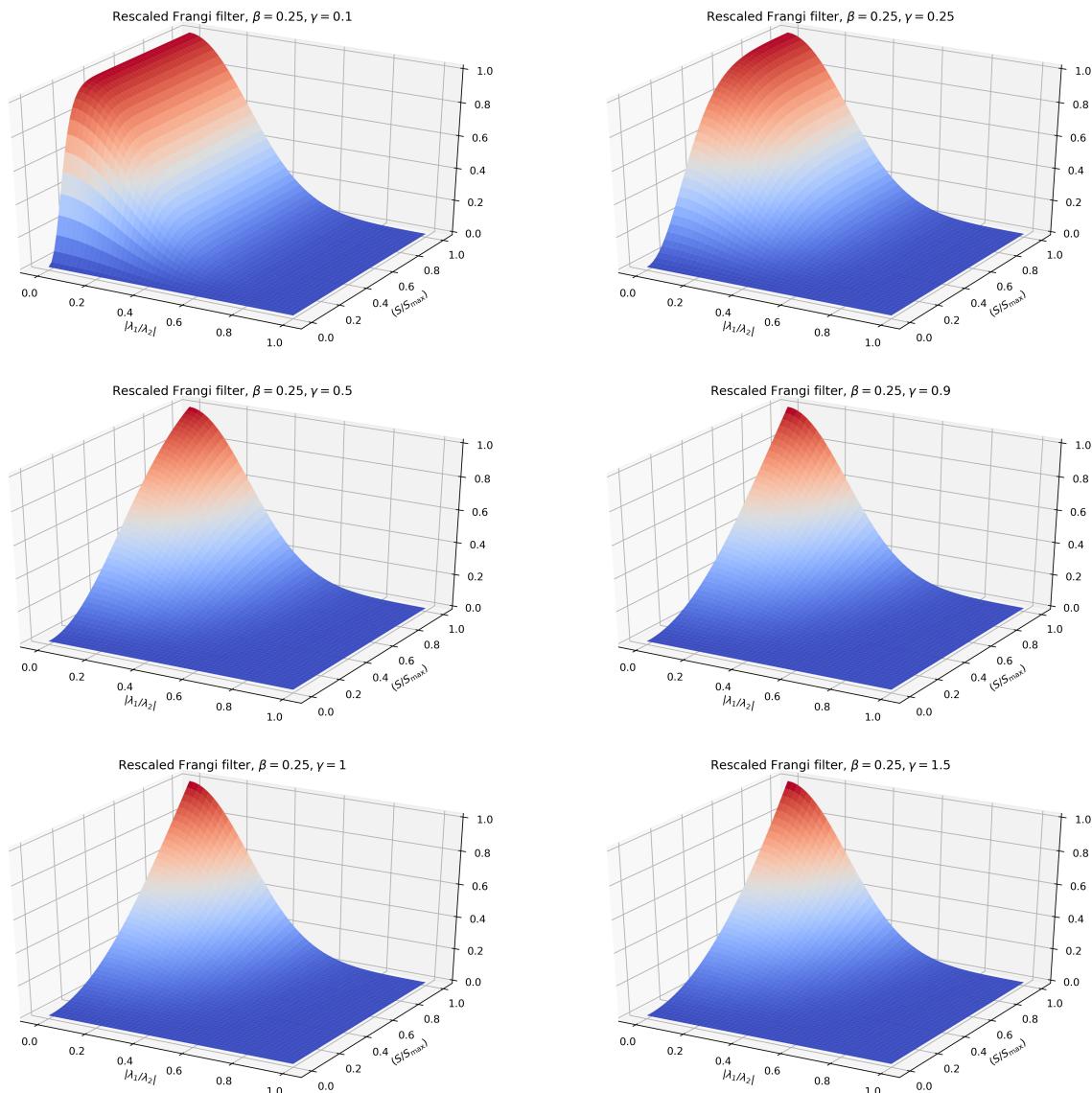


FIGURE 35: 3D graph of the Frangi Vesselness Measure, variable γ , $\beta = 0.25$

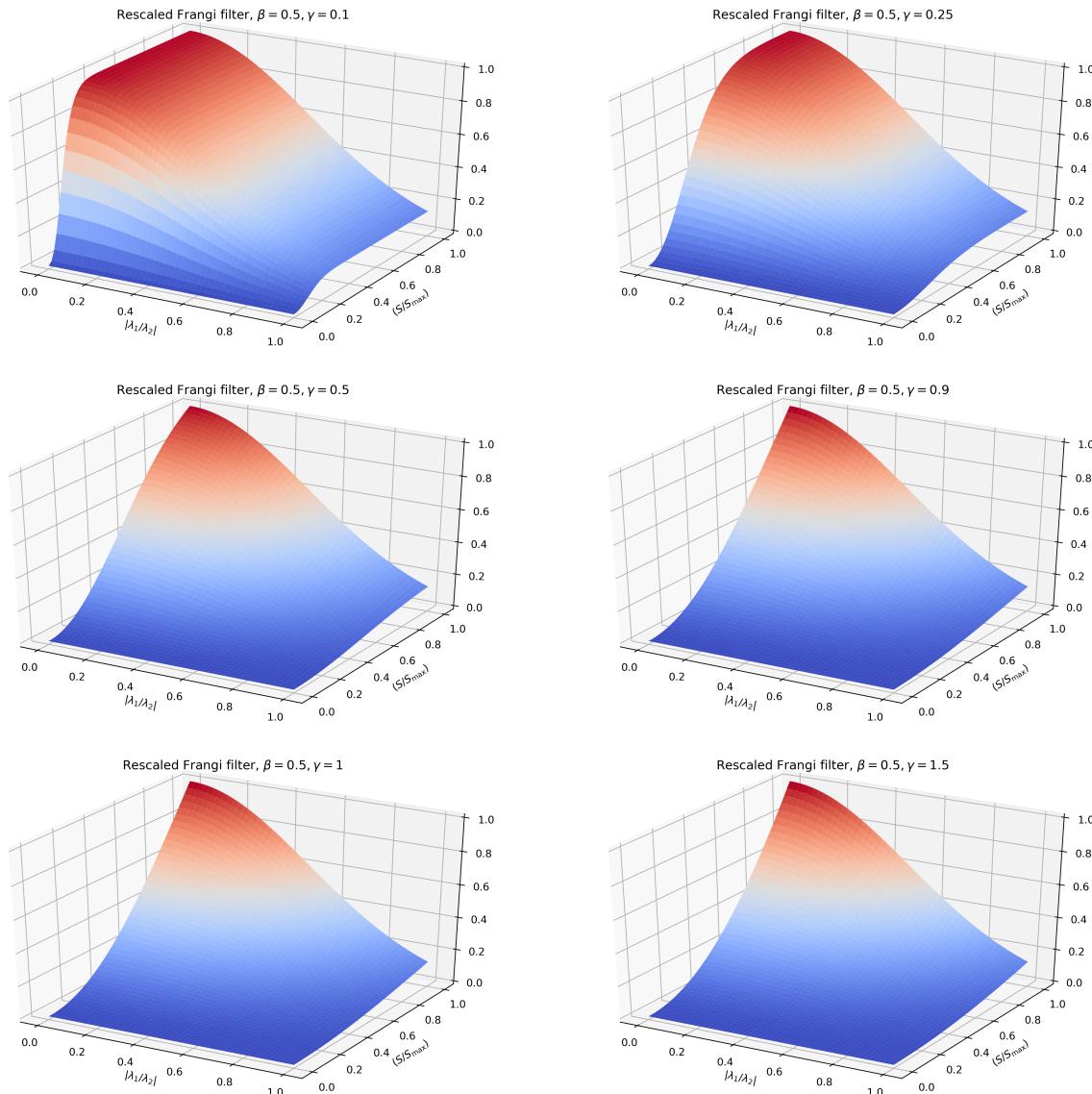


FIGURE 36: 3D graph of the Frangi Vesselness Measure, variable γ , $\beta = 0.5$

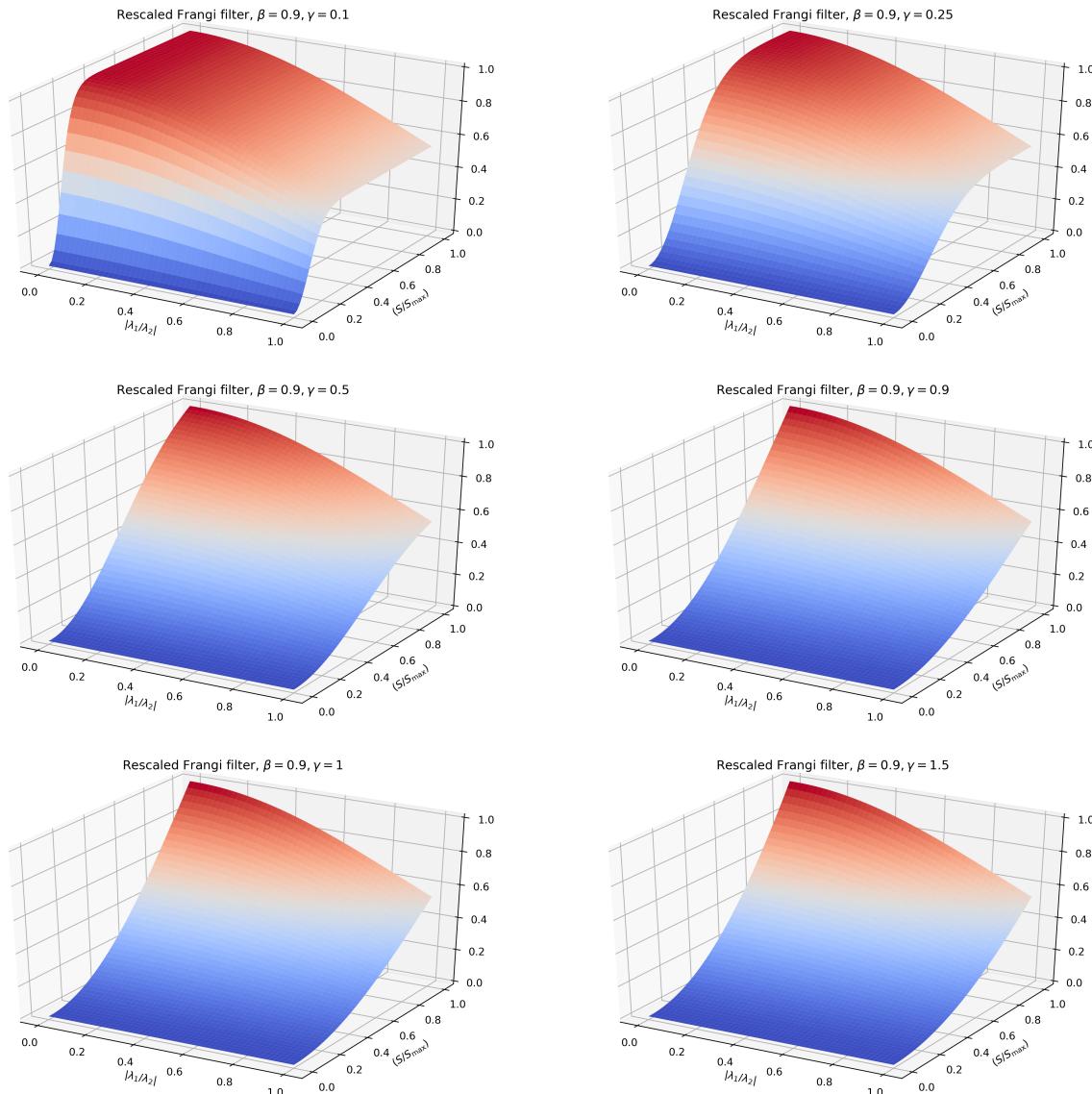


FIGURE 37: 3D graph of the Frangi Vesselness Measure, variable γ , $\beta = 0.9$

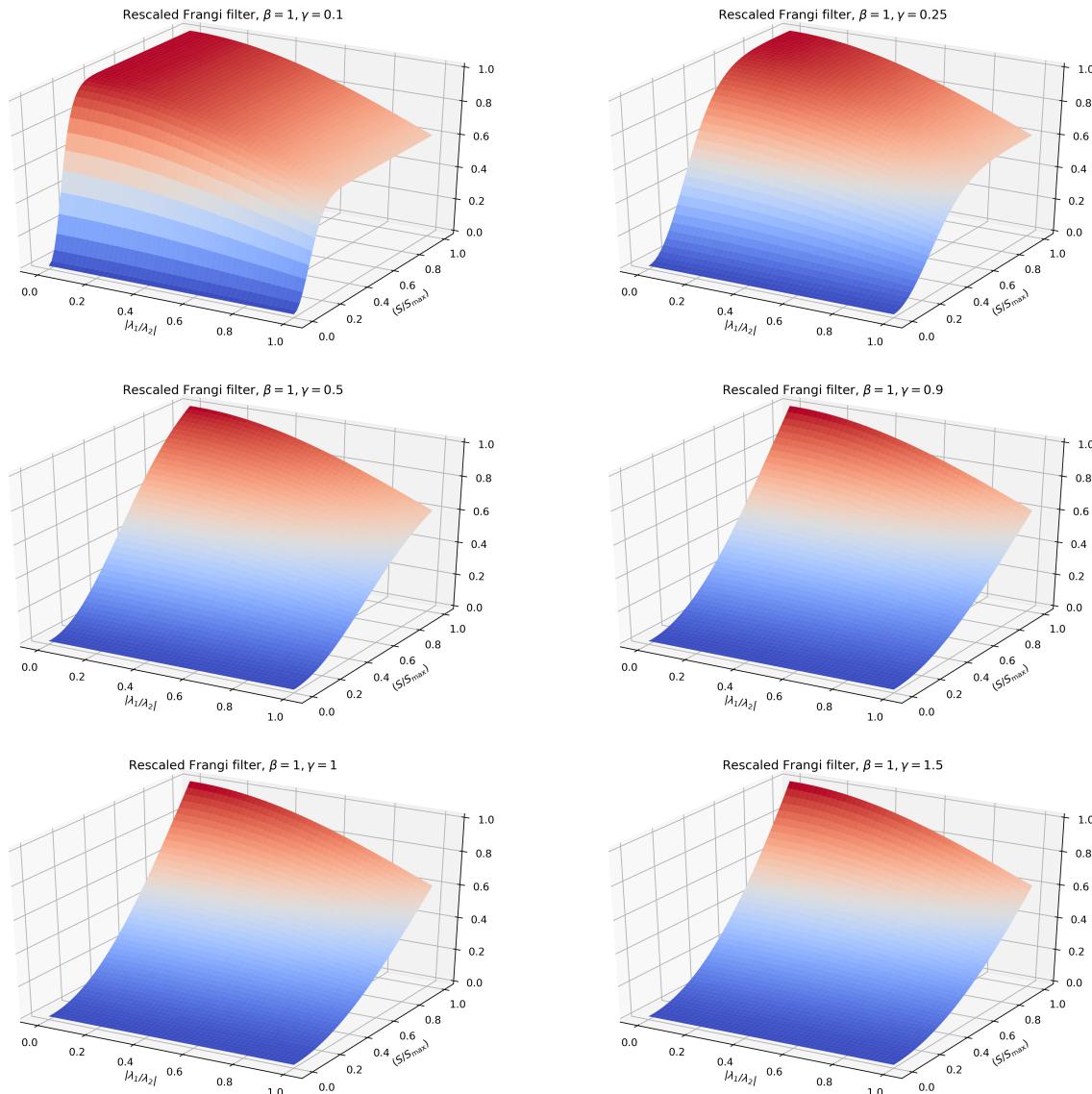


FIGURE 38: 3D graph of the Frangi Vesselness Measure, variable γ , $\beta = 1$

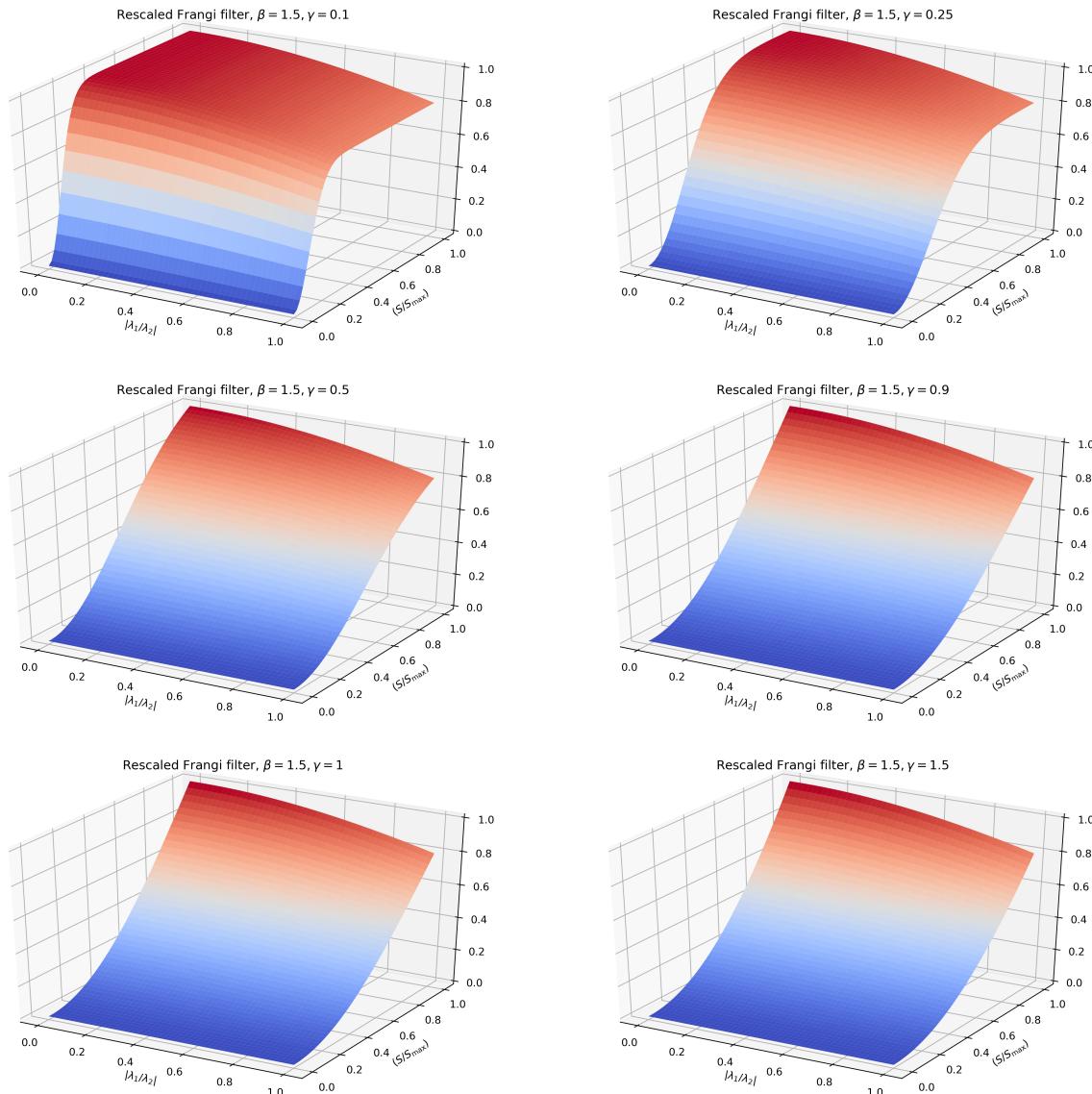


FIGURE 39: 3D graph of the Frangi Vesselness Measure, variable γ , $\beta = 1.5$

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BIBLIOGRAPHY

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