ABSTRACT

AN OPTIMIZED FRANGI FILTER FOR FAST VASCULAR SEGMENTATION TOWARDS A FAST AUTOMATIC PLACENTAL CHORIONIC SURFACE VASCULAR NETWORK EXTRACTION

By

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

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

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

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

We demonstrate the effectiveness of our sped-up implementation of the Frangi filter by performing a large (N=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.

AN OPTIMIZED FRANGI FILTER FOR FAST VASCULAR SEGMENTATION TOWARDS A FAST AUTOMATIC PLACENTAL CHORIONIC SURFACE VASCULAR NETWORK EXTRACTION

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Thank you to people for things.

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 was 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 are 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 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 demonstrate several approaches to merging the multiscale result into an approximation of the PCSVN and compare these to manual tracings of the network. Our ability to take many more scales into consideration allows us to be pickier about our thresholding, as well as our choice of parameters, which significantly reduces noise experienced in previous efforts. We finally suggest several ways to improve upon our approximation, namely by using the Frangi result as a prefilter for more robust techniques.

CHAPTER 2

MATHEMATICAL METHODS

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 suitiable 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 MxN array of pixels, whose intensity is given by an integer value between 0 and 255.

Definition 2.1 (Image as a pixel matrix)**.**

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

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)**.**

$$h : \mathbb{R}^2 \to \mathbb{R} \quad with \quad h \in C^2\left(\mathbb{R}^2\right), \quad where \quad h(i,j) = \mathtt{I}_{ij}\ \forall (i,j) \in \{0,...,M\}\times\{0,...,N\} \subset \mathbb{N}^2$$

That is, the function h is identical to the pixel matrix $\mathtt{I}$ 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 3.1), 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 2.4, we ultimately use these techniques because we find them successful to our problem.

Differential Geometry

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

Preliminaries of Differential Geometry

Given an open subset $U \subset \mathbb{R}^2$ and a twice differentiable function $h : U \to \mathbb{R}$ (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*

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

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.
$p = f(u) = f(u_1, u_2) = \Big(u_1, u_2, h(u_1, u_2)\Big)$, 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*

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

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

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

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 $U \to \mathbb{R}^3$ 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. □

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 $c : I \to \mathbb{R}^3$ parametrized along some closed interval $I \in \mathbb{R}$ (that is, a differentiable, one-to-one curve where $c'(s) = 1 \ \ \forall s \in I$), 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 $c : I \to \mathbb{R}^3$ a surface curve in the event that* $\text{image}(c) \subset \text{image}(f)$ *entirely. The one-to-one-ness of*

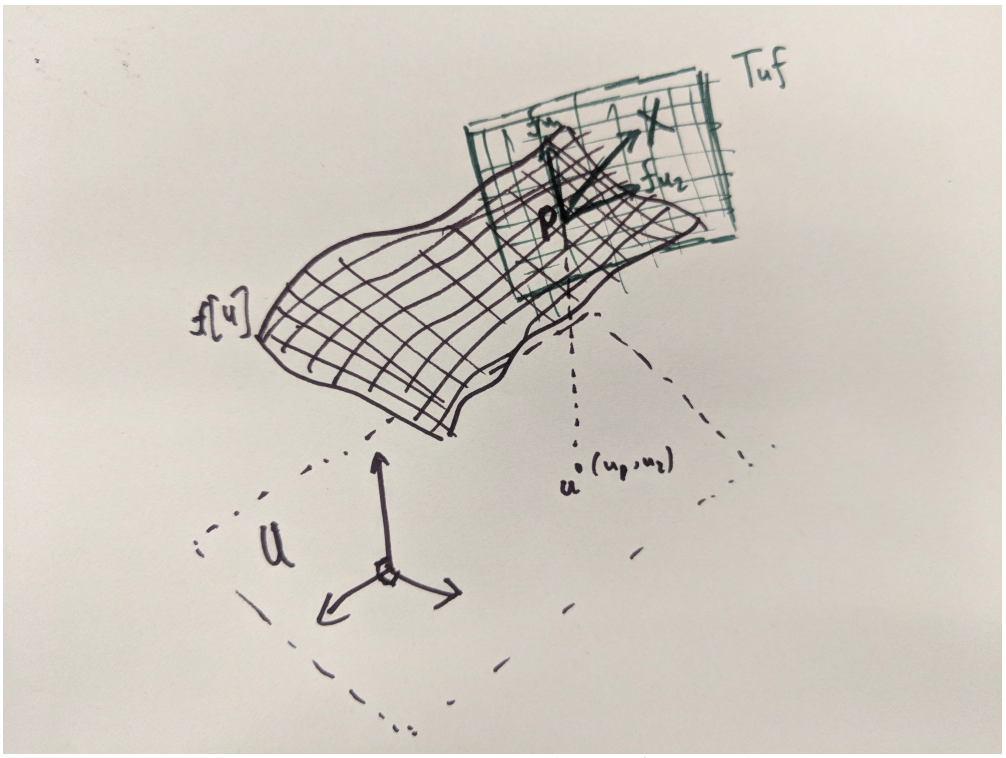


FIGURE 1: Tangent plane of a graph

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,

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

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 $T_u f$. This can be seen by an elementary application of chain rule:

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

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

$$= \theta_1'(t)\left(\frac{\partial f}{\partial u_1}\right) + \theta_2'(t)\left(\frac{\partial f}{\partial u_2}\right) \in T_u f. \tag{2.3}$$

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 $c : I \to \text{image}(f)$ 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*

$$\nu : U \to \mathbb{R}^3 \quad by \quad \nu(u) := \frac{\frac{\partial f}{\partial u_1} \times \frac{\partial f}{\partial u_2}}{\| \frac{\partial f}{\partial u_1} \times \frac{\partial f}{\partial u_2} \|}$$

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 $\nu \perp \frac{\partial f}{\partial u_i}$ 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 $\left\{\frac{\partial \nu}{\partial u_1}, \frac{\partial \nu}{\partial u_2}\right\} \in T_u f$, first note that at any particular $u \in U$, $\langle \nu, \nu \rangle = 1 \implies \frac{\partial}{\partial u_i}\langle \nu, \nu \rangle = 0$, and so by chain rule $2\langle \frac{\partial \nu}{\partial u_i}, \nu \rangle = 0 \implies \frac{\partial \nu}{\partial u_i} \perp \nu$. Since $\nu \perp \text{span}\left\{\frac{\partial f}{\partial u_i}\right\}$ as well (since ν its outer product), in $\mathbb{R}^3$, this implies $\text{span}\left\{\frac{\partial \nu}{\partial u_i}\right\} \parallel \text{span}\left\{\frac{\partial f}{\partial u_i}\right\}$.

Thus, we have $\text{span}\left\{\frac{\partial \nu}{\partial u_1}, \frac{\partial \nu}{\partial u_2}\right\} \subset T_u f$ 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 $\frac{\partial c}{\partial t}(u) = X$ 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 $u = \theta_c(p)$)

$$c'' = \langle c'', X\rangle X + \langle c'', \nu\rangle \nu \tag{2.4}$$

.

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:

$$\begin{aligned}
\langle c'', \nu\rangle &= \frac{\partial}{\partial t}[\langle c', \nu\rangle] - \langle c', \frac{\partial \nu}{\partial t}\rangle && (2.5)\\
&= \frac{\partial}{\partial t}[\langle X, \nu\rangle] - \langle c', \frac{\partial \nu}{\partial t}\rangle && (2.6)\\
&= 0 - \langle X, \frac{\partial \nu}{\partial t}\rangle && (2.7)
\end{aligned}$$

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

$$\begin{aligned}
\|c''\| = \|\langle c'', X\rangle X + \langle c'', \nu\rangle \nu\| &= \|0 + \langle c'', \nu\rangle \nu\| && (2.8)\\
&= -\langle X, \frac{\partial \nu}{\partial t}\rangle \|\nu\| && (2.9)\\
&= -\langle X, \frac{\partial \nu}{\partial t}\rangle && (2.10)\\
&= \langle X, -\frac{\partial \nu}{\partial t}\rangle && (2.11)
\end{aligned}$$

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

$$-\frac{d\nu}{dt} = -\frac{d}{dt}\Big[\nu(u_1, u_2)\Big] \tag{2.12}$$

$$= -\frac{d}{dt}\Big[\nu(\theta_1(t), \theta_2(t))\Big] \tag{2.13}$$

$$= \theta_1'(t)\left(-\frac{\partial \nu}{\partial u_1}\right) + \theta_2'(t)\left(-\frac{\partial \nu}{\partial u_2}\right) \tag{2.14}$$

Identifying $\text{span}\left\{-\frac{\partial \nu}{\partial u_i}\right\}_{i=1,2}$ 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)**.**

$$\mathsf{L} : T_u f \to T_u f \quad \textit{given by the composition} \quad \mathsf{L} = D\nu \circ (Df)^{-1}.$$

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

$$-\frac{d\nu}{dt} = \theta_1'(t)\left(-\frac{\partial \nu}{\partial u_1}\right) + \theta_2'(t)\left(-\frac{\partial \nu}{\partial u_2}\right) \tag{2.15}$$

$$= \theta_1'(t)\left(\mathsf{L}\left(\frac{\partial f}{\partial u_1}\right)\right) + \theta_2'(t)\left(\mathsf{L}\left(\frac{\partial f}{\partial u_2}\right)\right) \tag{2.16}$$

$$= \mathsf{L}\left[\theta_1'(t)\left(\frac{\partial f}{\partial u_1}\right) + \theta_2'(t)\left(\frac{\partial f}{\partial u_2}\right)\right] \tag{2.17}$$

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

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

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

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. □

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_ν at point u in the direction X is given by*

$$\kappa_\nu := \langle X, \mathsf{L}(X) \rangle$$

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 $\mathsf{L}(\frac{\partial f}{\partial u_i}) = -\frac{\partial \nu}{\partial u_i}$.

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 $\left\{-\frac{\partial \nu}{\partial u_1}, -\frac{\partial \nu}{\partial u_2}\right\}$.

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 $\widehat{\mathsf{L}} \in R^{2\times 2}$) we simply wish to find a linear transformation such that $\widehat{\mathsf{L}} \left.\frac{\partial f}{\partial u_i}\right|_{T_u f} = -\left.\frac{\partial \nu}{\partial u_i}\right|_{T_u f}$ for $i = 1, 2$ where

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

$$\left[\widehat{\mathsf{L}}\right]\begin{bmatrix} | & | \\ \left.\frac{\partial f}{\partial u_1}\right|_{T_uf} & \left.\frac{\partial f}{\partial u_2}\right|_{T_uf} \\ | & | \end{bmatrix} = \begin{bmatrix} | & | \\ \widehat{\mathsf{L}}\left.\frac{\partial f}{\partial u_1}\right|_{T_uf} & \widehat{\mathsf{L}}\left.\frac{\partial f}{\partial u_2}\right|_{T_uf} \\ | & | \end{bmatrix} \tag{2.20}$$

$$= \begin{bmatrix} | & | \\ -\left.\frac{\partial \nu}{\partial u_1}\right|_{T_uf} & -\left.\frac{\partial \nu}{\partial u_2}\right|_{T_uf} \\ | & | \end{bmatrix} \tag{2.21}$$

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

$$\implies \left[\widehat{\mathsf{L}}\right]\begin{bmatrix} - & \frac{\partial f}{\partial u_1} & - \\ - & \frac{\partial f}{\partial u_2} & - \end{bmatrix}\begin{bmatrix} | & | \\ \frac{\partial f}{\partial u_1} & \frac{\partial f}{\partial u_2} \\ | & | \end{bmatrix} = \begin{bmatrix} - & \frac{\partial f}{\partial u_1} & - \\ - & \frac{\partial f}{\partial u_2} & - \end{bmatrix}\begin{bmatrix} | & | \\ -\frac{\partial \nu}{\partial u_1} & -\frac{\partial \nu}{\partial u_2} \\ | & | \end{bmatrix} \tag{2.22}$$

We can simplify this greatly by defining

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

so that

$$\left[\widehat{\mathsf{L}}\right]\begin{bmatrix} g_{11} & g_{12} \\ g_{21} & g_{22} \end{bmatrix} = \begin{bmatrix} h_{11} & h_{12} \\ h_{21} & h_{22} \end{bmatrix} \tag{2.24}$$

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

$$\widehat{\mathsf{L}} = \begin{bmatrix} h_{11} & h_{12} \\ h_{21} & h_{22} \end{bmatrix} \begin{bmatrix} g_{11} & g_{12} \\ g_{21} & g_{22} \end{bmatrix}^{-1} \tag{2.25}$$

where $\left[g_{ij}\right]$ 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 $f : U \to \mathbb{R}^3$ 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 $\nabla_v\langle v, Av\rangle$:

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

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

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

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

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

$$\implies \nabla_v \langle v, Av\rangle = 2Av. \tag{2.31}$$

□

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 $\kappa_\nu = \langle \mathsf{L}X, X\rangle$ 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 $\widehat{\mathsf{L}}$. Using the method of Lagrange multipliers, we define the Lagrangian:

$$\mathscr{L}(X;\lambda) := \langle \widehat{\mathsf{L}}X, X\rangle - \lambda\Big(\langle X, X\rangle - 1\Big) \tag{2.32}$$

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

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

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

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

which implies that X is an eigenvector of $\widehat{\mathsf{L}}$ 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. □

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 $f : U \to \mathbb{R}^3$ where $(x, y) \mapsto (x, y, h(x, y))$, the matrix representation of its Weingarten map is given by*

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

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

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

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

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

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

and we have the unit normal vector (Gauss map)

$$\nu(u_1, u_2) = \frac{\frac{\partial f}{\partial x} \times \frac{\partial f}{\partial y}}{\| \frac{\partial f}{\partial x} \times \frac{\partial f}{\partial y} \|} \tag{2.37}$$

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

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

We then calculate each h_{ij} as

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

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

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

To calcuate the second, we use

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

and thus

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

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

Thus the matrix of the Weingarten map $\widehat{\mathsf{L}}$ 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 $\widehat{\mathsf{L}}$ and $\mathrm{Hess}(h)$ 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 $\widehat{\mathsf{L}}$ 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:

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

We can then rewrite eq. (2.35) as

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

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 $\widehat{\mathsf{L}} \approx \text{Hess}(h)$ 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

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

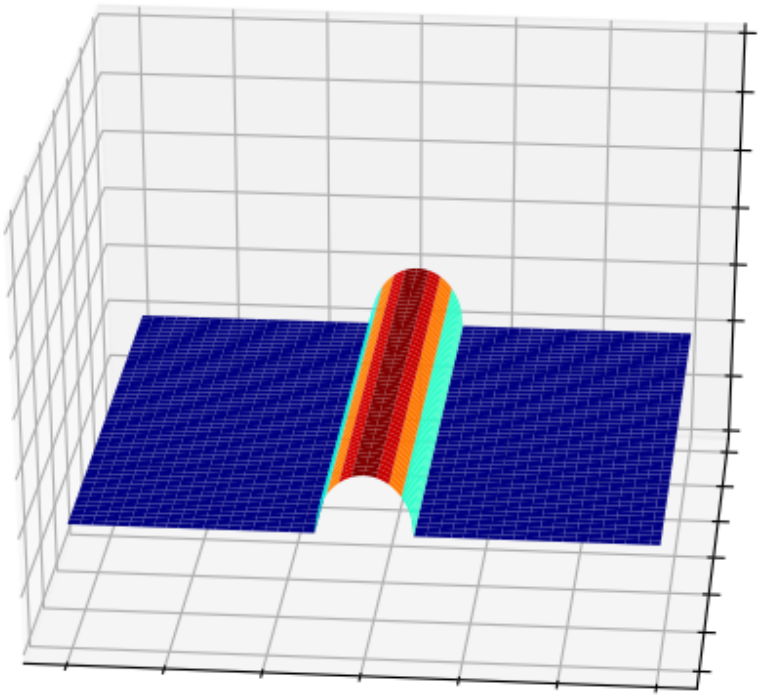


FIGURE 2: The graph of a cylindrical ridge of radius r

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

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

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

The gauss map is given by

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

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

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

$$[h_{ij}] = \frac{1}{\sqrt{1 + h_x^2 + h_y^2}} \mathrm{Hess}(h) = \frac{1}{\sqrt{1 + \left(\frac{x^2}{r^2 - x^2}\right)}} \begin{bmatrix} \frac{-r^2}{\sqrt{r^2 - x^2}^3} & 0 \\ 0 & 0 \end{bmatrix} = \begin{bmatrix} \frac{-r}{r^2 - x^2} & 0 \\ 0 & 0 \end{bmatrix} \tag{2.51}$$

$$[g_{ij}]^{-1} = \begin{bmatrix} \frac{r^2 - x^2}{r^2} & 0 \\ 0 & 1 \end{bmatrix} \tag{2.52}$$

$$\implies \widehat{\mathsf{L}} = [h_{ij}][g_{ij}]^{-1} = \begin{bmatrix} \frac{-r}{r^2 - x^2} & 0 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{r^2 - x^2}{r^2} & 0 \\ 0 & 1 \end{bmatrix} \tag{2.53}$$

$$= \begin{bmatrix} -\frac{1}{r} & 0 \\ 0 & 0 \end{bmatrix} \tag{2.54}$$

We see that $u_2 = (0, 1)$ and $u_1 = (1, 0)$ are eigenvectors for $\widehat{\mathsf{L}}$ 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:

$$\text{Hess}(x, y) = \begin{bmatrix} L_{xx}(x, y) & L_{xy}(x, y) \\ L_{yx}(x, y) & L_{yy}(x, y) \end{bmatrix} \tag{2.55}$$

At any point (x, y) we denote the two eigenpairs of $\text{Hess}(x, y)$ as

$$\text{Hess}(x, y)u_i = \kappa_i u_i \,, \quad i = 1, 2 \tag{2.56}$$

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

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

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

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

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

[1] To 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 $L(x, y)$.

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 orignally 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:

$$V_\sigma(x_0, y_0) = \begin{cases} 0 & \text{if} \quad \lambda_2 > 0 \\ \exp\left\{-\frac{A^2}{2\beta^2}\right\}\left(1 - \exp\left\{-\frac{S^2}{2c^2}\right\}\right) & \text{otherwise} \end{cases} \tag{2.57}$$

where

$$A := |\lambda_1/\lambda_2| \quad \text{and} \quad S := \sqrt{\lambda_1^2 + \lambda_2^2} \tag{2.58}$$

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. (2.57), and in particular, the ratios defined in eq. (2.58). A and S are known as the anisotropy measure and structureness measure, respectively. Consequently, we'll refer to the two factors in eq. (2.57) 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

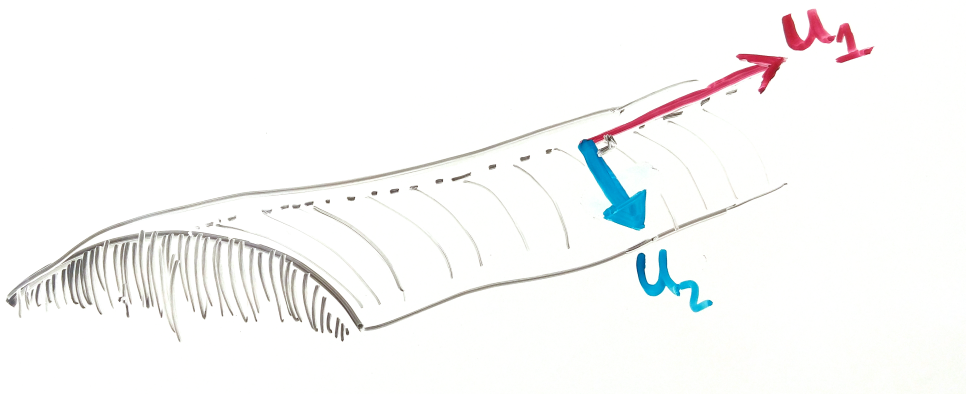


FIGURE 3: The principal eigenvectors at a ridge like structure

(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 tor 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.

Similiarly, the vessel we 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 3.1), 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 section 2.5.

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 6.1.

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. (2.57) in which a factor of exp{...} and $(1-\exp\{...\})$ 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. (2.57), 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 $\exp\{\frac{-A^2}{2\beta^2}\}$ and the structureness factor $(1-\exp\{\frac{-S^2}{2c^2}\})$ 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,

$$\begin{aligned}\max\{V_\sigma\} &\le \max\left(\exp\left\{\frac{-A^2}{2\beta^2}\right\}\right)\max\left(\left(1-\exp\left\{\frac{-S^2}{2(\gamma S_{\max})^2}\right\}\right)\right)\\ &\le \max\left\{\left(1-\exp\left\{\frac{-S^2}{2(\gamma S_{\max})^2}\right\}\right)\right\}\\ &= \left(1-\exp\left\{\frac{-(S_{\max})^2}{2(\gamma S_{\max})^2}\right\}\right) = \left(1-\exp\left\{\frac{-1}{2\gamma^2}\right\}\right)\end{aligned} \tag{2.59}$$

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 $\max\{V_\sigma\} \le 1-\exp\{-1\} \approx .8647$. 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

$$V_\sigma(x_0, y_0) = \begin{cases} 0 & \text{if} \quad \lambda_2 > 0 \\ a_\gamma \exp\left\{\frac{-A^2}{2\beta^2}\right\}\left(1-\exp\left\{\frac{-S^2}{2(\gamma S_{\max})^2}\right\}\right) & \text{otherwise} \end{cases} \tag{2.60}$$

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

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

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

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

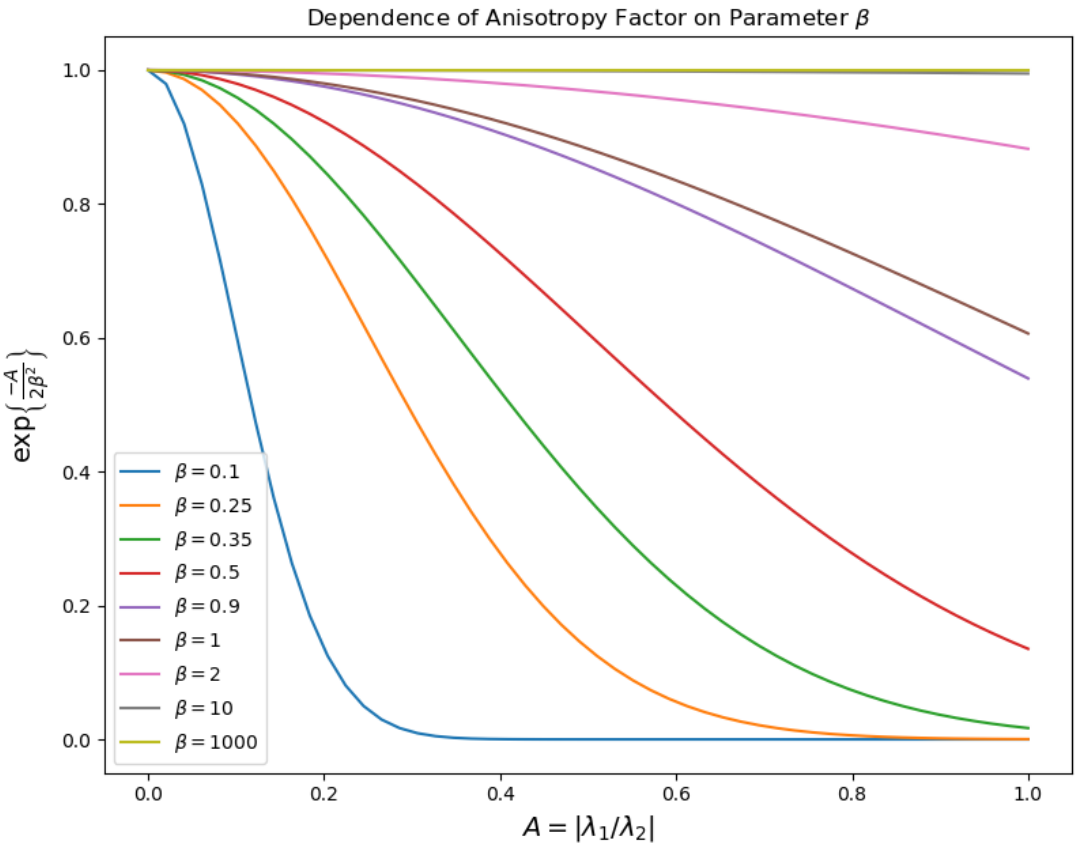


FIGURE 4: Dependence of the Anisotropy Factor on its Parameter

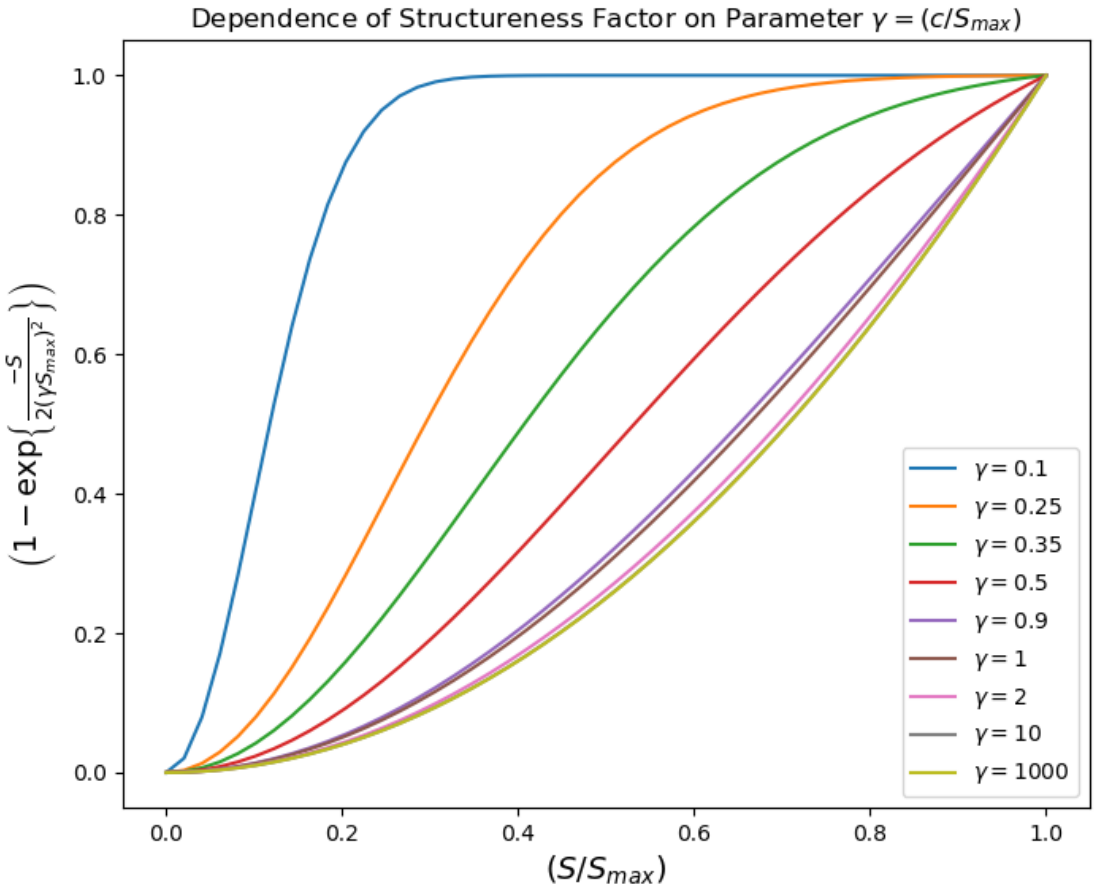


FIGURE 5: Dependence of the Structureness Factor on its Parameter

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

$$\Delta K(x,y,\sigma) = K_\sigma(x,y,\sigma) \text{ for } \sigma \geq 0 \text{ such that } K(x,y,0) = u_0(x,y). \tag{2.61}$$

where $K : \mathbb{R}^3 \to \mathbb{R}$ and $u_0 : \mathbb{R}^2 \to \mathbb{R}$: 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 to 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 2.1 (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 2.2 (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

$$Au_0 = \lim_{\sigma \downarrow 0} \frac{T_\sigma u_0 - u_0}{\sigma} \tag{2.62}$$

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

$$\partial_\sigma K(x, y; \sigma) = \lim_{\sigma \downarrow 0} \frac{K(\cdot; \sigma + h) - K(\cdot; \sigma)}{h} = A(T_\sigma u) = A(K(\cdot, \sigma)) \tag{2.63}$$

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

Axiom 2.3 (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.*

$$T_\sigma u = T_{\sigma_1 + \sigma_2} u \tag{2.64}$$

Axiom 2.4 (Causality Conditon)**.** *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.

$$\begin{cases} \nabla K(x_0, y_0; \sigma_0) = 0 \\ \Delta K(x_0, y_0; \sigma_0) < 0 \end{cases} \implies K(x_0, y_0; \sigma_1) \leq K(x_0, y_0; \sigma_0) \; \forall \; \sigma_1 \geq \sigma_0 \tag{2.65}$$

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.

$$\begin{cases} \nabla K(x_0, y_0; \sigma_0) = 0 \\ \Delta K(x_0, y_0; \sigma_0) > 0 \end{cases} \implies K(x_0, y_0; \sigma_1) \geq K(x_0, y_0; \sigma_0) \; \forall \; \sigma_1 \geq \sigma_0 \tag{2.66}$$

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. (2.61) 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,

$$K(x, y; \sigma) = T_\sigma u_0 = G_\sigma \star u_0 \quad \text{where} \quad G_\sigma := \frac{1}{2\pi\sigma^2} e^{\left(-|x|^2/(2\sigma^2)\right)} \tag{2.67}$$

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.

$$u : \mathbb{R}^2 \supset \Omega \to \mathbb{R} \text{ with } u(\boldsymbol{x}, t) : \begin{cases} \frac{\partial u}{\partial t}(\boldsymbol{x}, t) = \Delta u(\boldsymbol{x}, t) \quad , \ t \geq 0 \\ u(\boldsymbol{x}, 0) = u_0(\boldsymbol{x}) \end{cases} \tag{2.68}$$

We show that

$$u(\boldsymbol{x}, t) = \left(G_{\sqrt{2t}} \star u_0\right)(\boldsymbol{x}) \tag{2.69}$$

solves (the above tagged equation), where

$$s$$

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

Lemma 2.9. *Derivative of a convolution is the way that it is (obviously rewrite this).*

Proof. For a single variable,

$$\frac{\partial}{\partial \alpha}\left[f(\alpha) \star g(\alpha)\right] = \frac{\partial}{\partial \alpha}\left[\int f(t) g(\alpha - t) dt\right] \tag{2.70}$$

$$= \int f(t) \frac{\partial}{\partial \alpha}\left[g(\alpha - t)\right] dt \tag{2.71}$$

$$= \int f(t) \left(\frac{\partial g}{\partial \alpha}\right) g(\alpha - t) dt \tag{2.72}$$

$$= f(\alpha) \star g'(\alpha) \tag{2.73}$$

By symmetry of convolution we can also conclude

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

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

$$\Delta(f \star g) = \Delta(f) \star g = f \star \Delta(g) \tag{2.74}$$

□

Theorem 2.10. *$u(\boldsymbol{x}, t) = \left(G_{\sqrt{2t}} \star u_0\right)(\boldsymbol{x})$ solves the heat equation.*

Proof. We focus on the particular kernel

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

Then

$$\begin{aligned}
\frac{\partial u}{\partial t}(\boldsymbol{x}, t) &= \frac{\partial}{\partial t}\left(G_{\sqrt{2t}}(\boldsymbol{x}, t) \star u_0(\boldsymbol{x})\right) && (2.75)\\
&= \frac{\partial}{\partial t}\left(G_{\sqrt{2t}}(\boldsymbol{x}, t)\right) \star u_0(\boldsymbol{x}) && (2.76)\\
&= \frac{\partial}{\partial t}\left(\frac{1}{4\pi t} e^{\left(-|x|^2/(4t)\right)}\right) \star u_0(\boldsymbol{x}) && (2.77)\\
&= \left[-\frac{1}{4\pi t^2} e^{\left(-|x|^2/(4t)\right)} + \frac{1}{4\pi t}\left(\frac{-|x|^2}{4t^2}\right) e^{-|x|^2/(4t)}\right] \star u_0(\boldsymbol{x}) && (2.78)\\
&= -\frac{1}{4t^2}\left(e^{\left(-|x|^2/(4t)\right)} + |\boldsymbol{x}|^2 G_{\sqrt{2t}}(\boldsymbol{x}, t)\right) \star u_0(\boldsymbol{x}) && (2.79)
\end{aligned}$$

and from the previous lemma,

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

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

$$\frac{\partial}{\partial x}G_\sigma(x,y) = A\left(\frac{-2x}{2\sigma^2}\right)\exp\left(-\frac{x^2+y^2}{2\sigma^2}\right)$$

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

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

$$\Delta G_\sigma(x,y) = \frac{\partial^2}{\partial x^2}(G_\sigma)+\frac{\partial^2}{\partial y^2}(G_\sigma) = \frac{1}{\sigma^2}G_\sigma(x,y)\left[\frac{x^2+y^2}{\sigma^2}-2\right] \tag{2.80}$$

Then, given lemma 2.9, we conclude

$$\Delta\left[G_\sigma(x,y)\star u_0(x,y)\right] = \left(\frac{1}{\sigma^2}G_\sigma(x,y)\left[\frac{x^2+y^2}{\sigma^2}-2\right]\right)\star u_0(x,y) \tag{2.81}$$

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

$$\Delta\left[G_{\sqrt{2t}}(x,y)\star u_0(x,y)\right] = \left(\frac{1}{2t}G_{\sqrt{2t}}(x,y)\left[\frac{x^2+y^2}{2t}-2\right]\right)\star u_0(x,y) \tag{2.82}$$

$$= \left(G_{\sqrt{2t}}(x,y)\left[\frac{x^2+y^2}{4t^2}-\frac{1}{t}\right]\right)\star u_0(x,y) \tag{2.83}$$

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

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

$$\frac{\partial}{\partial t}\left[G_{\sigma(t)}(x,y) \star u_0(x,y)\right] = \frac{\partial}{\partial t}\left[G_{\sigma(t)}(x,y)\right] \star u_0(x,y) \tag{2.84}$$

$$= \frac{\partial}{\partial t}\left[G_{\sqrt{2t}}(x,y)\right] \star u_0(x,y) \tag{2.85}$$

$$= \frac{\partial}{\partial t}\left[\frac{1}{4\pi t}\exp\left(-\frac{x^2+y^2}{4t}\right)\right] \star u_0(x,y) \tag{2.86}$$

$$= \left[-\frac{1}{4\pi t^2}\exp\left(-\frac{x^2+y^2}{4t}\right) + \frac{1}{4\pi t}\left(\frac{x^2+y^2}{4t^2}\exp\left(-\frac{x^2+y^2}{4t}\right)\right)\right] \star u_0(x,y) \tag{2.87}$$

$$= \left(G_{\sqrt{2t}}(x,y)\left[\frac{x^2+y^2}{4t^2} - \frac{1}{t}\right]\right) \star u_0(x,y) \tag{2.88}$$

Combining these results, we find that

$$\frac{\partial}{\partial t}\left[G_{\sqrt{2t}} \star u_0\right] = \Delta\left[G_{\sqrt{2t}} \star u_0\right] \tag{2.89}$$

as desired. □

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 However, viewing our actual image definition 2.1 as a sample of a continuous surface definition 2.2, we might naïvely 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 2.13 (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

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

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 2.3), but–much less forgivably–the causality property (axiom 2.3). 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 2.4 and axiom 2.3:

Definition 2.14 (Discrete Gaussian Kernel)**.** *The discrete Gaussian kernel, which can be shown to be a suitable generator for scale space, is given by*

$$T(n;\sigma) = e^{-\alpha\sigma} I_n(\alpha\sigma), \quad I_n(\sigma) = I_{-n}(\sigma) = (-1)^n J_n(i\sigma) \quad n \geq 0, \sigma, \alpha > 0 \tag{2.90}$$

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

$$K(x, \sigma) = \sum_{n=-\infty}^{\infty} T(n; t) f(x - n) \quad \text{for} \quad x \in \mathbb{Z},\ t > 0 \tag{2.91}$$

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. (2.91) can be obtained by independent convolution of its dimensions (i.e. it is separable). We will make these ideas explicit in chapter 4 and the Appendix.

With the ideas of scale established, we may return to our discussion of the Frangi filter.

The Frangi Filter: A multiscale approach

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 2.3, 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:

$$V(x_0, y_0) = \max_{\sigma \in \Sigma} V_\sigma(x_0, y_0) \tag{2.92}$$

where $\Sigma := \{\sigma_0, \sigma_1, \cdots, \sigma_N\}$ 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:

$$\mathsf{V}_\Sigma := [V(x, y)]_{\substack{0 \le x < M \\ 0 \le y < N}} \tag{2.93}$$

Notably, Frangi [11] refrained from explicitly interpreting the probablility assigned by eq. (2.92); 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. (2.92) or eq. (2.93)

$$V_{\Sigma,\alpha}(x, y) = \begin{cases} 1 & \text{if} \quad V(x, y) \ge \alpha \\ 0 & \text{else} \end{cases}, \quad \alpha > 0 \text{ for } \alpha \text{ fixed.} \tag{2.94}$$

We will discuss alternatives methods of aggregating results from our multiscale

method, as well as optimal values for parameters and scales in chapter 4. As a final note, we admit that any future extensions of this work (as will be discussed in chapter 6) should not hold too much stock in this thresholded result, and analyzing the raw vesselness score eq. (2.93), 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 2.4.3, 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 4.

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 4.

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 $\mathcal{O}\left(N \cdot \log_2 N\right)$ 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:

$$f(t) = \sum_{-\infty}^{\infty} c_n e^{i\frac{2\pi n}{T}t}\,, \quad c_n = \frac{1}{T}\int_{-T/2}^{T/2} f(t)e^{-i\frac{2\pi n}{T}t}dt \tag{2.95}$$

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

$$F(\mu) := \mathscr{F}\{f(t)\} \;=\; \int_{-\infty}^{\infty} f(t)e^{i2\pi\mu}dt \tag{2.96}$$

An inverse transform will then recover our original signal:

$$f(t) = \mathscr{F}^{-1}\{F(\mu)\} = \int_{-\infty}^{\infty} F(\mu)e^{i2\pi\mu t}dt \tag{2.97}$$

Together, eq. (2.96) and eq. (2.97) 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:

$$s_{\Delta T}(t) := \sum_{n=-\infty}^{\infty} \delta[t - n\Delta T]\,, \quad \delta[t] = \begin{cases} 1\,, & t = 0 \\ 0\,, & t \neq 0 \end{cases} \tag{2.98}$$

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

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

$$\tilde{f}(t) = f(t)s_{\Delta T}(t) \tag{2.99}$$

From this we can calculate $\tilde{F}(t)$. Given the discrete signal $\tilde{f}$, we construct the

transform $\tilde{F}(\mu) = \mathscr{F}\{\tilde{f}(t)\}$. by expanding $\tilde{f}$ in the same infinite basis as the continuous case.

$$\tilde{F}(\mu) = \sum_{n=-\infty}^{\infty} f_n e^{-i2\pi\mu n\Delta T}, \quad f_n = \tilde{f}(n) = f(n\Delta T) \tag{2.100}$$

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

2D DFT Convolution Theorem .

Theorem 2.11 (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:*

$$F(u,v) := \mathcal{D}\{f(x,y)\} = \sum_{x=0}^{M-1}\sum_{y=0}^{N-1} f(x,y)e^{-2\pi i\left(\frac{ux}{M}+\frac{vy}{N}\right)} \tag{2.101}$$

$$H(u,v) := \mathcal{D}\{h(x,y)\} = \sum_{x=0}^{M-1}\sum_{y=0}^{N-1} h(x,y)e^{-2\pi i\left(\frac{ux}{M}+\frac{vy}{N}\right)} \tag{2.102}$$

and given the convolution of the two functions

$$(f \star h)(x,y) = \sum_{m=0}^{M-1}\sum_{n=0}^{N-1} f(m,n)h(x-m,y-n) \tag{2.103}$$

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

$$(f \star h)(x,y) = \mathcal{D}^{-1}\{MN \cdot F(u,v)H(u,v)\} \tag{2.104}$$

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

Proof.

$$(f \star h)(x,y) = \sum_{m=0}^{M-1}\sum_{n=0}^{N-1} f(m,n)h(x-m,y-n) \tag{2.105}$$

$$= \sum_{m=0}^{M-1}\sum_{n=0}^{N-1}\left(\sum_{p=0}^{M-1}\sum_{q=0}^{N-1} F(p,q)e^{2\pi i\left(\frac{mp}{M}+\frac{nq}{N}\right)}\right)\left(\sum_{u=0}^{M-1}\sum_{v=0}^{N-1} H(u,v)e^{2\pi i\left(\frac{u(x-m)}{M}+\frac{v(y-n)}{N}\right)}\right) \tag{2.106}$$

$$= \left(\sum_{u=0}^{M-1}\sum_{v=0}^{N-1} H(u,v)e^{2\pi i\left(\frac{ux}{M}+\frac{vy}{N}\right)}\right)\left(\sum_{p=0}^{M-1}\sum_{q=0}^{N-1} F(p,q)\left(\sum_{m=0}^{M-1} e^{2\pi i\left(\frac{m(p-u)}{M}\right)}\right)\left(\sum_{n=0}^{N-1} e^{2\pi i\left(\frac{n(q-v)}{N}\right)}\right)\right) \tag{2.107}$$

$$= \left(\sum_{u=0}^{M-1}\sum_{v=0}^{N-1} H(u,v)e^{2\pi i\left(\frac{ux}{M}+\frac{vy}{N}\right)}\right)\left(\sum_{p=0}^{M-1}\sum_{q=0}^{N-1} F(p,q)\left(M\cdot\hat{\delta}_M(p-u)\right)\left(N\cdot\hat{\delta}_M(q-v)\right)\right) \tag{2.108}$$

$$= \left(\sum_{u=0}^{M-1}\sum_{v=0}^{N-1} H(u,v)e^{2\pi i\left(\frac{ux}{M}+\frac{vy}{N}\right)}\right)\cdot MNF(u,v) \tag{2.109}$$

$$= MN\cdot\sum_{u=0}^{M-1}\sum_{v=0}^{N-1} F(u,v)H(u,v)e^{2\pi i\left(\frac{ux}{M}+\frac{vy}{N}\right)} \tag{2.110}$$

$$= MN\cdot\mathcal{D}^{-1}\{FH\} \tag{2.111}$$

where

$$\hat{\delta}_N(k) = \begin{cases} 1 & \text{when } k = 0 \mod N \\ 0 & \text{else} \end{cases} \tag{2.112}$$

□

Above, we make use of the following lemma

Lemma 2.12. *Let j and k be integers and let N be a positive integer. Then*

$$\sum_{n=0}^{N-1} e^{2\pi i\left(\frac{n(j-k)}{N}\right)} = N\cdot\hat{\delta}_N(j-k) \tag{2.113}$$

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

$$z^N - 1 \;=\; (z-1)\left(z^{n-1} + \cdots + z + 1\right) \;=\; (z-1)\sum_{n=0}^{N-1} z^n. \tag{2.114}$$

thus giving us

$$0 = \left(e^{2\pi i(j-k)/N} - 1\right)\sum_{n=0}^{N-1} e^{2\pi in(j-k)/N} \tag{2.115}$$

To prove the claim in eq. (2.113), we consider two cases: First, if $j-k$ is a multiple of N, we of course have $e^{2\pi in(j-k)/N} = \left(e^{2\pi i}\right)^{n(j-k)/N} = 1$ and thus the left side of eq. (2.113) 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. (2.115). 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. (2.112), giving us the result. □

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:

$$F(\mu,\nu) = \sum_{x=0}^{M-1}\sum_{y=0}^{N-1} f(x,y)e^{-i2\pi(\mu x/M+\nu y/N)} \tag{2.116}$$

$$= \sum_{x=0}^{M-1} e^{-i2\pi\mu x/M}\left[\sum_{y=0}^{N-1} f(x,y)e^{-i2\pi\nu y/N}\right] \tag{2.117}$$

$$= \sum_{x=0}^{M-1} e^{-i2\pi\mu x/M}\,\mathscr{F}_x\{f(x,y)\} \tag{2.118}$$

$$= \mathscr{F}_y\{\mathscr{F}_x\{f(x,y)\}\} \tag{2.119}$$

where $\mathscr{F}_{x'}$ 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 $x \in 0,\cdots,M-1$. 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

$$F(u) = \sum_{x=0}^{M-1} f(x) W_M^{ux}, \quad \text{where} \quad W_m := e^{-i2\pi/m} \tag{2.120}$$

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

$$F(u) = \sum_{x=0}^{2K-1} f(x) W_{2K}^{ux} \tag{2.121}$$

$$= \sum_{x=0}^{K-1} f(2x) W_{2K}^{u(2x)} + \sum_{x=0}^{K-1} f(2x+1) W_{2K}^{u(2x+1)} \tag{2.122}$$

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

$$W_{(2m)}^{(2n)} = e^{\frac{-i2\pi(2m)}{2m}} = e^{\frac{-i2\pi m}{n}} = W_m^n \tag{2.123}$$

$$W_m^{(u+m)x} = e^{\frac{-i2\pi(u+m)x}{m}} = e^{\frac{-i2\pi unx}{m}} e^{\frac{-i2\pi mx}{m}} = e^{\frac{-i2\pi ux}{m}}(1) = W_m^{ux} \tag{2.124}$$

$$W_{2m}^{(u+m)} = e^{\frac{-i2\pi(u+m)}{2m}} = e^{\frac{-i2\pi ux}{2m}} e^{-i\pi} = W_{2m}^u e^{-i\pi} = -W_{2m}^u \tag{2.125}$$

Thus we can rewrite eq. (2.122) as

$$F(u) = \sum_{x=0}^{K-1} f(2x) W_{2K}^{2ux} + \sum_{x=0}^{K-1} f(2x+1) W_{2K}^{2ux} W_{2K}^u \tag{2.126}$$

$$\implies \quad F(u) = \left(\sum_{x=0}^{K-1} f(2x) W_K^{ux} \right) + \left(\sum_{x=0}^{K-1} f(2x+1) W_K^{ux} \right) W_{2K}^u \tag{2.127}$$

The major advance comes via using the identities eq. (2.123) to consider the

Fourier transform K frequencies later :

$$F(u+K) = \left(\sum_{x=0}^{K-1} f(2x) W_K^{(u+K)x}\right) + \left(\sum_{x=0}^{K-1} f(2x+1) W_K^{(u+K)x}\right) W_{2K}^{(u+K)} \tag{2.128}$$

$$\implies F(u+K) = \left(\sum_{x=0}^{K-1} f(2x) W_K^{ux}\right) - \left(\sum_{x=0}^{K-1} f(2x+1) W_K^{ux}\right) W_K^u \tag{2.129}$$

Comparing eq. (2.127) and eq. (2.129), we see that the expressions within parentheses are identical. What's more, these parentetical expressions are functionally identical to discrete fourier transforms themselves. Let's notate them as follows:

$$\mathscr{D}_u\{f_{\text{even}}(t)\} := \sum_{x=0}^{K-1} f(2x) W_K^{ux} \tag{2.130}$$

$$\mathscr{D}_u\{f_{\text{odd}}(t)\} := \sum_{x=0}^{K-1} f(2x+1) W_K^{ux} \tag{2.131}$$

If we're calculating an M point transform (i.e. we're wishing to calculate $F(1),...,F(M)$), once we've calculated the first K discrete frequencies (i.e. $F(1),\cdots,F(K)$) we may simply reuse the two values we've calculated in eq. (2.130) to calculate the next $F(K+1),..,F(K+K) = F(M)$. 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 $F(1),..,F(M)$. 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. (2.130) 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. (2.116).

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 3

RESEARCH PROTOCOL

Samples / Image Domain

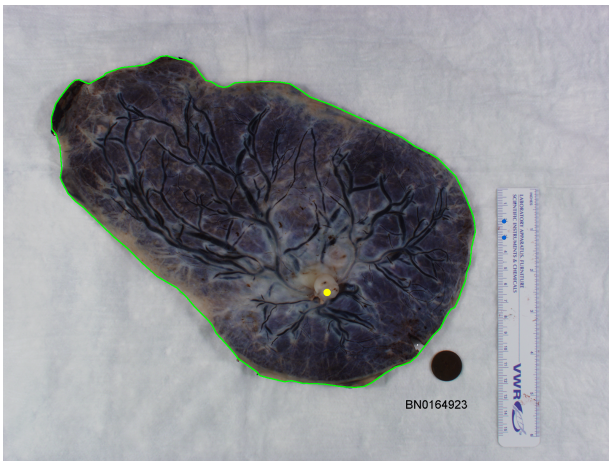
We ultimately perform a multiscale Frangi filter to estimate the PCSVN from a subset of 201 color placental images from a private database provided by the National Children's Study, which had been prepared for a different study. A detailed description of the data set is given in [1], and a description 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

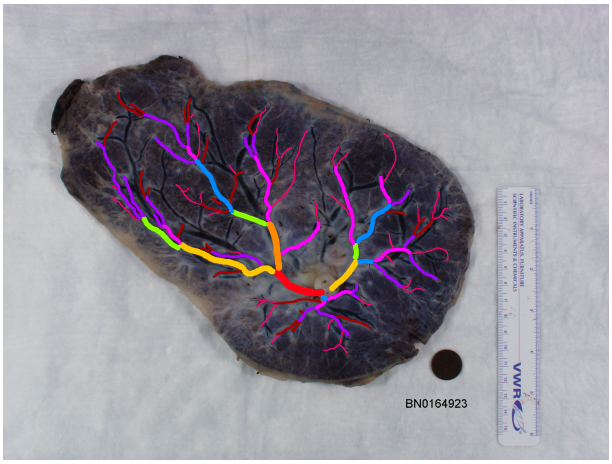
The layers together give a hand tracing of the vascular network and perimeter. A sample of overlaid layers in a representative sample (with ID number "BN0164923") is given in fig. 6.

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 rule 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 infig. 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

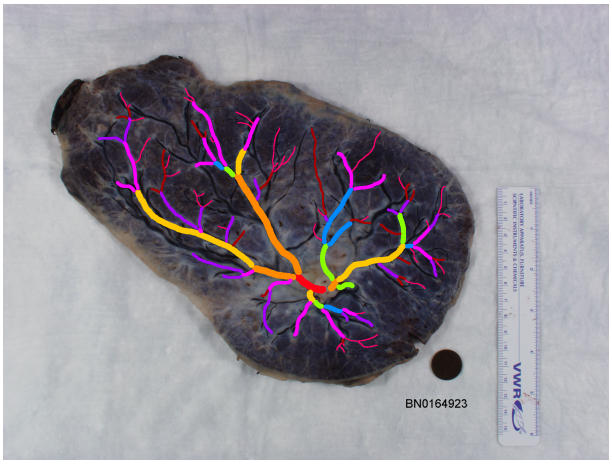
(a) Fixed Placental Sample



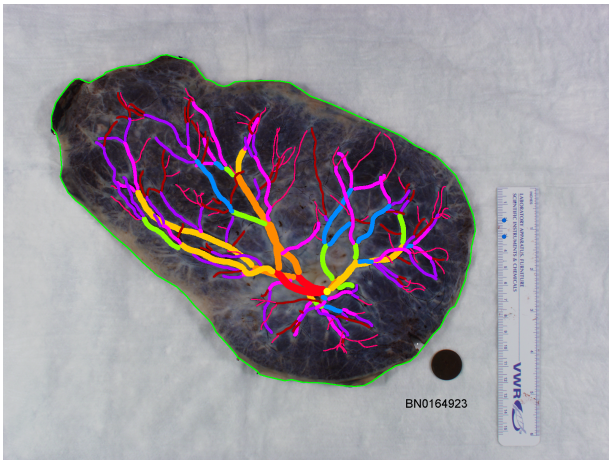
(b) Perimeter tracing



(c) Arterial tracing



(d) Venous tracing



(e) Total Vascular Network

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 pixel s	#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.

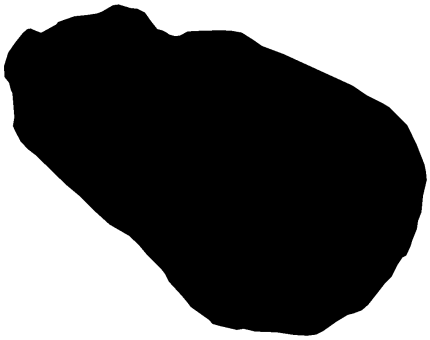
Finally, we will consider the location of the umbilical insertion point as a "known", as the vessels around it are frequently impossible to see and we wish to exclude them from consideration. It is not unreasonable, however, to consider this to be a known–in future preparations of samples, we could simply 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

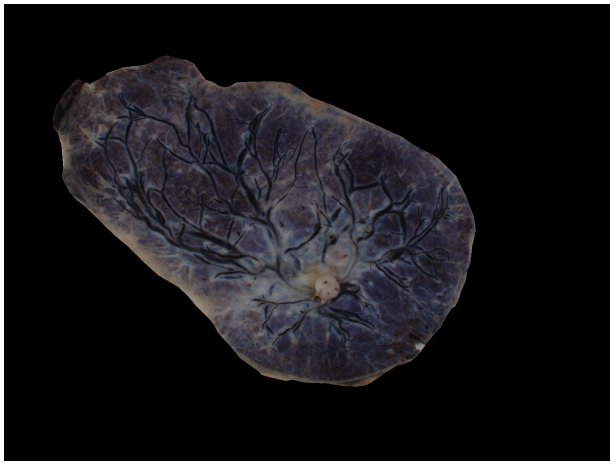
Building a sample suitable for use in our algorithm from fig. 6 is relatively simple. We zero outside the boundary of the plate (so as to not waste computational time calculating the differential geometry of a ruler, say), and also generate a binary mask to identify the plate. Finally, our vessel layers are combined and given as a binary trace. Our preprocessed samples used by the algorithm are given in section 3.2.

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.

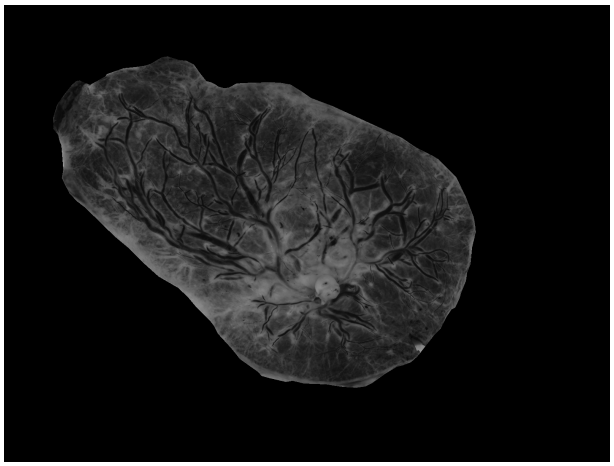
As a point of technicality, the grayscale image in fig. 7c is not actually produced directly by the extractor plug-in, but created when the 3 channel RGB image fig. 7b is



(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 descaleed 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:

$$L = \frac{299}{1000} R + \frac{587}{1000} G + \frac{114}{1000} B \tag{3.1}$$

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 descaleed 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 affect 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

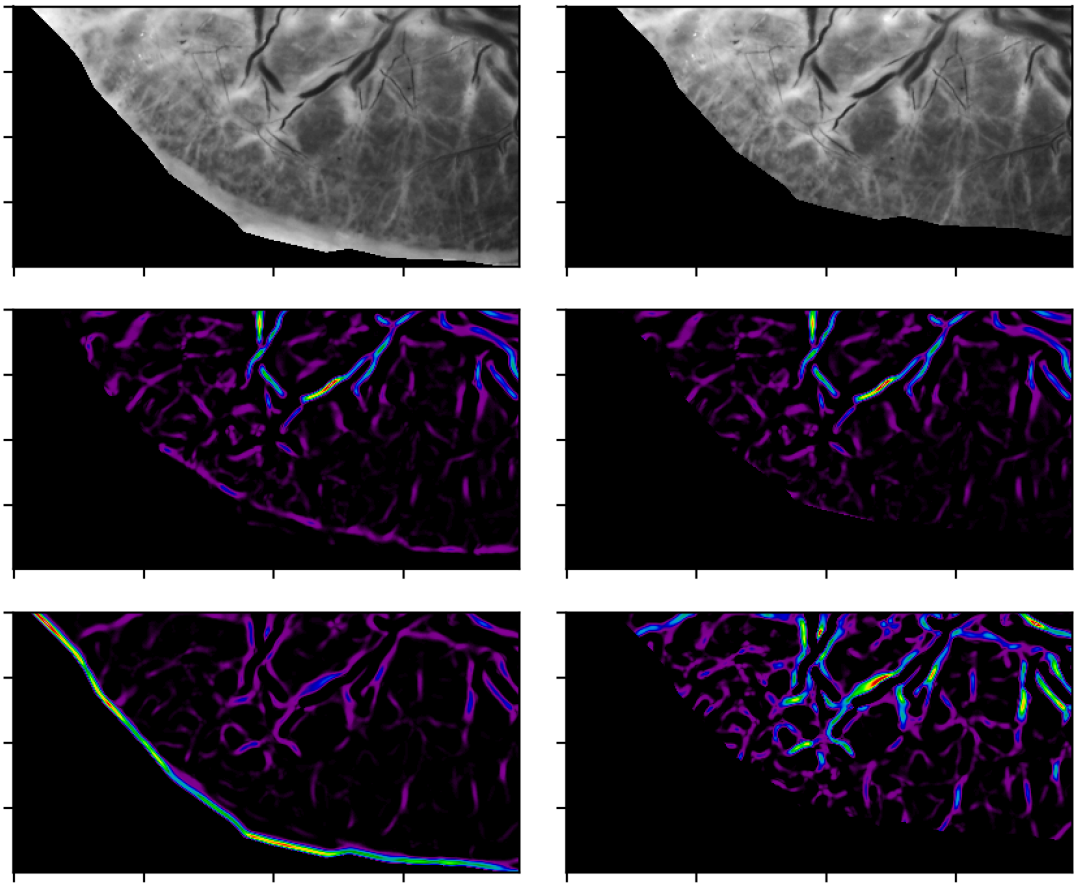


FIGURE 8: Effect of boundary dilation on Frangi responses

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

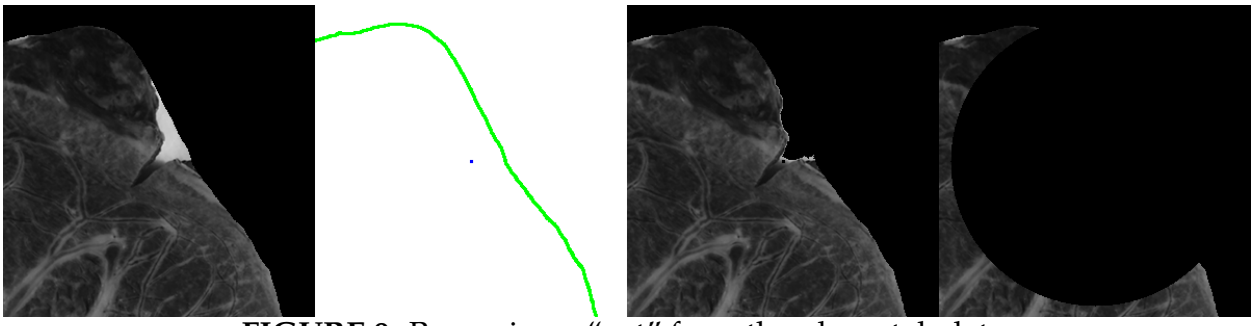


FIGURE 9: Removing a "cut" from the placental plate.

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 umbilicial cord insertion point. This is demonstrated in fig. 9. From left to right, we have the original masked placental sample, the cut mark notated 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.

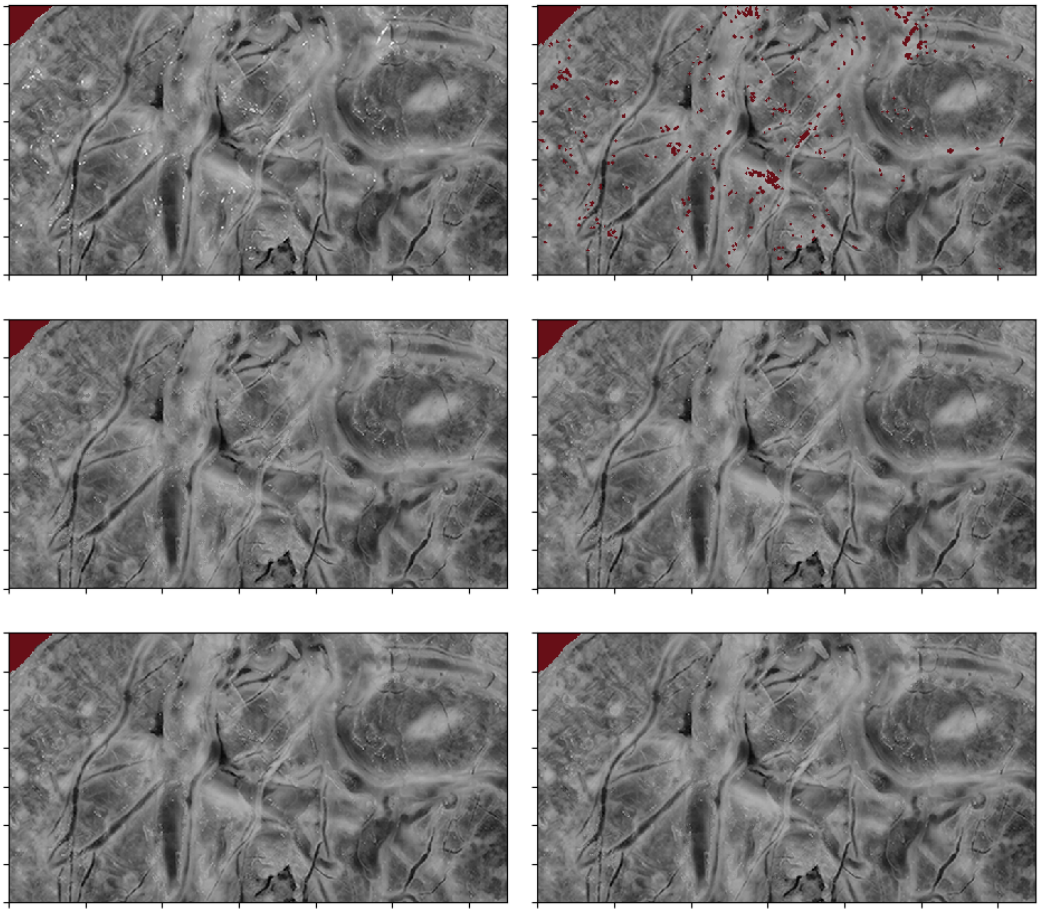


FIGURE 10: Deglaring a sample using a hybrid inpainting method

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

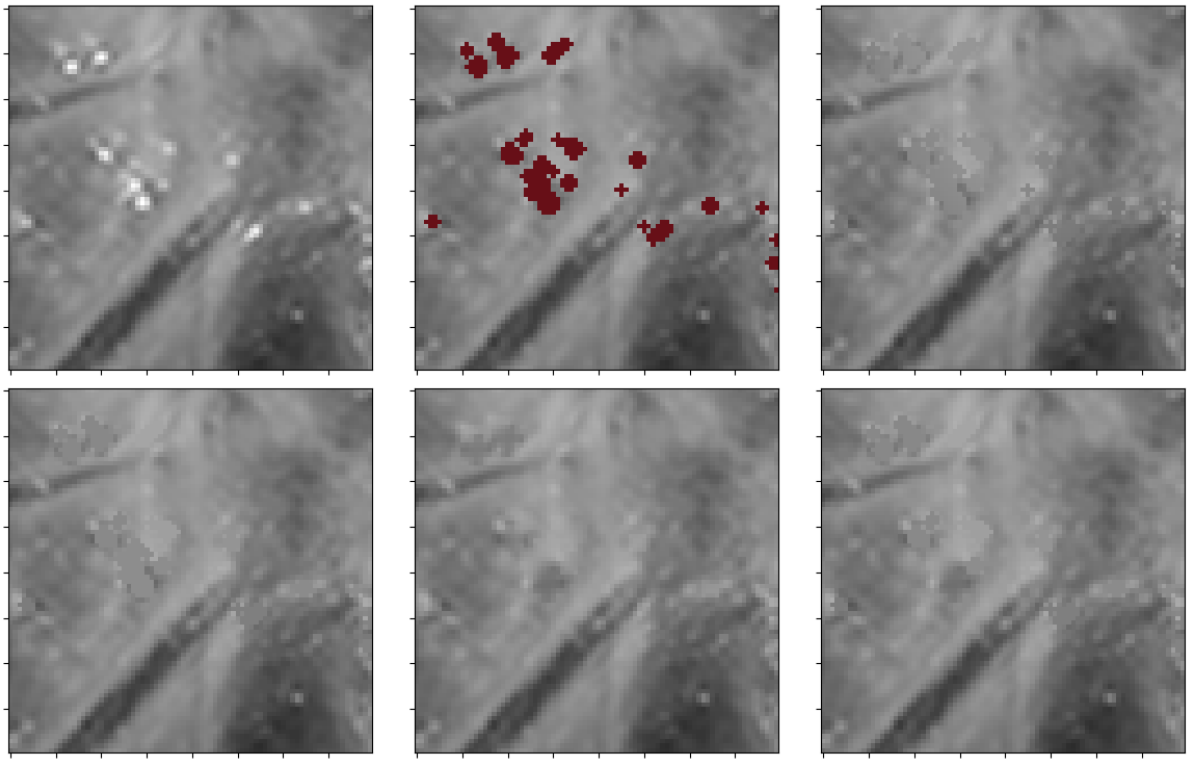


FIGURE 11: Comparison of glare inpainting methods (detail)

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.

```
In [1]: %timeit inpaint_with_boundary_median(img)
1 loop, best of 3: 3.99 s per loop

In [2]: %timeit inpaint_with_biharmonic(img)
1 loop, best of 3: 22.3 s per loop

In [3]: %timeit inpaint_hybrid(img)
1 loop, best of 3: 6.49 s per loop

In [4]: px_inpainted = np.sum(np.logical_and(masked.mask, np.invert(img.mask)))
In [5]: px_plate = np.sum(np.invert(img.mask))
In [6]: px_inpainted / px_plate  # ratio of inpainted pixels to total plate
```

```
Out[6]: 0.011444460505513942
```

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 $\Sigma := \{\sigma_1, \sigma_2, \ldots, \sigma_N\}$.

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

$$\sigma_1 = 2^m \ , \ \sigma_j = 2^{\left(m + \frac{M-m}{N-1} j\right)} \ , \ \sigma_N = 2^M \tag{3.2}$$

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 2.3 and section 2.5. 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, Hyy
    c) find eigenvalues of hessian at each point (using np.eig)
       and sort by magnitude
    d) zero out principal directions according to Dilate Per Scale
    e) zero out hessian according to max(ceil(sigma),10)
    f) Calculate Frangi Vesselness Measure
C) Estimate PCSVN
  1) Approximate using strategy
    a) Calculate Fmax and Fmax.where -> Fmax
    b) Threshold at 95th percentile -> approx
    c) Threshold at fixed alpha
    d) Margin adding to one of the above
    e) Random walker after margin adding
  2) Compare to Trace
  3) Calculate Network Coverage and MCC score
```

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

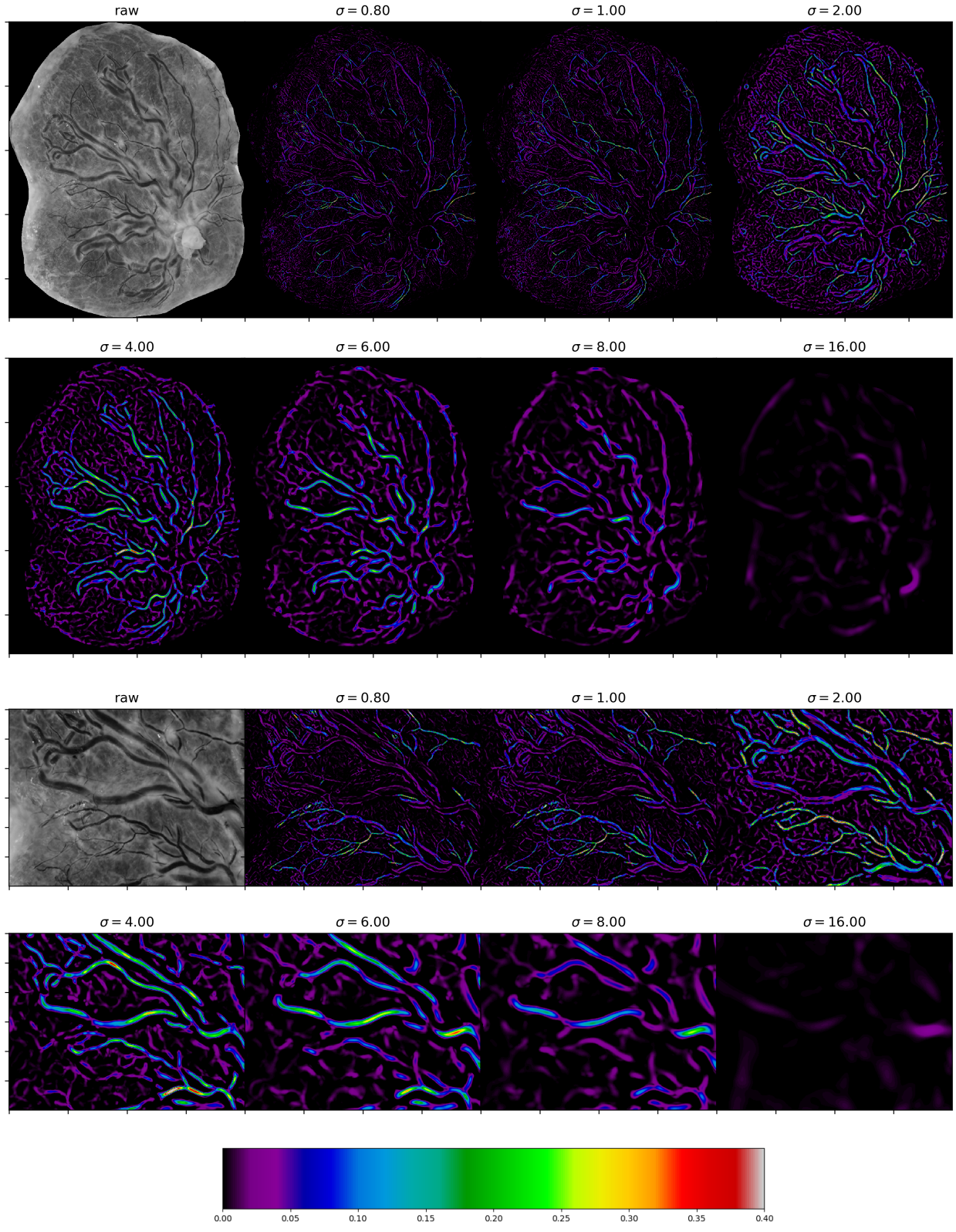


FIGURE 12: Signed Frangi output (plate and inset) (Example 1)

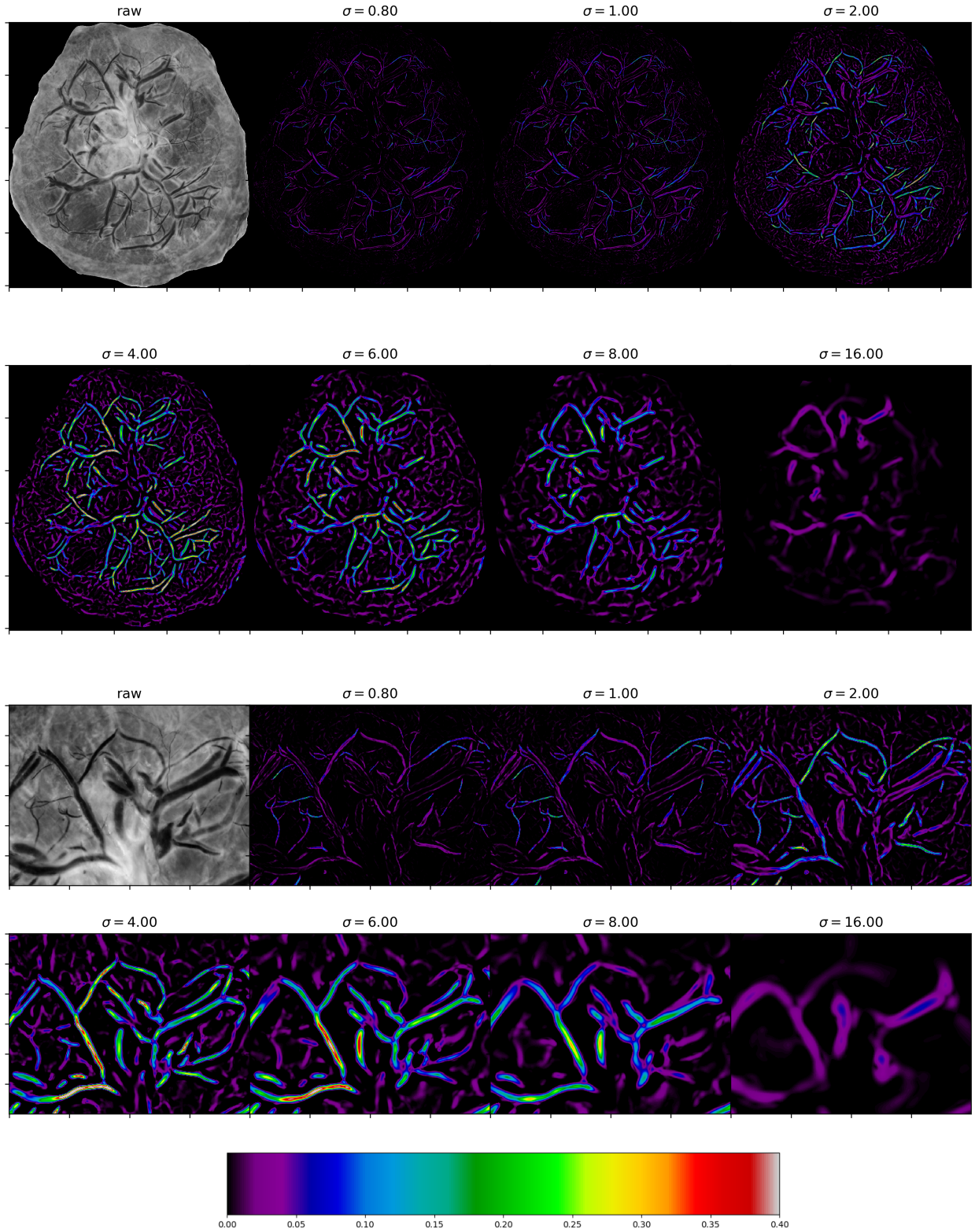


FIGURE 13: Signed Frangi output (plate and inset) (Example 1)

CHAPTER 4

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 noticable after

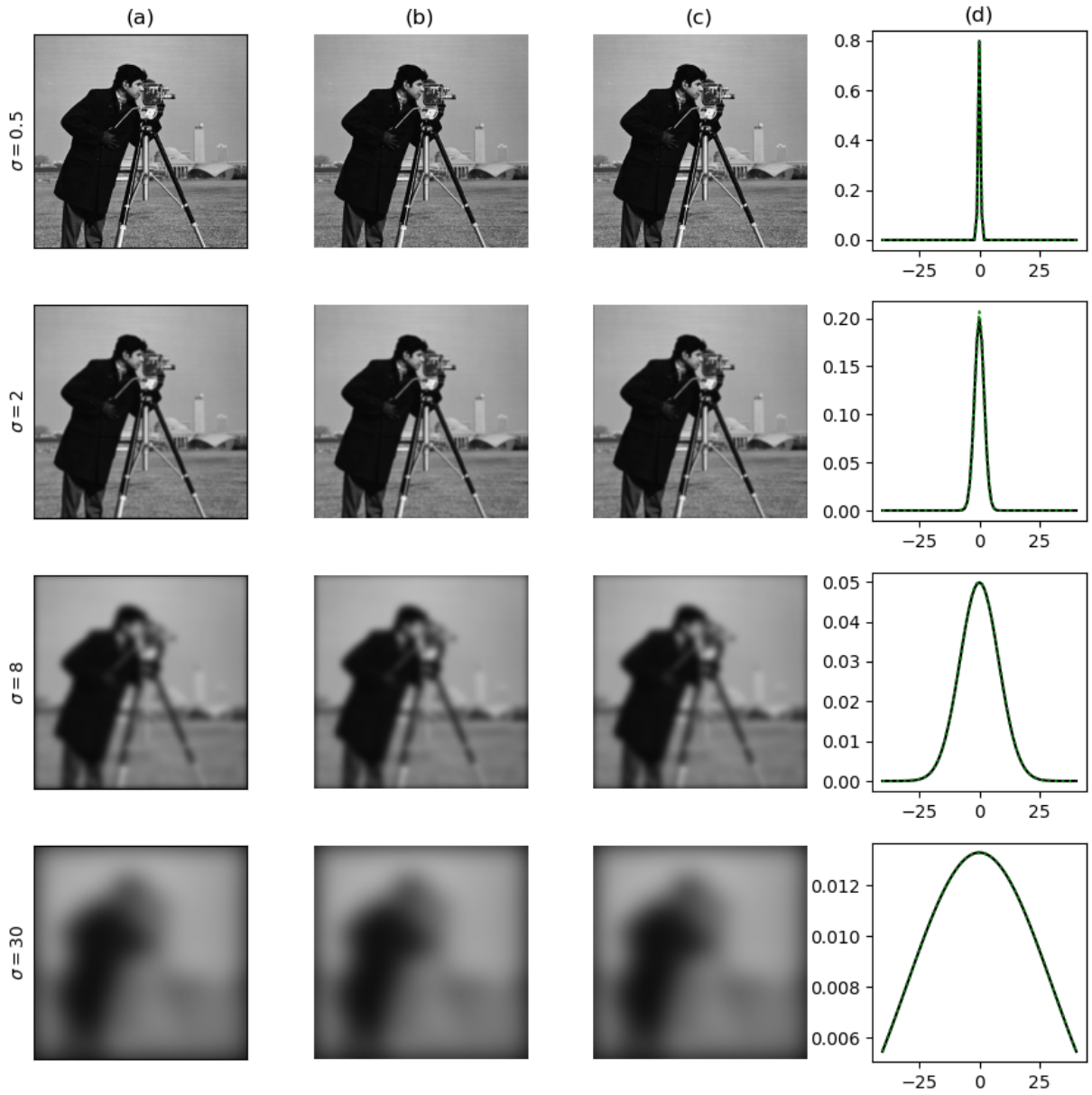


FIGURE 14: Compatibility of Gaussian convolution strategies

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 of an image ($\sigma = 0.3$)

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

TABLE 3: MSE of Frangi scores $\sigma = 0.3$

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

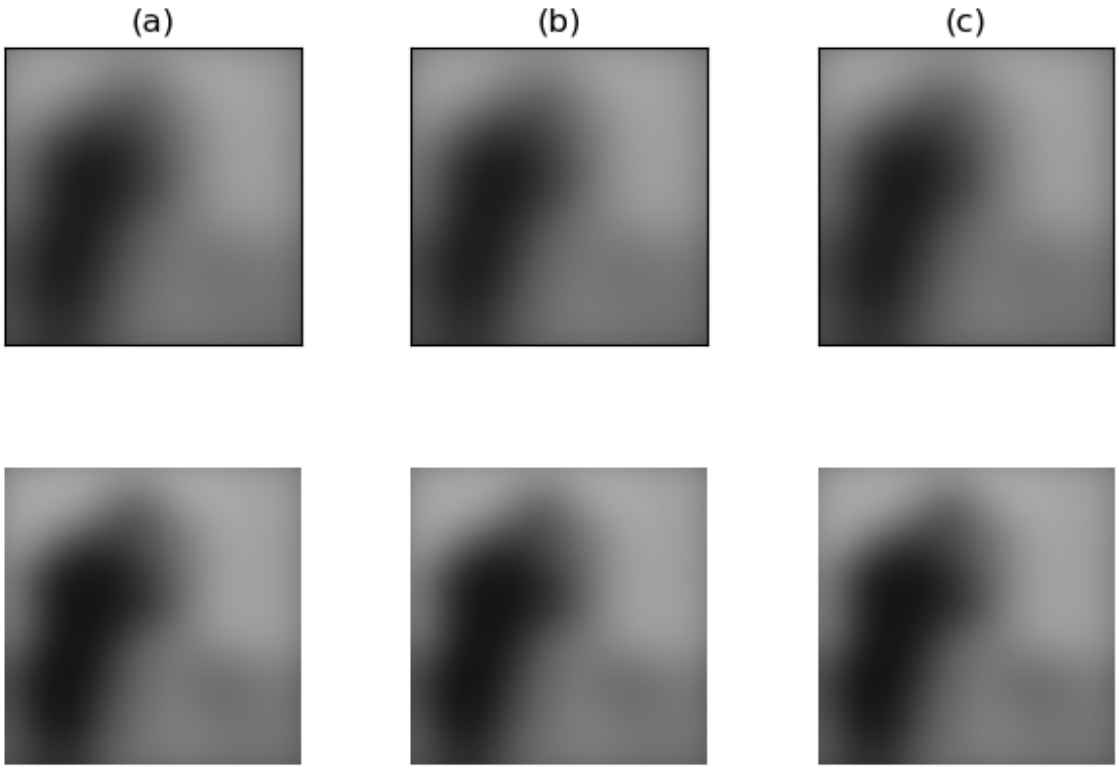


FIGURE 15: Iterative Gaussian blur

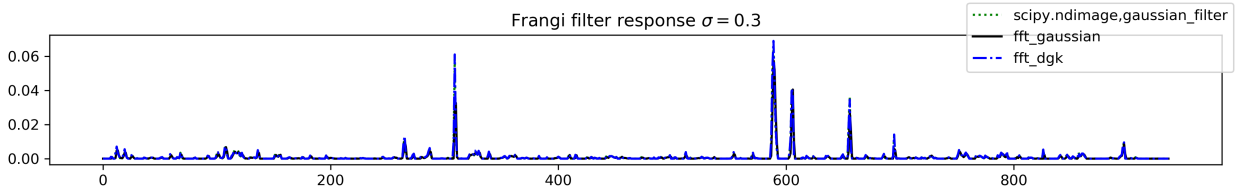


FIGURE 16: Image cross-section of Gaussian blurred images

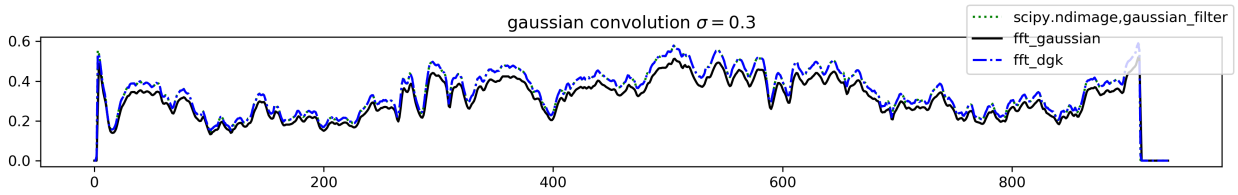


FIGURE 17: Image cross-section of Frangi targets images

	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 $\sigma = 5$

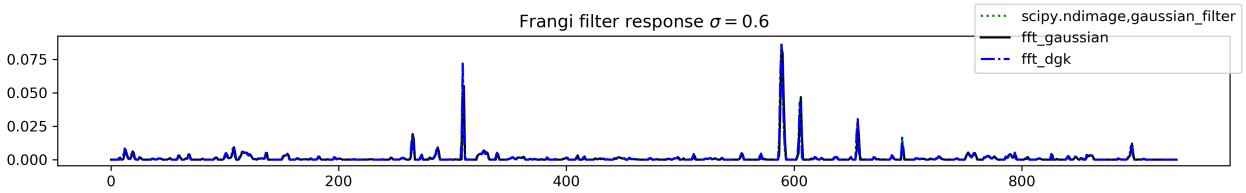


FIGURE 18: Image cross-section of Gaussian blurred images $\sigma = 5$

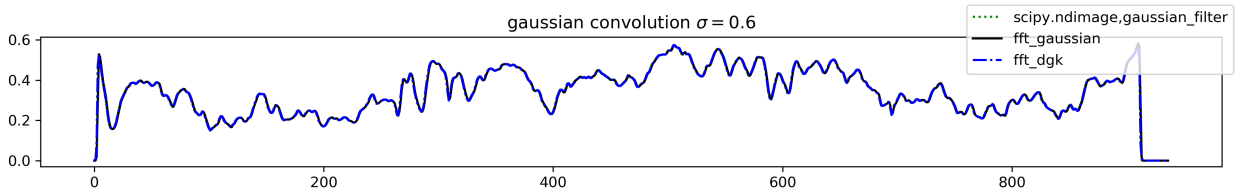


FIGURE 19: Image cross-section of Frangi targets images $\sigma = 5$

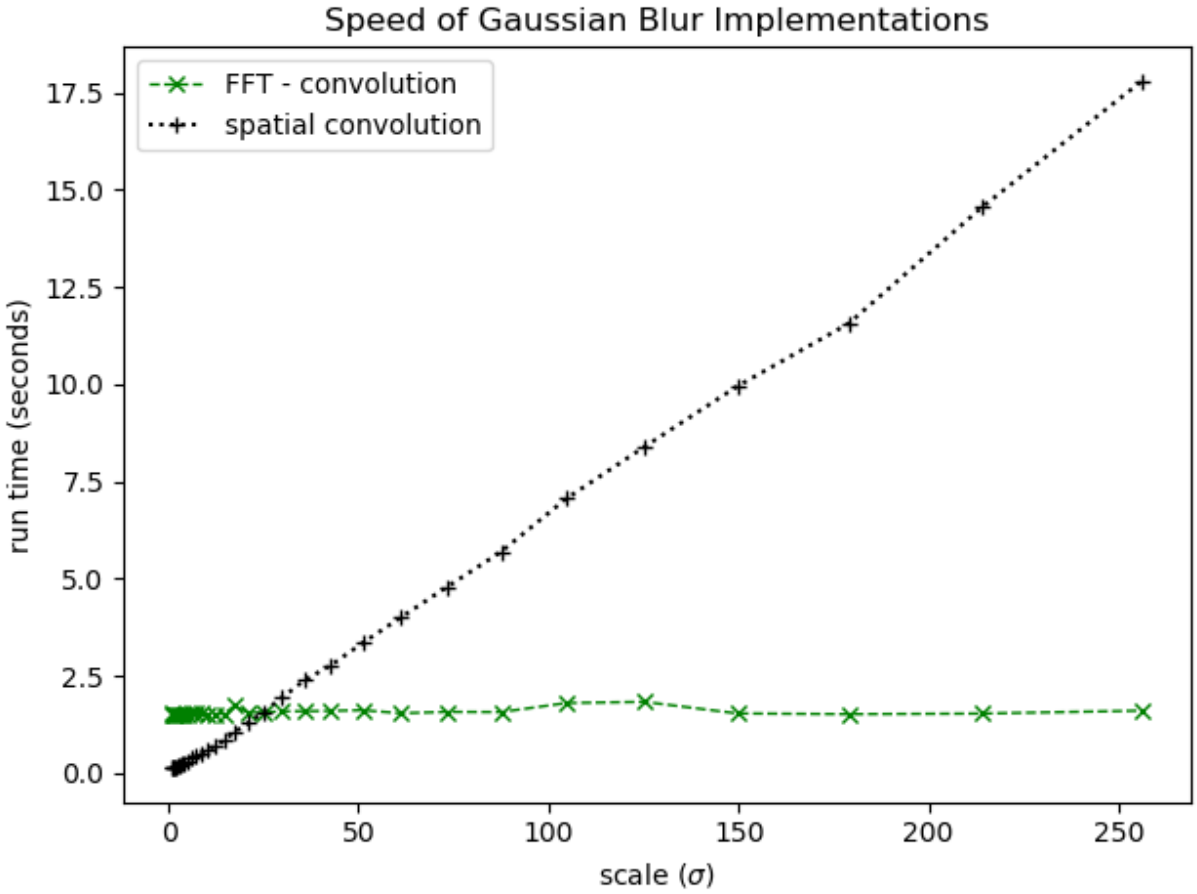


FIGURE 20: Time required

(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. (2.92). 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 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 boster this by requiring that any selected pixels be in the 95th percentile of nonzero and unmasked pixels–otherwise the average is artificially low due to the large background and pixels with zero Frangi score. The use of percentiles 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 $\sigma_{\min}$ and $\sigma_{\max}$.

Method C: Scale-Based Random Walker

This method isn't working well and I should remove it, but the idea is to use a fill to the edge of the vessel and connect them.

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.

CHAPTER 5

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 $\beta = .35$, with scales spaced logarithmcally 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. 21 and fig. 22 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 Classificaitons 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.

use MCC [30]

A Source of "False Negatives" in the NCS data set

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.

Variations in the Data Set and Imperfections of the Ground Truth

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

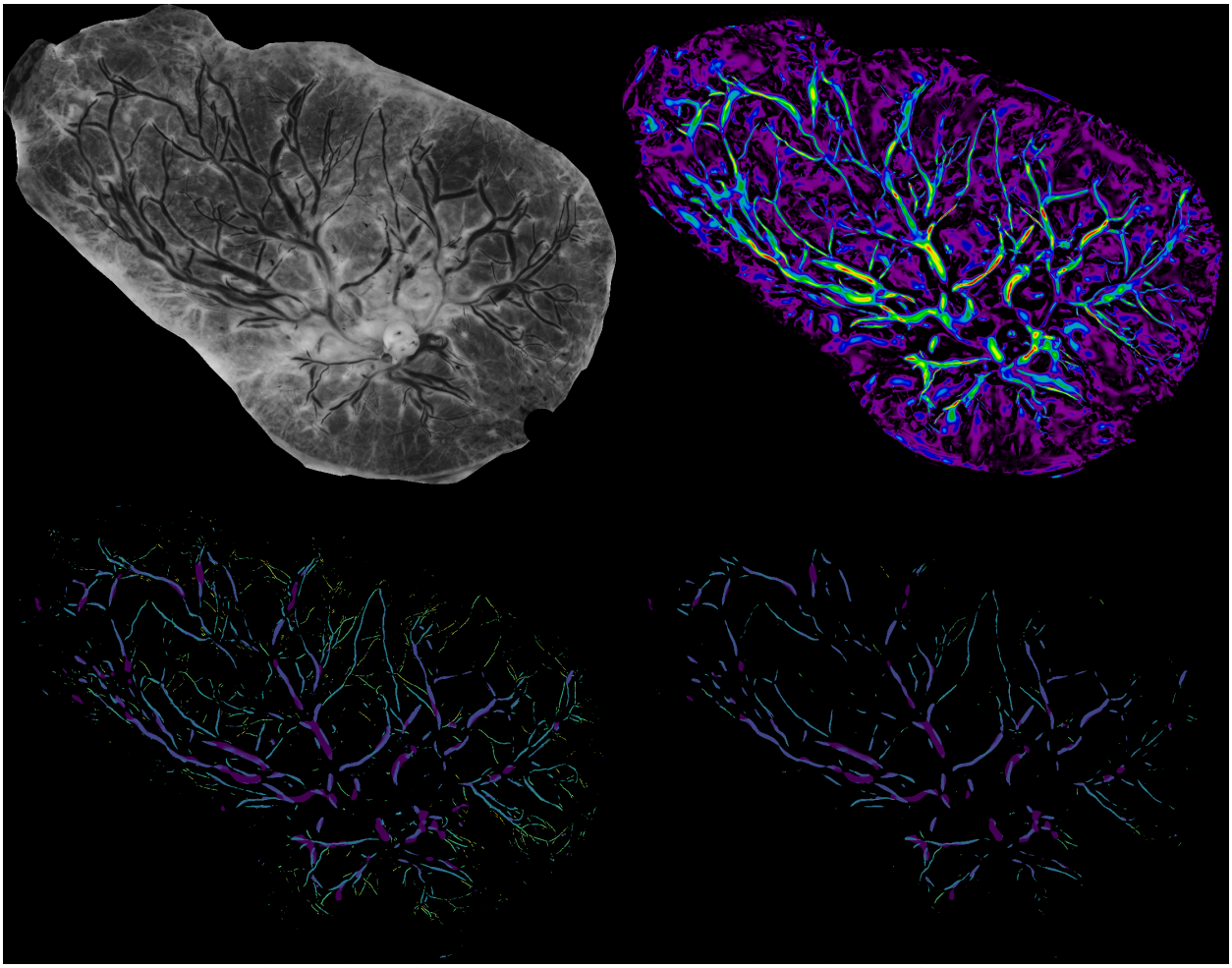


FIGURE 21: Sample Multiscale Frangi output ($\beta = 0.35$) with simple segmentation strategies (Example 1)

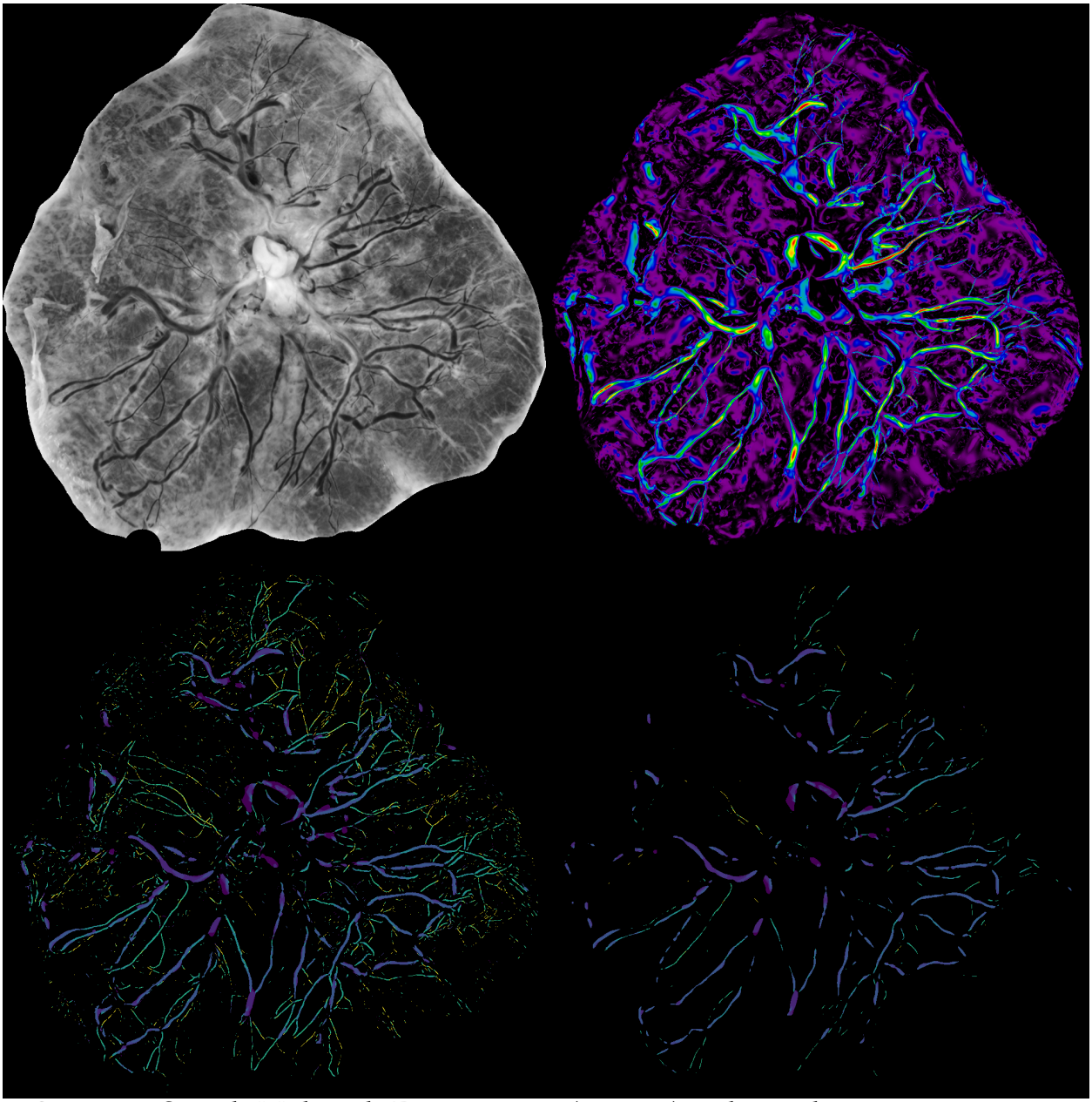


FIGURE 22: Sample Multiscale Frangi output ($\beta = 0.35$) with simple segmentation strategies (Example 2)

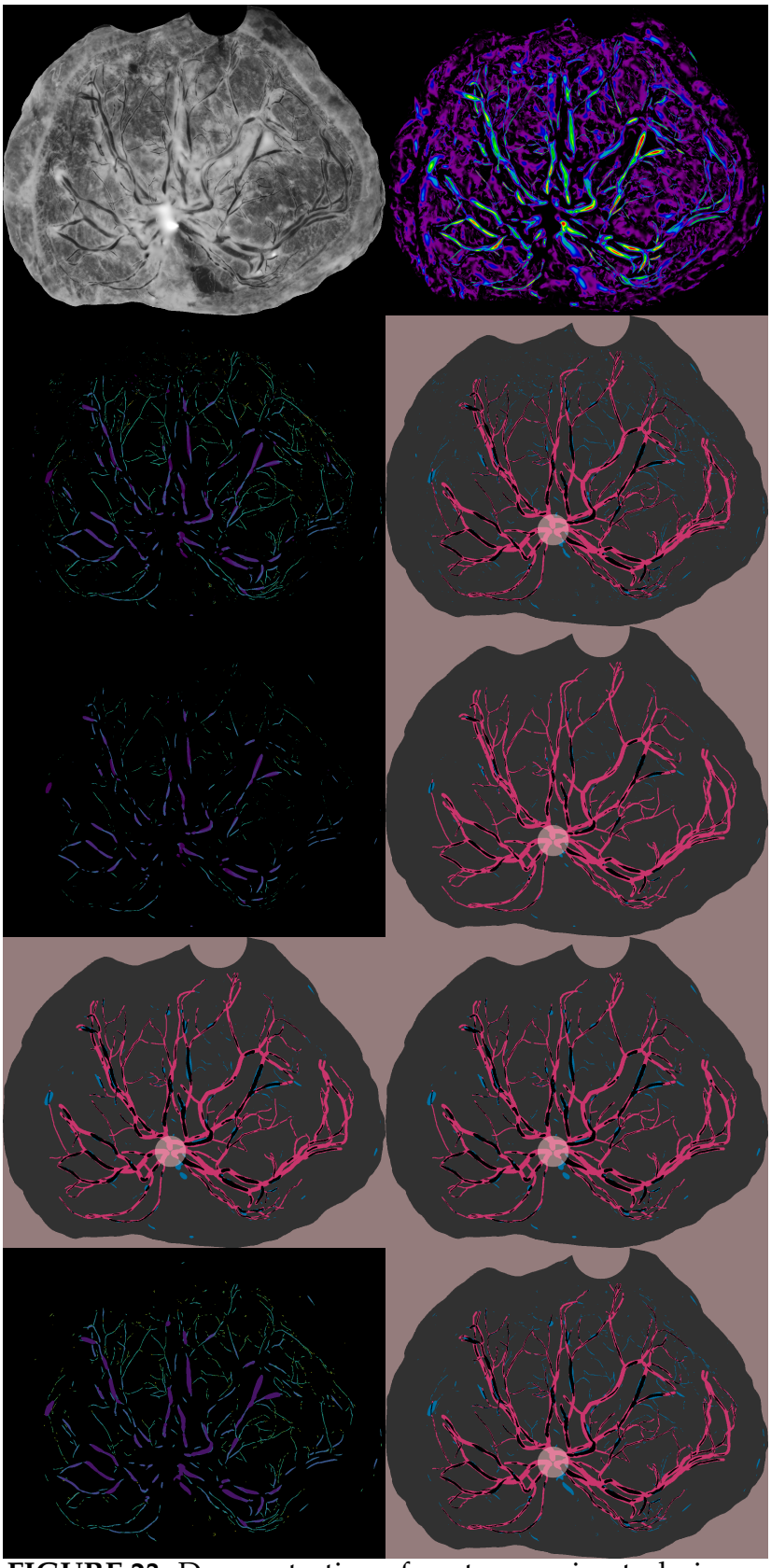


FIGURE 23: Demonstration of postprocessing techniques

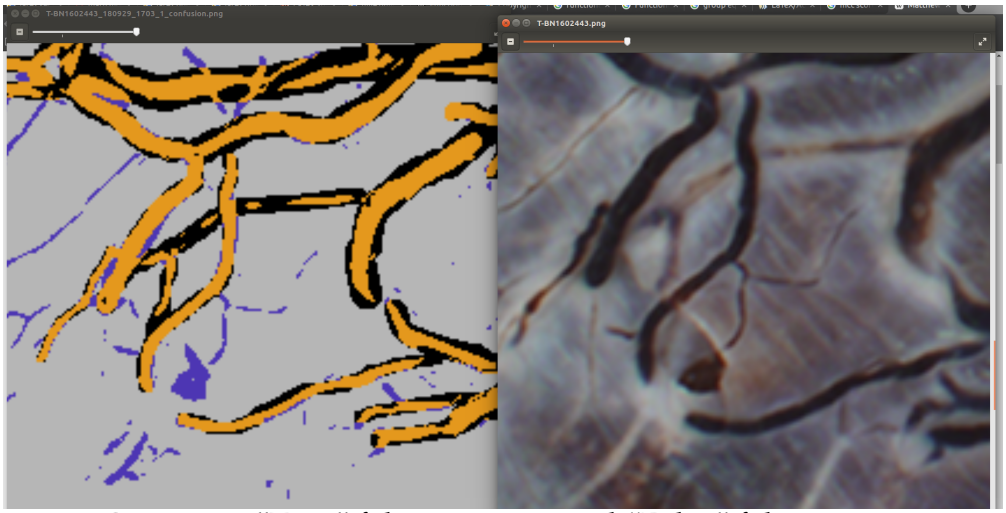


FIGURE 24: "True" false positives and "False" false positives

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 obviouslly 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. Umbillical 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

This is a list of particular things I'd like to explore if I have time:

- Relationship between traced pixelwidths vs the scale they were pulled from.
- Frangi behavior at max scale length and if there's anything that gets too large (related to first derivatives maybe?
- calculate the actual weingarten map eigenvectors (although this is probably gonna be very fake in a discrete sense).
- difference between using green channel and non-green channel.

Answer Research Questions

CHAPTER 6

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

- Solve the Network Connection Problem (PICTURE OF GAPS) Try something like [31] 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).

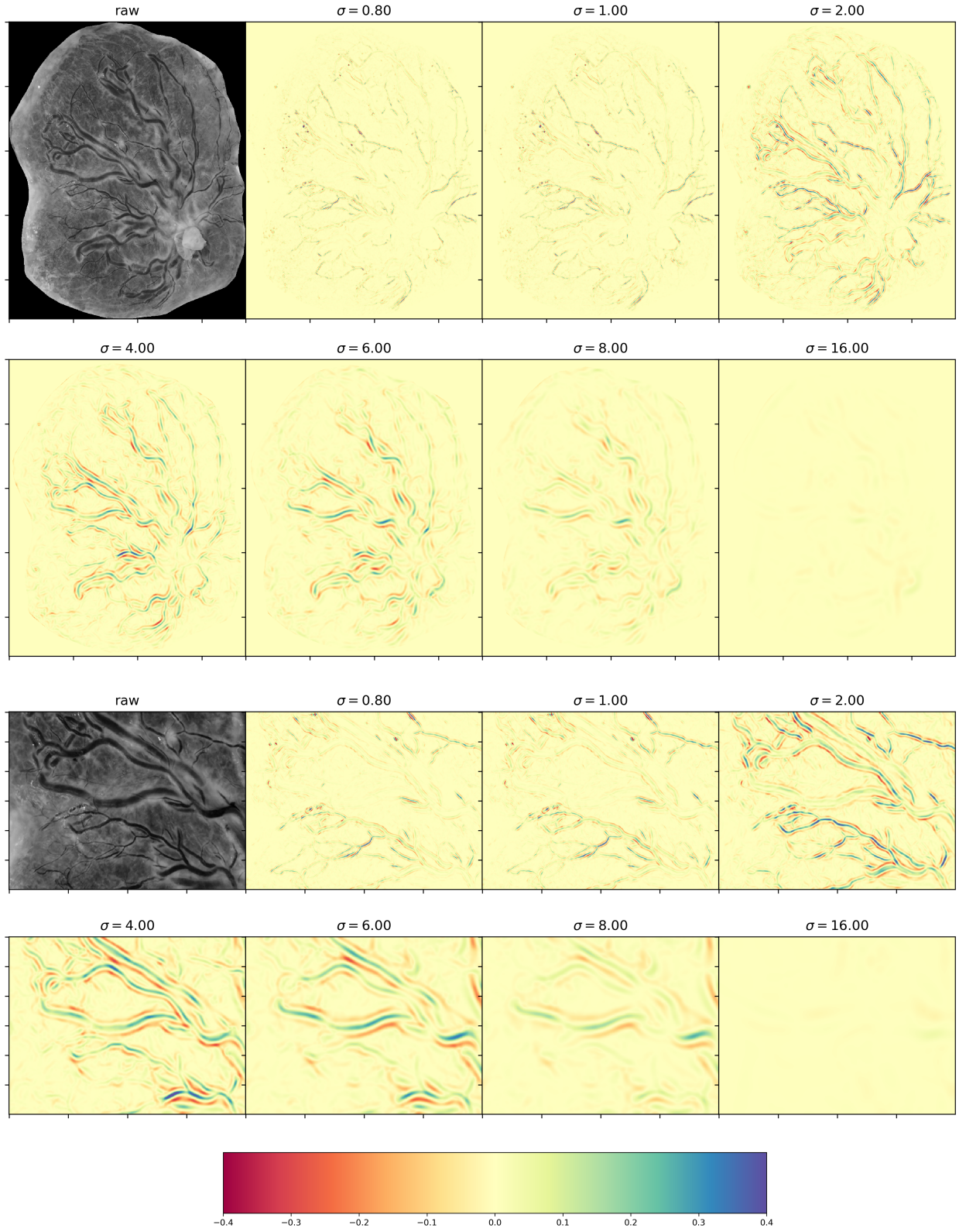


FIGURE 25: Signed Frangi output (plate and inset) (Example 1)

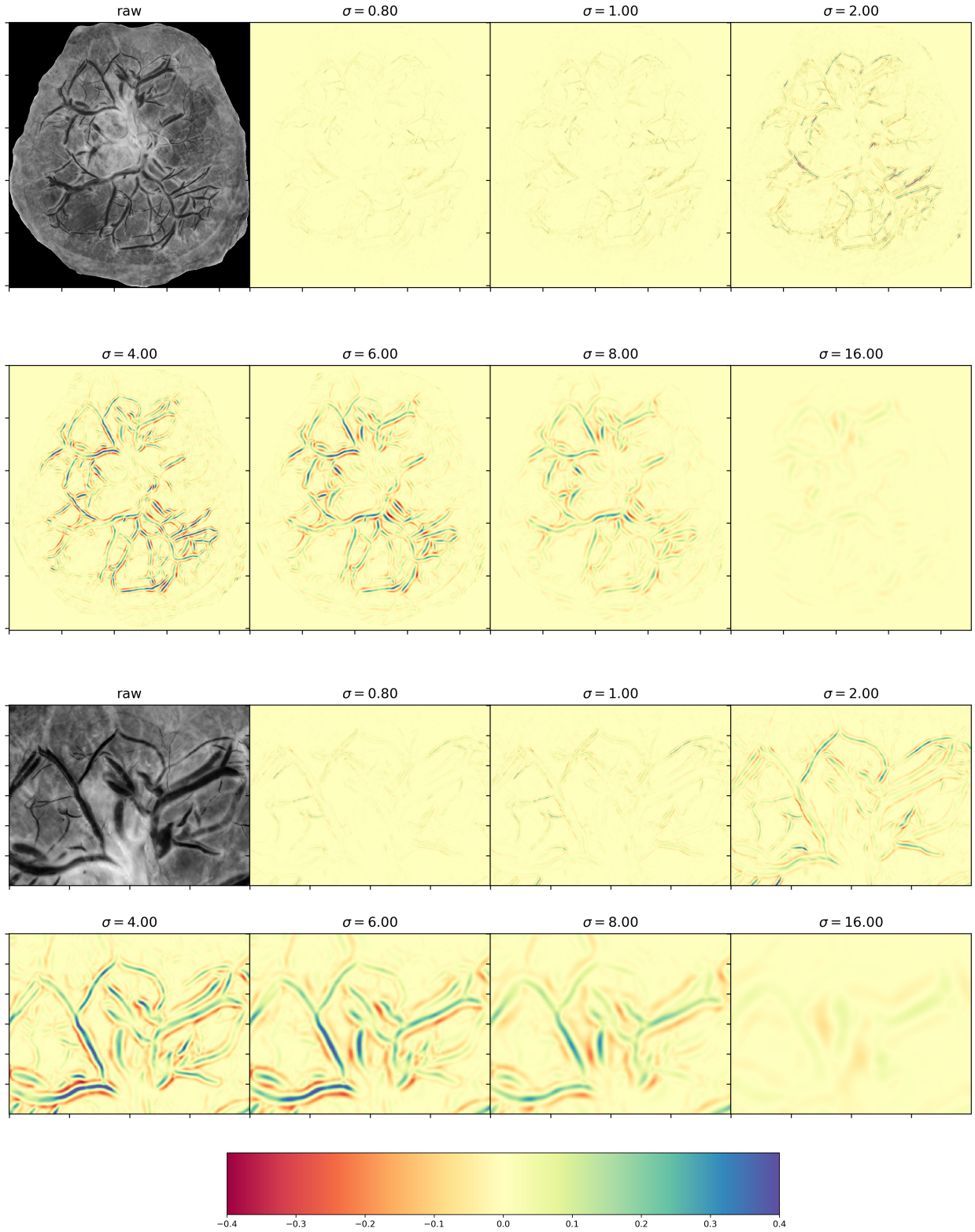


FIGURE 26: Signed Frangi output (plate and inset) (Example 1)

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

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

from skimage.filters import sobel
from frangi import frangi_from_image
from plate_morphology import dilate_boundary
from skimage.morphology import remove_small_holes, remove_small_objects
from merging import nz_percentile

s = sobel(img)
s = dilate_boundary(s, mask=img.mask, radius=20)
finv = frangi_from_image(s, sigma=0.8, dark_bg=True)

finv_thresh = nz_percentile(finv, 80)

margins = remove_small_objects((finv > ft).filled(0), min_size=32)

margins_added = remove_small_holes(np.logical_or(margins, approx),
                                   min_size=100, connectivity=2)

markers = np.zeros(img.shape, dtype=np.uint8)

markers[ Fmax < .1 ] = 1
markers[ margins_added] = 2

rw = random_walker(img, markers)
approx_rw = (rw==2)
confusion_rw = confusion(approx_rw, trace, bg_mask=ucip_mask)
mccs_rw = mccs(approx_rw, trace, bg_mask=ucip_mask)
pnc_rw = np.logical_and(skeltrace, rw2==2).sum() / skeltrace.sum()
```

listings/cut_demo.py

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

import numpy as np
import matplotlib.pyplot as plt

from placenta import (open_typefile, list_placentas, get_named_placenta)
from plate_morphology import mask_cuts_simple, dilate_boundary

from skimage.color import gray2rgb
from skimage.morphology import thin, binary_dilation, disk, square
import numpy.ma as ma
import os.path

def l2_dist(p,q):
    return int(np.round(np.sqrt((p[0]-q[0])**2 + (p[1]-q[1])**2)))

placentas = list_placentas('T-BN')
samples_with_cuts = list()

for filename in list_placentas('T-BN'):

    # this one has two cuts, another one has two cuts as well
    #if filename != "T-BN2459820.png":
    #       continue

    img = get_named_placenta(filename)
    ucip = open_typefile(filename, 'ucip')

    #C, has_cut = mask_cuts(img, ucip, return_success=True, in_place=False)

    #if has_cut:

    #    dilcut = img.copy()

    #    print(filename, "has a cut!")
    #    samples_with_cuts.append(filename)

    #    B = np.all(ucip==(0,0,255), axis=-1)
    #    G = np.all(ucip==(0,255,0), axis=-1)

    #    cutmarks = np.nonzero(thin(B))
    #    perimeter = np.nonzero(G)

    #    #for array in the tuple that comes out of np.nonzero(thin(B))
    #    # or just one if it's just a single thing i guess?

    #    # the x, y points of the cutmarks are in columns
    #    cutinds = np.stack(cutmarks)

    #    for P in cutinds.T:

    #        # consider larger and larger window sizes
    #        for W in [100,200,300]:
    #            # consider all perimeter elements within these bounds

    #            rmin, rmax = max(0, P[0]-W), min(img.shape[0], P[0]+W)
    #            cmin, cmax = max(0, P[1]-W), min(img.shape[1], P[1]+W)
    #            window = np.s_[rmin:rmax, cmin:cmax]

    #            # perimeter indices within the window
    #            pinds = [(x,y) for x, y in zip(*perimeter)
    #                        if x > rmin and x < rmax and y > cmin and y < cmax
```

```
    #                         ]
    #             if pinds:
    #                 break
    #     if pinds:

    #         # max distance to boundary point in the window
    #         # we really only need to keep the largest; deque?
    #         dists = sorted([(pp, l2_dist(P,pp)) for pp in pinds],
    #                        key=lambda t: t[1])
    #         r = int(dists[-1][1]) + 1 # get largest radius but closest point
    #         P = dists[0][0]
    #         B = np.zeros_like(img.mask)

    #         B[cutmarks] = True

    #         # center a disk of found radius there
    #         D = disk(r)
    #         winx = max(P[0]-r,0), min(P[0]+r+1,B.shape[0])
    #         winy = max(P[1]-r,0), min(P[1]+r+1,B.shape[1])
    #         try:
    #             B[winx[0]:winx[1] , winy[0]:winy[1]] = D
    #         except ValueError:
    #             # they're out of bounds so it's a size mismatch. fix it
    #             # by starting/ending D index with opposite sign of the initial
    #             # p +/- radius that was out of bounds
    #             # for example P[0]-r was -9 and everything else was fine
    #             # so you just need to set left side to D[9:,:]
    #             # but you should  wrap this up in a function so the three times
    #             # you do it here and the one time in ucip all gets the same
    #             # code
    #             pass
    #         dilcut[B] = ma.masked

    #     else:
    #         # this is probably not going to happen, but just in case no
    #         # nearby perimeter was found, just... give up
    #         pass

    #     rminv, rmaxv = max(0, rmin-W//2), min(img.shape[0], rmax+W//2)
    #     cminv, cmaxv = max(0, cmin-W//2), min(img.shape[1], cmax+W//2)
    #     view = np.s_[rminv:rmaxv, cminv:cmaxv]
    #     montage = np.hstack((gray2rgb(img.filled(0)[view]),
    #                          ucip[view],
    #                          gray2rgb(C.filled(0)[view]),
    #                          gray2rgb(dilcut.filled(0)[view])))
    #     filestub, _ = os.path.splitext(filename)
    #     plt.imsave(f'demo_output/cut_demo/{filestub}_cutopts.png', montage)
    #     #plt.imshow(montage)
    #     plt.show()
    #     plt.close()
    mimg, success = mask_cuts_simple(img, ucip, return_success=True)
    if success:
        montage = np.hstack((img.filled(0),
                             mimg.filled(0)))
        plt.imshow(montage)
        plt.show()
        plt.close()
print("*"*80)
print(f"there were {len(placentas)} total samples",
      f"and {len(samples_with_cuts)} of them had cuts")
```

listings/diffgeo.py

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

import numpy as np
import numpy.ma as ma

from skimage.feature import hessian_matrix, hessian_matrix_eigvals
from numpy.linalg import eig


def principal_curvatures(img, sigma=1.0, H=None):
    """Calculate the approximated principal curvatures of an image

    Return the (approximated) principal curvatures { 1 ,  2 } of an image,
    that is, the eigenvalues of the Hessian at each point (x,y). The output
    is arranged such that |  1 | <= |  2 |.  Note that the Hessian of the image,
    if not provided, is computed using skimage.feature.hessian_matrix, which
    can be very slow for large sigmas.

    Parameters
    ----------
    img: array or ma.MaskedArray

        An ndarray representing a 2D or multichannel image. If the image is
        multichannel (e.g. RGB), then each channel will be proccessed
        individually. Additionally, the input image may be a masked array-- in
        which case the output will preserve this mask identically.

    sigma: float, optional
        Standard deviation of the Gaussian (used to calculate the hessian
        matrix).
    H:  list of array, optional
        The hessian itself (Hxx,Hxy,Hyy) whose eigenvalues will be calculated.
        Use this option if you're going to calculate the Hessian using faster
        means, e.g. via FFT.

    Returns
    -------
    (K1, K2):   tuple of arrays
        K1, K2 each are the exact dimension of the input image, ordered in
        magnitude such that |  1 | <= |  2 | in all locations.

    Examples
    --------
        >>> K1, K2 = principal_curvatures(img)
        >>> K1.shape == img.shape
        True
        >>> (K1 <= K2).all()
        True
        >>> K1.mask == img.mask
        True
    """

    # determine if multichannel
    multichannel = (img.ndim == 3)

    if not multichannel:
        # add a trivial dimension
        img = img[:,:,np.newaxis]

    K1 = np.zeros_like(img, dtype='float64')
    K2 = np.zeros_like(img, dtype='float64')

    for ic in range(img.shape[2]):
```

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

```
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[subs]:
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
221     pass
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()
```

```
    #     print('time elapsed: ', toc - tic)
    #     tic = time.time()
    #     print('calculating principal curvatures for   ={} (fast)'.format(sigma))
    #     k1,k2 = principal_curvatures(img, sigma=sigma, H=h)

    #     toc = time.time()
    #     print('time elapsed: ', toc - tic)
    #     tic = time.time()

    #     #####

    #     print('calculating targets for   ={}'.format(sigma))
    #     T = get_targets(K1,K2, threshold=False)

    #     toc = time.time()
    #     print('time elapsed: ', toc - tic)
    #     tic = time.time()

    #     print('calculating targets for   ={} (fast)'.format(sigma))
    #     t = get_targets(k1,k2, threshold=False)

    #     toc = time.time()
    #     print('time elapsed: ', toc - tic)

    #     ######

    #     print('extending masks')

    #     # extend mask over nontargets items
    #     img1 = ma.masked_where( T < T.mean(), img)
    #     img2 = ma.masked_where( t < t.mean(), img)

    #     tic = time.time()
    #     print('calculating principal directions for   ={}'.format(sigma))
    #     T1,T2 = principal_directions(img1, sigma=sigma, H=H)
    #     toc = time.time()
    #     print('time elapsed: ', toc - tic)
    #     tic = time.time()

    #     print('calculating principal directions for   ={} (fast)'.format(sigma))
    #     t1,t2 = principal_directions(img2, sigma=sigma, H=h)
    #     toc = time.time()
    #     print('time elapsed: ', toc - tic)
```

listings/extract_NCS_pcsvn.py

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

"""
This is the main program. It approximates the PCSVN of a list of samples.
It does not do network completion.

"""

from placenta import (get_named_placenta, cropped_args, cropped_view,
                      list_placentas, list_by_quality, open_typefile,
                      open_tracefile, add_ucip_to_mask, measure_ncs_markings)

from merging import nz_percentile, apply_threshold, sieve_scales, view_slices

from scoring import (compare_trace, rgb_to_widths, merge_widths_from_traces,
                     filter_widths, mcc, confusion, skeletonize_trace)

```

```
from pcsvn import extract_pcsvn, scale_label_figure, get_outname_lambda
from preprocessing import inpaint_hybrid

import numpy as np
import numpy.ma as ma

import matplotlib.pyplot as plt

import os.path
import os
import json
import datetime
import pandas

# for some post_processing, this needs to be moved elsewhere
from skimage.filters import sobel
from frangi import frangi_from_image
from plate_morphology import dilate_boundary, mask_cuts_simple
from skimage.morphology import remove_small_holes, remove_small_objects
from skimage.segmentation import random_walker
from postprocessing import random_walk_fill, random_walk_scalewise


# INITIALIZE SAMPLES ____________________________________________________
#   There are several ways to initialize samples. Uncomment one.

# load all 201 samples
# placentas = list_placentas('T-BN')
# load placentas from a certain quality category 0=good, 1=okay, 2=fair, 3=poor

placentas = list_by_quality(0, N=1)
#placentas = list()
#placentas.extend(list_by_quality(1))
#placentas.extend(list_by_quality(2))
#placentas.extend(list_by_quality(3))

# load from a file (sample names are keys of the json file)
# placentas = list_by_quality(json_file='manual_batch.json')

# for a single named sample, use a 1 element list.
# placentas = ['T-BN0204423.png']

#placentas = ['barium1.png',]
# RUNTIME OPTIONS _______________________________________________________
#   Where to save and whether or not to use old targets.

MAKE_NPZ_FILES = False # pickle frangi targets if you can
USE_NPZ_FILES = False # use old npz files if you can
NPZ_DIR = 'output/181201-L'  # where to look for npz files
OUTPUT_DIR = 'output/181201-L'  # where to save outputs

# add in a meta switch for verbosity (or levels)
#VERBOSE = False

# FRANGI / EXTRACT_PCSVN OPTIONS ________________________________________

# Find bright curvilinear structure against a dark background -> True
# Find dark curvilinear structure against a bright background -> False
# DARK_BG -> ignore and return signed Frangi scores
DARK_BG = False

# Along with the above, this will return "opposite" signed frangi scores.
# if this is True, then DARK_BG controls the "polarity" of the filter.
# See frangi.get_frangi_targets for details.
```

```
SIGNED_FRANGI = False

# Do not calculate hessian scores close to the boundary (this is important
# mainly in terms of ensuring that the hessian is very large on the edge of
# the plate (which would influence gamma calculation)
DILATE_PER_SCALE = True

# Attempt to remove glare from sample (some are OK, some are bad)
FLATTEN_MODE = 'L' # 'G' or 'L'
REMOVE_GLARE = True
REMOVE_CUTS = True

# Which scales to use
SCALE_RANGE = (-1.0, 3.5); SCALE_TYPE = 'logarithmic'
#SCALE_RANGE = (.2, 12); SCALE_TYPE = 'linear'
N_SCALES = 20

# use this if you want to use a custom argument (comment out the above)
SCALES = None
#SCALE_RANGE = None, SCALE_TYPE == 'custom'


# Explicit Frangi Parameters (pass a scalar, array as long as scales)
BETAS = 0.35
GAMMAS = 0.5
CS = None # pass scalar, array, or None
ALPHAS = None # set custom alphas or calculate later
FIXED_ALPHA = .3

RESCALE_FRANGI = True
GRADIENT_FILTER = False


# Scoring Decisions (don't need to touch these)
UCIP_RADIUS = 50  # area around the umbilical cord insertion point to ignore
INV_SIGMA = 0.8
# some other initializations, don't mind me




# CODE BEGINS HERE ____________________________________________________________

if SCALES is None:
    if SCALE_TYPE == 'linear':
        scales = np.linspace(*SCALE_RANGE, num=N_SCALES)
    elif SCALE_TYPE == 'logarithmic':
        scales = np.logspace(*SCALE_RANGE, num=N_SCALES, base=2)
else:
    scales = SCALES
    SCALE_TYPE = 'custom'  # this and the next three lines are just for logging
    N_SCALES = len(SCALES)
    SCALES = (min(SCALES), max(SCALES))

mccs = dict()  # empty dict to store MCC's of each sample
pncs = dict()  # empty dict to store percent network covered for each sample

n_samples = len(placentas)

if not os.path.exists(OUTPUT_DIR):
    os.makedirs(OUTPUT_DIR)

print(n_samples, "samples total!")

```

```
for i, filename in enumerate(placentas):

    print('*'*80)
    print(f'extracting PCSVN of {filename}\t ({i} of {n_samples})')

    # --- Setup, Preprocessing, Frangi Filter (it's mixed up) -----------------

    raw_img = get_named_placenta(filename, mode=FLATTEN_MODE)

    ucip = open_typefile(filename, 'ucip')

    if REMOVE_CUTS:
        img, has_cut = mask_cuts_simple(raw_img, ucip, return_success=True)
        img.data[img.mask] = 0 # actually zero out that area
    else:
        img = raw_img.copy()

    if REMOVE_GLARE:
        img = inpaint_hybrid(img)


    if USE_NPZ_FILES:
        # find the first npz file with the sample name in it in the
        # specified directory.
        stub = filename.rstrip('.png')
        for f in os.scandir(NPZ_DIR):
            if f.name.endswith('npz') and f.name.startswith(stub):
                npz_filename = os.path.join(NPZ_DIR, f.name)
                print(f'using the npz file {npz_filename}')
                break  # we'll just use the first one we can find.
        else:
            print(f'no npz file found for {filename}.')
            npz_filename = None
    else:
        npz_filename = None

    # set a lambda function to make output file names
    outname = get_outname_lambda(filename, output_dir=OUTPUT_DIR)

    if npz_filename is not None:

        F = np.load(npz_filename)['F']

        # in case preprocessing happens inside extract_pcsvn, do it out here

        print('successfully loaded the frangi targets!')

    else:
        print('finding multiscale frangi targets')

        # F is an array of frangi scores of shape (*img.shape, N_SCALES)
        F, jfile = extract_pcsvn(img, filename, dark_bg=DARK_BG, beta=BETAS,
                                 scales=scales, gamma=GAMMAS, c=CS,
                                 kernel='discrete', dilate_per_scale=True,
                                 verbose=False, signed_frangi=SIGNED_FRANGI,
                                 generate_json=True, output_dir=OUTPUT_DIR,
                                 rescale_frangi=RESCALE_FRANGI,
                                 gradient_filter=GRADIENT_FILTER)

        if MAKE_NPZ_FILES:
            npzfile = ".".join((outname("F").rsplit('.', maxsplit=1)[0], 'npz')
                               )
            print("saving frangi targets to ", npzfile)
            np.savez_compressed(npzfile, F=F)
```

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

```
274
275     # fix labels to incorporate offset
276     #labs_LO = (labs_LO != 0)*(labs_LO + LO_offset)
277
278     # confusion matrix against default trace
279     confuse = confusion(approx, trace, bg_mask=ucip_mask)
280     #confuse_LO = confusion(approx_LO, trace, bg_mask=ucip_mask)
281     confuse_FA = confusion(approx_FA, trace, bg_mask=ucip_mask)
282
283     m_score, counts = mcc(approx, trace, ucip_mask, return_counts=True)
284     m_score_FA, counts_FA = mcc(approx_FA, trace, ucip_mask,
285                                 return_counts=True)
286
287     # this all just verifies that the 4 categories were added up
288     # correctly and match the total number of pixels in the reported
289     # placental plate.
290     TP, TN, FP, FN = counts # return these for more analysis?
291
292     total = np.sum(~ucip_mask)
293     #print(f'TP: {TP}\t TN: {TN}\nFP: {FP}\tFN: {FN}')
294     # just a sanity check
295     #print(f'TP+TN+FP+FN={TP+TN+FP+FN}\ttotal pixels={total}')
296
297
298     #approx_rw, markers, margins_added = random_walk_fill(img, Fmax, .3, .01,
299     #                                                     DARK_BG)
300
301     approx_rw, labs_rw = random_walk_scalewise(F, .4, return_labels=True)
302     #confuse_margins = confusion(margins_added, trace, bg_mask=ucip_mask)
303
304     high_alphas = np.array([nz_percentile(F[..., k], 98.0)
305                             for k in range(N_SCALES)]
306                            )
307     high_frangi = apply_threshold(F,high_alphas, return_labels=False)
308     confuse_rw = confusion(approx_rw, trace, bg_mask=ucip_mask)
309     m_score_rw, counts_rw = mcc(approx_rw, trace, ucip_mask,
310                                 return_counts=True)
311     pnc_rw = (skeltrace & approx_rw).sum() / skeltrace.sum()
312
313
314     # --- Generating Visual Outputs-----------------------------------------------
315     crop = cropped_args(img)  # these indices crop out the mask significantly
316
317     # save the raw, unaltered image
318     plt.imsave(outname('0_raw'), raw_img[crop].filled(0), cmap=plt.cm.gray)
319
320     # save the preprocessed image
321     plt.imsave(outname('1_img'), img[crop].filled(0), cmap=plt.cm.gray)
322
323     # save the maximum frangi output over all scales
324     plt.imsave(outname('2_fmax'), Fmax[crop], vmin=0, vmax=1.0,
325                cmap=plt.cm.nipy_spectral)
326
327     # only save the colorbar the first time
328     save_colorbar = (i==0)
329     scale_label_figure(labs, scales, crop=crop,
330                        savefilename=outname('3_labeled'), image_only=True,
331                        save_colorbar_separate=save_colorbar,
332                        output_dir=OUTPUT_DIR)
333
334     scale_label_figure(labs_rw, scales, crop=crop,
335                        savefilename=outname('A_labeled_rw'), image_only=True,
336                        save_colorbar_separate=save_colorbar,
337                        output_dir=OUTPUT_DIR)
```

```
    plt.imsave(outname('4_confusion'), confuse[crop])

    plt.imsave(outname('7_confusion_FA'), confuse_FA[crop])
    plt.imsave(outname('B_confusion_rw'), confuse_rw[crop])
    #plt.imsave(outname('A_markers_rw'), markers[crop])
    #plt.imsave(outname('9_margin_for_rw'), confuse_margins[crop])
    percent_covered = (skeltrace & approx).sum() / skeltrace.sum()
    percent_covered_FA = (skeltrace & approx_FA).sum() / skeltrace.sum()



    st_colors = {
        'TN': (79,79,79),  # true negative# 'f7f7f7'
        'TP': (0, 0, 0),  # true positive  # '000000'
        'FN': (201,53,108),  # false negative # 'f1a340' orange
        'FP': (92,92,92),  # false positive
        'mask': (247, 200, 200)  # mask color (not used in MCC calculation)
    }

    plt.imsave(outname('5_coverage'), confusion(approx, skeltrace,
                                                colordict=st_colors)[crop])
    plt.imsave(outname('8_coverage_FA'), confusion(approx_FA, skeltrace,
                                                   colordict=st_colors)[crop])
    plt.imsave(outname('C_coverage_rw'), confusion(approx_rw, skeltrace,
                                                   colordict=st_colors)[crop])

    # make the graph that shows what scale the max was pulled from

    scale_label_figure(labs_FA, scales, crop=crop,
                       savefilename=outname('6_labeled_FA'), image_only=True,
                       save_colorbar_separate=False, output_dir=OUTPUT_DIR)

    V = np.transpose(F, axes=(2, 0, 1))

    #view_slices(F[crop], axis=-1, scales=scales)

    print('starting to sieve')
    sieved = sieve_scales(V, 98, 95)

    approx_S, labs_S = (sieved != 0), sieved
    confuse_S = confusion(approx_S, trace, bg_mask=ucip_mask)

    scale_label_figure(labs_S, scales, crop=crop,
                       savefilename=outname('D_labeled_S'), image_only=True,
                       save_colorbar_separate=False, output_dir=OUTPUT_DIR)

    plt.imsave(outname('E_confusion_S'), confuse_S[crop])

    m_score_S, counts_S = mcc(approx_S, trace, ucip_mask, return_counts=True)
    pnc_S = (skeltrace & approx_S).sum() / skeltrace.sum()

    mccs[filename] =  (m_score, m_score_FA, m_score_rw, m_score_S )
    pncs[filename] = (percent_covered, percent_covered_FA, pnc_rw, pnc_S)

    print('percentage of skeltrace covered:(percentile filtering)',
          f'{percent_covered:.2%}')
    print('percentage of skeltrace covered (fixed alpha):',
          f'{percent_covered_FA:.2%}')
    print('percentage of skeltrace covered (random_walker):',
          f'{pnc_rw:.2%}')
    print('percentage of skeltrace covered (sieving):',
          f'{pnc_S:.2%}')
```

```
    print(f'mcc score of {m_score:.3} for percentile filtering')
    print(f'mcc score of {m_score_FA:.3} with fixed alpha {FIXED_ALPHA}')
    print(f'mcc score of {m_score_rw:.3} after random walker')
    print(f'mcc score of {m_score_S:.3} after sieving')
    ### THIS IS ALL A HORRIBLE MESS. FIX IT

    # why don't you just return the dict instead
    with open(jfile, 'r') as f:
        slog = json.load(f)

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

    slog['counts'] = c2d(counts)
    slog['counts_FA'] = c2d(counts_FA)
    slog['counts_rw'] = c2d(counts_rw)
    slog['pnc'] = pncs[filename]
    slog['mcc'] = mccs[filename]
    slog['scale_maxes'] = list(scale_maxes)
    slog['ALPHAS'] = list(ALPHAS)

    with open(jfile, 'w') as f:
        json.dump(slog, f)

    plt.close('all')

# Post-run Meta-Output and Logging ____________________________________________

timestring = datetime.datetime.now()
timestring = timestring.strftime("%y%m%d_%H%M")

mccfile = os.path.join(OUTPUT_DIR, f"runlog_{timestring}.json")

runlog = {
    'time': timestring,
    'DARK_BG': DARK_BG,
    'DILATE_PER_SCALE': DILATE_PER_SCALE,
    'SCALE_RANGE': SCALE_RANGE,
    'SCALE_TYPE' : SCALE_TYPE,
    'N_SCALES': N_SCALES,
    'scales': list(scales),
    'ALPHAS': list(ALPHAS),
    'BETAS': None,
    'use_npz_files': False,
    'remove_glare': REMOVE_GLARE,
    'files': list(placentas),
    'MCCS': mccs,
    'PNC': pncs
}

# save to a json file
with open(mccfile, 'w') as f:
    json.dump(runlog, f, indent=True)
```

listings/frangi_graphing.py

```
import matplotlib as mpl
from mpl_toolkits.mplot3d import Axes3D
import matplotlib.pyplot as plt
import numpy as np
from numpy import exp
from skimage.io import imread
from skimage.util import montage
```

```
from itertools import product

def s(x, gamma):
    """normalized structureness factor.
    x is the ratio of the input to the maximum possible structureness factor
    (smax) at that scale (which would cancel out with the c in the denominator)
    """
    return (1 - exp(-x**2 / (2*gamma**2))) / (1 - exp(-1/(2*gamma**2)))


def r(y, beta):
    """normalized anistropy factor
    y is the ratio |k1 / k2|, so y=0 corresponds to perfectly isotropic
    and y->1 corresponds to highly anisotropic
    """
    return np.exp(-y**2 / (2*beta**2))

#plt.rc('text', usetex=True)
#plt.rc('font', family='serif')


dom = np.linspace(0, 1)

plt.close('all')

# show dependence of structureness factor on its parameter
for gamma in [0.1, 0.25, 0.35, 0.5, 0.9, 1, 2, 10, 1000]:
    plt.plot(dom, s(dom, gamma), label=r'$\gamma={}$'.format(gamma))

plt.ylabel(r'$\left(1-\exp\left\{\frac{-S}{2(\gamma S_{max})^2}\right\}\right)$',
           fontsize=14)
plt.xlabel(r'$(S / S_{max})$', fontsize=14)
plt.title(r'Dependence of Structureness Factor on Parameter $\gamma=(c/S_{max})$')
plt.legend()

#plt.show()
plt.close('all')

for beta in [0.1, 0.25, 0.35, 0.5, 0.9, 1, 2, 10, 1000]:
    plt.plot(dom, r(dom, beta), label=r'$\beta={}$'.format(beta))

plt.ylabel(r'$\exp\left\{ \frac{-A}{2\beta^2}\right \}$',
           fontsize=14)
plt.xlabel(r'$ A = \left|\lambda_1 / \lambda_2\right|$', fontsize=14)
plt.title(r'Dependence of Anisotropy Factor on Parameter $\beta$')
plt.legend()

#plt.show()
plt.close('all')

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

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

    fig = plt.figure(figsize=(8,5))
    ax = fig.gca(projection='3d')
    X, Y = np.meshgrid(dom, dom)

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

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

    ax.set_xlabel(r'$\left|\lambda_1 / \lambda_2 \right|$')
    ax.set_ylabel(r'$ ( S / S_{\max} )$ ')
```

```
72
73      ax.set_title(r"Rescaled Frangi filter, "
74                   r"$\beta={}, \gamma={}$".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.
```

```
    signed_frangi: bool, optional
        if signed is True, the result will be the same as if dark_bg is set
        to None, except that the sign will change to match the desired
        features. See example below.
    return_debug info: bool, optional
        will return a large dict consisting of several large matrices,
        calculated hessian, etc.

        scale_dict = {'sigma': sigma,
                      'beta': beta,
                      'gamma': gamma,
                      'c': c,
                      'H': hesh,
                      'F': targets,
                      'k1': k1,
                      'k2': k2,
                      'border_radius': dilation_radius
                      }
    Returns
    -------
    ...

    Notes
    -----
    Although default is 0.5, this means that the structureness factor of the
    Frangi score will only be 0.86 at its maximum. Larger values of gamma
    will only dampen the frangi filter more. Smaller values toward 0 will
    result in a "looser" filter. For example, if gamma = .25, then the
    maximum score is (1-exp{-8}) around .999 (it may be desirable that the
    franginess score should be able to achieve a score of 1).

    This function will accept 0 an input, and the structureness factor will
    be set to 1 everywhere (the limiting case as gamma -> 0)

    Frangi structureness factor is (1 - exp((-S**2)/(2*c**2))
    """
    hesh = fft_hessian(img, sigma, kernel=kernel)  # the triple (Hxx,Hxy,Hyy)
    # calculate principal curvatures with |k1| <= |k2|


    k1, k2 = principal_curvatures(img, sigma, H=hesh)

    if dilation_radius is not None:
        # pass None to just get the mask back
        collar = dilate_boundary(None, radius=dilation_radius, mask=img.mask)

        # get rid of "bad" K values before you calculate gamma and Frangi
        k1[collar] = 0
        k2[collar] = 0
        hesh[0][collar] = 0
        hesh[1][collar] = 0
        hesh[2][collar] = 0
    else:
        collar = img.mask.copy()


    # no need to set gamma or c anymore. will be set inside get_frangi_targets
    #if c is None:
    # Frangi suggested 'half the max Hessian norm' as an empirical
    # half the max spectral radius is easier to calculate so do that
    # shouldn't be affected by mask data but should make sure the
    # mask is *well* far away from perimeter
    # we actually calculate half of max hessian norm
```

```
    # using frob norm = sqrt(trace(AA^T))
    # alternatively you could use gamma = .5 * np.abs(k2).max()
    #hnorm = hessian_norm(hesh, mask=collar)
    #print(f'  ={sigma:2f}')
    #gamma0 = .5*hessian_norm(hesh).max()
    #print(f'\t{gamma0:.5f} = frob-norm    pre-dilation')

    #gamma1 = .5*hessian_norm(hesh, mask=collar).max()
    #print(f'\t{gamma1:.5f} = frob-norm    post-collar dilation {dilation_radius}')
    #l2gamma = .5*np.max(np.abs(k2))
    #print(f'\t{l2gamma:.5f} =  from L2-norm    (K2 with collar)')

    #hdilation = int(max(np.ceil(sigma),10))
    #hcollar = dilate_boundary(None, radius=hdilation, mask=img.mask)
    #gamma = .5 * max_hessian_norm(hesh, mask=hcollar)

    #print(f'\t{gamma:.5f} =    post-hdilation (radius {hdilation}) (old   )')

    #print('changing    to L2-norm with collar')
    #gamma = max(gamma1, l2gamma, gamma, gamma0)

    # wish this scaled a little better

    # a very large gamma here will make the Frangi score zero
    # a very small gamma means that we are artificially inflating the
    # structureness measure
    #import matplotlib.pyplot as plt
    #plt.imshow(hnorm*(~collar))
    #plt.show()
    #print(hnorm[~collar].min(), hnorm[~collar].max())
    #if hnorm[~collar].max() < 0.1:
    #    print(f'max hessian norm is very small at this scale ({sigma},{hnorm[~collar].max
    #          'you should maybe skip this scale')
    #elif hnorm[~collar].min() <  0.001:
    #    # only trigger if the first one didn't
    #    print(f'min hessian norm is very small at this scale ({sigma}, {hnorm[~collar].mi
    #         'be carefully of artificially inflated scores')
    #S = np.sqrt(k1**2 + k2**2)
    #import matplotlib.pyplot as plt
    #plt.imshow(S)
    #plt.show()
    #plt.close()
    #print('max hessian norm (Frob): ', hnorm.max())
    #print('max structureness: ', S.max())
    #c = gamma*S.max()

    if verbose:
        print(f'finding Frangi targets with   ={beta} and   ={c:.2}')

    targets = get_frangi_targets(k1, k2, beta=beta, gamma=gamma, c=c,
                                 dark_bg=dark_bg, signed=signed_frangi,
                                 rescale_frangi=rescale_frangi)

    if gradient_filter:
        # obviously you could compute this at the same time as the hessian :/

        g = fft_gradient(img, sigma)
        g = dilate_boundary(g, radius=20, mask=img.mask)

        # you could technically pass a function to switch between these
        # behaviors
        low_g = (g < nz_percentile(g, 50)).filled(0)

        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
193 def get_frangi_targets(K1, K2, beta=0.5, gamma=0.5, c=None,
194                        dark_bg=True, signed=False, rescale_frangi=False):
195     """Calculate the Frangi vesselness measure from eigenvalues.
196
197     Parameters
198     ----------
199         K1, K2 : ndarray (each)
200             each is an ndarray of eigenvalues (approximated principal
201             curvatures) for some image.
202         beta: float
203             the anisotropy parameter (default is 0.5)
204         gamma: float or None
205             Scaling factor for the the structureness parmeter. The structurness
206             parameter c will be set to gamma times the maximum of the Hessian
207             norm, sqrt(K1**2 + K2**2). Default is 0.5
208         c: float or None
209             The frangi structurness 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     --------
```

```
    >>>f1 = get_frangi_targets(K1,K2, dark_bg=True, signed=True)
    >>>f2 = get_frangi_targets(K1,K2, dark_bg=False, signed=True)
    >>>np.all(f1 == -f2)
    True

    >>> F = get_frangi_targets(K1,K2, gamma=0.5)
    >>> Falt = get_frangi_targets(K1,K2, c=0.5*np.sqrt(K1**2 + K2**2))
    >>> np.all(F == Falt)
    True
    """

    A = anisotropy(K1, K2, beta=beta)
    S = structureness(K1, K2, gamma=gamma, c=c)

    anisotropy_factor = np.exp(-A)
    structureness_factor = (1 - np.exp(-S))

    F = anisotropy_factor * structureness_factor

    if rescale_frangi:
        if c is not None:
            # more like will not
            print('c was set to an arbitrary value. cannot rescale')
        else:
            max_theoretical = (1 - np.exp(-1/(2*gamma**2)))
            F = F / max_theoretical

    # now just filter/ change sign as appropriate.
    if not signed:
        # calculate the regular frangi filter
        if dark_bg is None:
            #keep F the way it is
            pass
        elif dark_bg:
            # zero responses from positive curvatures
            F = (K2 < 0)*F
        else:
            # zero responses from negative curvatures
            F = (K2 > 0)*F
    else:
        if dark_bg is None:
            # output is already signed
            pass
        elif dark_bg:
            # positive curvature spots will be made negative
            F[K2 > 0] = -1 * F[K2 > 0]
        else:
            # negative curvature spots will be made positive
            F[K2 < 0] = -1 * F[K2 < 0]

    # finally, reapply the mask if the inputs came with one
    if numpy.ma.is_masked(K1):
        F = numpy.ma.masked_array(F, mask=K1.mask)

    return F


def hessian_norm(hesh, mask=None):
    """Calculate Frobenius norm of Hessian.

    Calculates the maximal value (over all pixels of the image) of the
    Frobenius norm of the Hessian. This should be the same as the square root
    of unscaled structureness.

```

```
    Parameters
    ----------
    hesh: a tuple of ndarrays
        The tuple hxx,hxy,hyy which are all the same shape. The hessian at
        the point (m,n) is then [[hxx[m,n], hxy[m,n]],
                                 [hxy[m,n], hyy[m,n]]]

    Returns
    -------
    float
    """

    hxx, hxy, hyy = hesh

    # frob norm is just sqrt(trace(AA^T)) which is easy for a 2x2
    hnorm = (hxx**2 + 2*hxy**2 + hyy**2)

    if mask is not None:
        hnorm[mask] = 0

    hnorm = np.sqrt(hnorm)
    return hnorm


def anisotropy(K1,K2, beta=0.5):
    """Convenience function for the exponential argument in the Frangi
    anisotropy factor.

    According to Frangi (1998) this is technically (A**2) / (2*beta**2)
    unless beta is None, in which case just A**2 is returned

    The frangi vesselness factor is formally (np.exp(-R))
    where R is what's returned by this function
    """

    A = (K1 / K2) ** 2
    #print(f'inside anisotropy,   ={beta}')
    if beta == 0:
        return np.zeros_like(A)  # the limiting case as beta -> 0

    elif beta == 'inf' or np.isinf(beta):
        return np.ones_like(A)  # the limiting case as beta -> inf

    elif beta is None:
        return A  # just return the A**2 part (why though)
    else:
        return A / (2*beta**2)


def structureness(K1, K2, gamma=0.5, c=None):
    """Convenience function for Structureness measure.
    According to Frangi (1998) this is technically S**2
    """
    S = K1**2 + K2**2


    # is c is not provided, calculate it
    if c is None:
        c = gamma * np.sqrt(S).max()  # the max Frob norm of the Hessian

    #print(f'inside structureness,   ={gamma}, c={c}')

    if c == 0:
        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                        mimg_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')
```

```
        ax[0].axis('off')
        ax[0].set_title(f'Standard Frangi   ={sigma:.2f}', fontsize=10)

        ax[1].imshow(f1.filled(0)[crop], vmin=0, vmax=1, cmap='nipy_spectral')
        ax[1].axis('off')
        ax[1].set_title(f'w/ gradient filter', fontsize=10)

        #ax[2].imshow(g_filter[crop].T, cmap='nipy_spectral')
        #ax[2].axis('off')
        #ax[2].set_title(f'Gradient filter   ={sigma:.2f}')

        #plt.show()
        plt.tight_layout()
        plt.savefig(os.path.join(OUTPUT_DIR, f'gf_scale_{n:0{2}}.png'))
        plt.close('all')

    F0.append(f0)
    F1.append(f1)

F0 = np.stack(F0)
F1 = np.stack(F1)


if MAKE_OUTPUTS:
    fig, ax = plt.subplots(ncols=2, nrows=1, figsize=(10,4))

    ax[0].imshow(F0.max(axis=0).filled(0)[crop], vmin=0, vmax=1,
            cmap='nipy_spectral')
    ax[0].axis('off')
    ax[0].set_title(f'Standard Frangi F_max', fontsize=10)

    ax[1].imshow(F1.max(axis=0).filled(0)[crop], vmin=0, vmax=1,
            cmap='nipy_spectral')
    ax[1].axis('off')
    ax[1].set_title(f'w/ gradient filter', fontsize=10)

    plt.tight_layout()
    #plt.show()
    plt.savefig(os.path.join(OUTPUT_DIR, f'gf_Fmax.png'))
    plt.close('all')
```

listings/hfft_accuracy.py

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

"""
here you want to show  the accuracy of hfft.py

BOILERPLATE

show that gaussian blur of hfft is accurate, except potentially around the
boundary proportional to sigma.

or if they're off by a scaling factor, show that the derivates
(taken the same way) are proportional.

pseudocode

A = gaussian_blur(image, sigma, method='convential')
B = gaussian_blur(image, sigma, method='fourier')

zero_order_accurate = isclose(A, B, tol)

```

```
J_A= get_jacobian(A)
J_B = get_jacobian(B)

first_order_accurate = isclose(J_A, J_B, tol)

A_eroded = zero_around_plate(A, sigma)
B_eroded = zero_around_plate(B, sigma)

J_A_eroded = zero_around_plate(A, sigma)
J_B_eroded = zero_around_plate(B, sigma)

zero_order_accurate_no_boundary = isclose(A_eroded, B_eroded, tol)
first_order_accurate = isclose(J_A_eroded, J_B_eroded, tol)

"""

from placenta import get_named_placenta, cropped_args

from itertools import combinations_with_replacement
from skimage.exposure import rescale_intensity

from hfft import fft_hessian, fft_gaussian, fft_dgk
from scipy.ndimage import gaussian_filter
import matplotlib.pyplot as plt
from placenta import show_mask, list_by_quality

from scoring import mean_squared_error
from itertools import combinations
import numpy as np
from scipy.ndimage import laplace
import numpy.ma as ma

from skimage.segmentation import find_boundaries
from skimage.morphology import disk, binary_dilation

from plate_morphology import dilate_boundary

from diffgeo import principal_curvatures
from frangi import structureness, anisotropy, get_frangi_targets

from skimage.util import img_as_float

def plot_image_slices(arrs, fixed_axis=0, fixed_index=None, labels=None,
                      formats=None, title=None):
    """
    arrs needs to be the same shape and dimension
    could pass it to np.stack and check for a value error?

    """
    fig, ax = plt.subplots(figsize=(12,2))
    # hopefully the fixed axis is 0 or 1. this gets the other one
    it_axis = 1 if fixed_axis==0 else 0

    # if it's a tuple, make it an array, etc. etc.
    arrs = np.stack(arrs)

    # make sure we can iterate over it if there's just as single image
    if arrs.ndim < 3:
        arrs = np.expand_dims(arrs,0)

    if labels is None:
        labels = [None for a in arrs]
    if formats is None:
```

```
        formats = ['' for a in arrs]

    if fixed_index is None:
        # find halfway point of the appropriate dimension from the first array
        fixed_index = arrs[0].shape[fixed_axis] // 2

    for a, lab, fmt in zip(arrs, labels, formats):
        ax.plot(np.arange(a.shape[it_axis]),
                 np.moveaxis(a, fixed_axis, 0)[fixed_index, :],
                 fmt, label=lab)

    if title is not None:
        ax.set_title(title)

    # can this be at least a little object-oriented? :(
    fig.legend()

def multiway_comparison(arrs, scorefunc):

    scores = np.zeros((len(arrs), len(arrs)))

    for j in range(len(arrs)):
        for k in range(j+1,len(arrs)):
            scores[j,k] = scorefunc(arrs[j], arrs[k])

    return scores

filename = list_by_quality(0)[5]

img = get_named_placenta(filename)

# so that scipy.ndimage.gaussian_filter doesn't use uint8 precision (jesus)
img = ma.masked_array(img_as_float(img), mask=img.mask)

test_sigmas = [.3, .6, 1.0, 5.0, 15, 30, 60, 90]

for sigma in test_sigmas:

    print("*"*80, '\n\n', f"  ={sigma}")
    #print('applying standard gauss blur')

    # this is exactly how it's passed to skimage.feature.hessian_matrix(...)
    A = gaussian_filter(img.filled(0), sigma, mode='constant', cval=0)

    #print('applying fft gauss blur')
    B = fft_gaussian(img, sigma, kernel='sampled')
    C = fft_gaussian(img, sigma, kernel='discrete')

    #print('calculating first derivatives')
    # zero the masks before calculating derivates if they're masked
    Agrad = np.gradient(A)
    Bgrad = np.gradient(B)
    Cgrad = np.gradient(C)


    axes = range(img.ndim)

    #print('calculating second derivatives')
    # this is the same way it's done in skimage.feature.hessian_matrix(...)
    H_A = [np.gradient(Agrad[ax0], axis=ax1)
        for ax0, ax1 in combinations_with_replacement(axes, 2)]
    H_B = [np.gradient(Bgrad[ax0], axis=ax1)
        for ax0, ax1 in combinations_with_replacement(axes, 2)]
    H_C = [np.gradient(Cgrad[ax0], axis=ax1)
```

```
        for ax0, ax1 in combinations_with_replacement(axes, 2)]

    #print('calculating eigenvalues of hessian')
    ak1, ak2 = principal_curvatures(img, sigma=sigma, H=H_A)
    bk1, bk2 = principal_curvatures(img, sigma=sigma, H=H_B)
    ck1, ck2 = principal_curvatures(img, sigma=sigma, H=H_C)


    #RA = anisotropy(ak1,ak2)
    #RB = anisotropy(bk1,bk2)
    #RC = anisotropy(ck1,ck2)

    #SA = structureness(ak1, ak2)
    #SB = structureness(bk1, bk2)
    #SC = structureness(ck1, ck2)

    ## ugh, apply masks here. too large to be conservative?
    ## otherwise structureness only shows up for small sizes
    new_mask = dilate_boundary(None, radius=int(3*sigma), mask=img.mask)

    crop = cropped_args(img)

    A = A[crop]
    B = B[crop]
    C = C[crop]

    ak1 = ma.masked_array(ak1,new_mask)[crop]
    ak2 = ma.masked_array(ak2,new_mask)[crop]
    bk1 = ma.masked_array(bk1,new_mask)[crop]
    bk2 = ma.masked_array(bk2,new_mask)[crop]
    ck1 = ma.masked_array(ck1,new_mask)[crop]
    ck2 = ma.masked_array(ck2,new_mask)[crop]

    FA = get_frangi_targets(ak1,ak2, dark_bg=False).filled(0)
    FB = get_frangi_targets(bk1,bk2, dark_bg=False).filled(0)
    FC = get_frangi_targets(ck1,ck2, dark_bg=False).filled(0)


    # the following shows a random vertical slice of A & B (when scaled)
    labels = ('scipy.ndimage,gaussian_filter', 'fft_gaussian', 'fft_dgk')
    formats = ('g:', 'k', 'b-.')
    plot_image_slices((A,B,C), labels=labels, formats=formats,
                      title=r'gaussian convolution $\sigma={}$'.format(sigma))
    plt.tight_layout()
    plt.savefig('Gslice_sigma={:d}.png'.format(int(sigma*10)), dpi=300)
    plot_image_slices((FA,FB,FC), labels=labels, formats=formats,
                      title=r'Frangi filter response $\sigma={}$'.format(sigma))
    plt.tight_layout()
    plt.savefig('Fslice_sigma={:d}.png'.format(int(sigma*10)), dpi=300)
    #plt.show()

    print('comparing gaussians (mean squared error)')
    print(multiway_comparison((A,B,C), mean_squared_error))
    print('comparing frangi response (mean squared error)')
    print(multiway_comparison((FA,FB,FC), mean_squared_error))
```

listings/hfft_demo.py

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

import numpy as np
from skimage.data import camera
```

```
from skimage.io import imread
from skimage.util import img_as_float

import matplotlib.pyplot as plt
from hfft import fft_gaussian, fft_hessian, fft_dgk
from scipy.ndimage import gaussian_filter

from scipy.linalg import norm
import timeit

#img = camera() / 255.
img = imread('samples/barium1.png', as_grey=True) / 255.
mask = imread('samples/barium1.mask.png', as_grey=True)

img = img_as_float(img)

# compare computation speed over sigmas

# N logarithmically spaced scales between 1 and 2^m
N = 32
m = 8
sigmas = np.logspace(0,m, num=N, base=2)

fft_results = list()
std_results = list()

for sigma in sigmas:
    # test statements to compare (fft-based gaussian vs convolution-based)
    fft_test_statement = "fft_gaussian(img,{},kernel='discrete')".format(sigma)
    std_test_statement = "gaussian_filter(img,{})".format(sigma)
    # run each statement 1 times (with 2 runs in each trial)
    # returns/appends the average of 3 runs
    fft_results.append(timeit.timeit(fft_test_statement,
                                     number=1, globals=globals()))
    std_results.append(timeit.timeit(std_test_statement,
                                     number=1, globals=globals()))

    # now actually evaluate both to compare
    f = eval(fft_test_statement)
    s = eval(std_test_statement)

    # normalize each matrix by frobenius norm and take difference
    # ideally should try to zero out the "mask" area
    diff = np.abs(f / norm(f) - s / norm(s))
    raw_diff = np.abs(f - s)
    # don't care if it's the background
    diff[mask==1] = 0
    raw_diff[mask==1] = 0

    # should format this stuff better into a legible table
    print(sigma, diff.max(), raw_diff.max())

lines = plt.plot(sigmas, fft_results, 'go', sigmas, std_results, 'bo')
plt.xlabel('sigma (gaussian blur parameter)')
plt.ylabel('run time (seconds)')
plt.legend(lines, ('fft-gaussian', 'conv-gaussian'))
plt.title('Comparision of Gaussian Blur Implementations')
```

listings/hfft.py

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

```

```
import numpy as np
from scipy import signal
import scipy.fftpack as fftpack
from scipy.special import iv, ive
from scipy.ndimage import gaussian_filter
from itertools import combinations_with_replacement

# for demos
import matplotlib.pyplot as plt

from skimage.data import camera
from skimage.util import img_as_float
from skimage.measure import compare_mse, compare_nrmse
"""
hfft.py is the implementation of calculating the hessian of a real

image based in frequency space (rather than direct convolution with a gaussian
as is standard in scipy, for example).

TODO: PROVIDE MAIN USAGE NOTES
"""

def fft_gaussian(img,sigma, kernel=None):

    """
    https://docs.scipy.org/doc/scipy/reference/generated/scipy.signal.fftconvolve.html

    in particular the example in which a gaussian blur is implemented.

    along with the comment:
    "Gaussian blur implemented using FFT convolution. Notice the dark borders
    around the image, due to the zero-padding beyond its boundaries. The
    convolve2d function allows for other types of image boundaries, but is far
    slower"

    (i.e. doesn't use FFT).

    note that here, you actually take the FFT of a gaussian (rather than
    build it in frequency space). there are ~6 ways to do this.
    """
    #create a 2D gaussian kernel to take the FFT of
    # output of signal.gaussian is normalized to 1 so you need to scale
    # it back to work
    #A = 1 / (2*np.pi*sigma**2) # scale factor for 2D

    if kernel in ('discrete', None):
        kern_x = discrete_gaussian_kernel(img.shape[0], sigma)
        kern_y = discrete_gaussian_kernel(img.shape[1], sigma)
    elif kernel == 'sampled':
        A = 1 / (np.sqrt((2*np.pi)*sigma**2))
        kern_x = A*signal.gaussian(img.shape[0], sigma)
        kern_y = A*signal.gaussian(img.shape[1], sigma)
    else:
        raise ValueError("Key must be 'discrete' or 'sampled'")

    kernel = np.outer(kern_x, kern_y)

    return signal.fftconvolve(img, kernel, mode='same')

def discrete_gaussian_kernel(n_samples, sigma):
    """
    sigma is the scale, n_samples is the number of samples to compute
    will return a window centered a zero
    i.e. arange(-n_samples//2, n_samples//2+1)
```

```
67
68      note! to make this work similarly to fft_gaussian, this uses
69      sigma = np.sqrt(t). Usually you'll find this in terms of t
70
71      by using scipy.special.ive instead we prevent blowups
72      """
73      dom = np.arange(-(n_samples//2), (n_samples//2) + 1)
74      #there should be a scaling parameter alpha but whatever
75      #return np.exp(-t) * iv(dom,t)
76      return ive(dom,sigma**2)
77
78  def fft_dgk(img,sigma,order=0,A=None):
79      """
80      This is the discrete gaussian kernel which is supposedly less crappy
81      than using a sampled gaussian.
82      """
83      m,n = img.shape
84      # i don't know if this will suck if there are odd dimensions
85      kernel = np.outer(discrete_gaussian_kernel(m,sigma**2),
86                        discrete_gaussian_kernel(n,sigma**2))
87
88      return signal.fftconvolve(img, kernel, mode='same')
89
90  def fft_fdgk(img,sigma):
91      """
92      convolve with discrete gaussian kernel in freq. space
93      """
94      # this would be a lot better since you wouldn't have to deal
95      # with an arbitrary cutoff of size of the discrete kernel
96      # since the freq. space version is just
97      # exp{\alpha*t (cos\theta - 1)}
98      # see formula 22 of lindeberg discrete paper
99
100     pass
101
102 def fft_hessian(image, sigma=1., kernel=None):
103     """
104     a reworking of skimage.feature.hessian_matrix that uses
105     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
```

```
    return H_elems


def fft_gradient(image, sigma=1.):
    """ returns gradient norm """

    gaussian_filtered = fft_gaussian(image, sigma=sigma)

    Lx, Ly = np.gradient(gaussian_filtered)

    return np.sqrt(Lx**2 + Ly**2)


def demo(img=None):
    """
    old main function for testing.

    This simply tests fft_gaussian on a test image,
    """

    if img is None:
        img = img_as_float(camera())
    else:
        img = img_as_float(img)

    sample_sigmas = (.5, 2, 8, 30)
    #sample_sigmas = (.2, 2)

    # build the graphs here side by side
    # show regular blur, sampled blur, discrete blur, 1d plot of signals
    # so a 4 by 4 grid

    fig, axes = plt.subplots(nrows=len(sample_sigmas), ncols=4,
                             figsize=(10, 10))

    for cax, sigma in enumerate(sample_sigmas):

        # convolve the image with a gaussian kernel, one of three ways
        fft_dgk = fft_gaussian(img, sigma, kernel='discrete')
        fft_sampled = fft_gaussian(img, sigma, kernel='sampled')
        xy_sampled = gaussian_filter(img, sigma, mode='constant', cval=0)

        # make the fancy sample
        N = 80
        dom = np.arange(-(N//2), N//2 + 1)
        dgk = discrete_gaussian_kernel(N,  sigma)
        A = np.sqrt(2*np.pi*sigma**2)
        A = 1 / A
        sgk = A * signal.gaussian(N+1, sigma)

        axes[cax, 0].imshow(xy_sampled, cmap='gray', vmin=0, vmax=1)
        axes[cax, 0].set_ylabel(r'$\sigma={}$'.format(sigma))
        #axes[cax, 0].set_title(f'ndi.gaussian_filter,   ={sigma}')
        #axes[cax, 0].axis('off')
        axes[cax, 0].set_xticks([])
        axes[cax, 0].set_yticks([])

        axes[cax, 1].imshow(fft_sampled, cmap='gray', vmin=0, vmax=1)
        #axes[cax, 1].imshow(fft_sampled, cmap='gray')
        #axes[cax, 1].set_title(f'fft sampled kernel,   ={sigma}')
        axes[cax, 1].axis('off')

        axes[cax, 2].imshow(fft_dgk, cmap='gray', vmin=0, vmax=1)
        #axes[cax, 2].set_title(f'fft discrete kernel,   ={sigma}')
```

```
        axes[cax, 2].axis('off')


        axes[cax, 3].plot(dom, sgk, 'k', dom, dgk, 'g:')
        #axes[cax, 3].set_title(f'discrete vs. sampled kernel   ={sigma}')
        #axes[cax, 3].axes.set_aspect('equal')

    # set titles for the first column
    axes[0,0].set_title('(a)')
    axes[0,1].set_title('(b)')
    axes[0,2].set_title('(c)')
    axes[0,3].set_title('(d)')

    plt.tight_layout()
    plt.show()

def compare_mae(arr1, arr2):

    assert arr1.shape == arr2.shape
    return np.abs(arr1 - arr2).sum() / arr1.size


def semigroup_demo(img=None):
    """
    the step ones don't look anywhere near as blurred as the initial image
    in any case! don't use this till it's good!
    """
    if img is None:
        img = img_as_float(camera())
    else:
        img = img_as_float(img)

    sigma = 45.
    n_steps = 2
    sigmas = (10,35)

    fft_discrete = fft_gaussian(img, sigma, kernel='discrete')
    fft_sampled = fft_gaussian(img, sigma, kernel='sampled')
    xy_sampled = gaussian_filter(img, sigma, mode='constant', cval=0)

    step_discrete = img.copy()
    step_fft_sampled = img.copy()
    step_xy_sampled = img.copy()

    #sigma_n = sigma / n_steps
    #sigma_n = np.power(sigma, 1/n_steps)
    counter = 0
    for sigma_n in sigmas:
        step_discrete = fft_gaussian(step_discrete, sigma_n, kernel='discrete')
        step_fft_sampled = fft_gaussian(step_fft_sampled, sigma_n,
                                        kernel='sampled')
        step_xy_sampled = gaussian_filter(step_xy_sampled, sigma_n,
                                          mode='constant', cval=0)
        counter += sigma_n
        #print(counter, end=' ')

    print()
    er = int(sigma)
    crop = np.s_[er:-er,er:-er]

    fft_discrete = fft_discrete[crop]
    fft_sampled = fft_sampled[crop]
    xy_sampled = xy_sampled[crop]
    step_discrete = step_discrete[crop]
```

```
    step_fft_sampled = step_fft_sampled[crop]
    step_xy_sampled = step_xy_sampled[crop]

    fig, axes = plt.subplots(ncols=3, nrows=2)
    axes[0,0].imshow(xy_sampled, vmin=0, vmax=1, cmap='gray')
    axes[0,0].set_title('(a)')
    axes[0,0].set_xticks([]), axes[0,0].set_yticks([])

    axes[0,1].imshow(fft_sampled, vmin=0, vmax=1, cmap='gray')
    axes[0,1].set_title('(b)')
    axes[0,1].set_xticks([]), axes[0,1].set_yticks([])

    axes[0,2].imshow(fft_discrete, vmin=0, vmax=1, cmap='gray')
    axes[0,2].set_title('(c)')
    axes[0,2].set_xticks([]), axes[0,2].set_yticks([])

    axes[1,0].imshow(step_xy_sampled, vmin=0, vmax=1, cmap='gray')
    axes[1,0].axis('off')
    axes[1,1].imshow(step_fft_sampled, vmin=0, vmax=1, cmap='gray')
    axes[1,1].axis('off')
    axes[1,2].imshow(step_discrete, vmin=0, vmax=1, cmap='gray')
    axes[1,2].axis('off')

    MSE_sampled = compare_mse(xy_sampled, step_xy_sampled)
    MSE_fft_sampled = compare_mse(fft_sampled, step_fft_sampled)
    MSE_discrete = compare_mse(fft_discrete, step_discrete)

    print(f'MSE sampled:{MSE_sampled}')
    print(f'MSE fft_sampled:{MSE_fft_sampled}')
    print(f'MSE discrete:{MSE_discrete}')
    print()
    #NRMSE_sampled = compare_nrmse(xy_sampled, step_xy_sampled)
    #NRMSE_fft_sampled = compare_nrmse(fft_sampled, step_fft_sampled)
    #NRMSE_discrete = compare_nrmse(fft_discrete, step_discrete)

    #print(f'NRMSE sampled:{NRMSE_sampled}')
    #print(f'MSE fft_sampled:{NRMSE_fft_sampled}')
    #print(f'NRMSE discrete:{NRMSE_discrete}')
    #for ax, title in zip(axes.ravel(), ['(a)', '(b)', '(c)', '(d)']):
    #    ax.axis('off')
    #    ax.set_title(title)


    MAE_sampled = compare_mae(xy_sampled, step_xy_sampled)
    MAE_fft_sampled = compare_mae(fft_sampled, step_fft_sampled)
    MAE_discrete = compare_mae(fft_discrete, step_discrete)

    print(f'MAE sampled:{MAE_sampled}')
    print(f'MAE fft_sampled:{MAE_fft_sampled}')
    print(f'MAE discrete:{MAE_discrete}')

    plt.show()

if __name__ == "__main__":
    from skimage.io import imread
    from placenta import list_by_quality, get_named_placenta
    #A = list_by_quality(0)[0]
    #A = get_named_placenta(A)
    #A = imread('samples/5.3.02.tiff')
    A = None
    demo(A)
    semigroup_demo(A)
```

listings/merging.py

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

import numpy as np
import numpy.ma as ma
from scipy.ndimage import label
from skimage.morphology import remove_small_objects
import matplotlib.pyplot as plt

def nz_percentile(A, q, axis=None, interpolation='linear'):
    """calculate np.percentile(...,q) on an array's nonzero elements only

    Parameters
    ----------
    A : ndarray
        matrix from which percentiles will be calculated. Percentiles
        are calculated on an elementwise basis, so the shape is not important
    q : a float
        Percentile to compute, between 0 and 100.0 (inclusive).

    (other arguments): see numpy.percentile docstring
    ...

    Returns
    -------
    out: float

    """

    if ma.is_masked(A):
        A = A.filled(0)

    return np.percentile(A[A > 0], q, axis=axis, interpolation=interpolation)


def apply_threshold(targets, alphas, return_labels=True):
    """Threshold targets at each scale, then return max target over all scales.

    A unique alpha can be given for each scale (see below). Return a 2D boolean
    array, and optionally another array representing what at what scale the max
    filter response occurred.

    Parameters
    ----------
    targets : ndarray
        a 3D array, where targets[:,:,k] is the result of the Frangi filter
        at the kth scale.
    alphas : float or array_like
        a list / 1d array of length targets.shape[-1]. each alphas[k] is a
        float which thresholds the Frangi response at the kth scale. Due to
        broadcasting, this can also be a single float, which will be applied
        to each scale.
    return_labels : bool, optional
        If True, return another ndarray representing the scale (see Notes
        below). Default is True.

    Returns
    -------
    out : ndarray, dtype=bool
        if return labels is true, this will return both the final
        threshold and the labels as two separate matrices. This is
        a convenience, since you could easily find labels with
    labels : ndarray, optional, dtype=uint8
```

```
        The scale at which the largest filter response was found after
        thresholding. Element is 0 if no scale passed the threshold,
        otherwise an int between 1 and targets.shape[-1] See Notes below.

    Notes / Examples
    ----------------
    Despite the name, this does *NOT* return the thresholded targets itself,
    but instead the maximum value after thresholding. If you wanted the
    thresholded filter responses alone, you should simply run

    >>>(targets > alphas)*targets

    The optional output `labels` is a 2D matrix indicating where the max filter
    response occured. For example, if the label is K, the max filter response
    will occur at targets[:,:,K-1].  In other words,

    >>>passed, labels = apply_threshold(targets,alphas)
    >>>targets.max(axis=-1) == targets[:,:,labels -1 ]
    True

    It should be noted that returning labels is really just for convenience
    only; you could construct it as shown in the following example:

    >>>manual_labels = (targets.argmax(axis=-1) + 1)*np.invert(passed)
    >>>labels == manual_labels
    True

    Similarly, the standard boolean output could just as easily be obtained.
    >>>passed == (labels != 0)
    True
    """

    # threshold as an array (even if it's a single element) to broadcast
    alphas = np.array(alphas)

    # if input's just a MxN matrix, expand it trivially so it works below
    if targets.ndim == 2:
        targets = np.expand_dims(targets, 2)

    # either there's an alpha for each channel or there's a single
    # alpha to be broadcast across all channels
    assert (targets.shape[-1] == alphas.size) or (alphas.size == 1)

    # pixels that passed the threshold at any level
    passed = (targets >= alphas).any(axis=-1)

    if not return_labels:
        return passed  # we're done already

    wheres = targets.argmax(axis=-1)  # get label of where maximum occurs
    wheres += 1  # increment to reserve 0 label for no match

    # then remove anything that didn't pass the threshold
    wheres[np.invert(passed)] = 0

    assert np.all(passed == (wheres > 0))

    return passed, wheres


def sieve_scales(multiscale, high_percentile, low_percentile, min_size=None,
                 axis=0):
    """
    multiscale is a 3 dimensional where 2 dimensions are image and `axis`
```

```
    parameter is which one is the scale space (i.e. resolution). hopefully
    axis is 0 or 1 (this won't handle stupider cases)

    this gathers points contiguous points at a low threshold and adds them
    to the output it contains at least only if that blob contains at least one
    high percentile point.

    min_size is a size requirement can either be an integer or an array of
    integers """

    assert multiscale.ndim == 3

    if axis in (-1, 2):
        # this won't change the input, just creates a view
        V = np.transpose(multiscale, axes=(2, 0, 1))

    elif axis == 0:
        V = multiscale  # just to use the same variable name
    else:
        raise ValueError('Please make resolution the first or last dimension.')

    if np.isscalar(min_size):
        min_size = [min_size for x in range(multiscale.shape[0])]

    # label matrix the size of one of the images
    sieved = np.zeros(V.shape[1:], dtype=np.int32)

    print('sieving ', end='')
    for n, v in enumerate(V):
        print('  ', end='', flush=True)

        if min_size is not None:
            z = remove_small_objects(v, min_size=min_size[n])
        else:
            z = v  # relabel to use same variable

        high_thresh = nz_percentile(v, high_percentile)
        low_thresh = nz_percentile(v, low_percentile)

        labeled, n_labels = label(z > low_thresh)
        high_passed = (z > high_thresh)

        for lab in range(n_labels):
            if lab == 0:
                continue
            if np.any(high_passed[labeled == lab]):
                sieved[labeled == lab] = n

    print()
    return sieved

def view_slices(multiscale, axis=0, scales=None, cmap='nipy_spectral',
                vmin=0, vmax=1.0, outnames=None, show_colorbar=True):
    """ scales is just to use for a figure title
        crop before you get in here.

        if outname is an iterable returning filenames, then we'll assume
        non-interative mode
        """
    assert multiscale.ndim == 3

    if axis in (-1, 2):
        # this won't change the input, just creates a view
        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  from placenta import get_named_placenta
4  from diffgeo import principal_directions
5  from frangi import frangi_from_image
6  from skimage.util import img_as_float
7  import numpy as np
8  from preprocessing import inpaint_hybrid
9
10 from merging import nz_percentile
11
12 from plate_morphology import dilate_boundary
13
14 import matplotlib.pyplot as plt
15 import matplotlib as mpl
16 import numpy.ma as ma
17
18 import os.path
19 import json
20 import datetime
21
22
23 def make_multiscale(img, scales, beta=0.5, gamma=0.5, c=None, dark_bg=True,
24                     find_principal_directions=False, dilate_per_scale=True,
25                     signed_frangi=False, kernel=None, verbose=True,
26                     rescale_frangi=False, gradient_filter=False):
27     """Returns an ordered list of dictionaries for each scale of Frangi info.
28
```

```
    beta, gamma, and c can all be vectors as long as scales or constants
    if c is None it will be set.

    Each element in the output contains the following info:
        {'sigma': sigma,
         'beta': beta,
         'gamma': gamma,
         'H': hesh,
         'F': targets,
         'k1': k1,
         'k2': k2,
         't1': t1, # if find_principal_directions
         't2': t2 # if find_principal_directions
         }

    is it necessary to lug all this shit around?
    """

    # store results of each scale (create as empty list)
    multiscale = list()

    img = ma.masked_array(img_as_float(img), mask=img.mask)

    vectorize = lambda x: np.repeat(x, len(scales)) if (x is None or np.isscalar(x)) else x

    # vectorize any scalar inputs here
    beta = vectorize(beta)
    gamma = vectorize(gamma)
    c = vectorize(c)
    print('finding multiscale targets ', end='')
    for i, (sigma, b, g, cx) in enumerate(zip(scales, beta, gamma, c)):

        print('  ', end='')

        if dilate_per_scale:
            if sigma > 20:
                radius = int(2*sigma)
            elif sigma < 3:
                radius = 12
            else:
                radius = int(4*sigma)
        else:
            radius = None

        targets, this_scale = frangi_from_image(img, sigma, beta=b, gamma=g,
                                                c=cx, dark_bg=dark_bg,
                                                dilation_radius=radius,
                                                kernel=kernel,
                                                signed_frangi=signed_frangi,
                                                return_debug_info=True,
                                                rescale_frangi=rescale_frangi,
                                                gradient_filter=gradient_filter)

        if find_principal_directions:
            # principal directions should only be computed for critical regions
            # this mask is where PD's will *NOT* be calculated
            # is targets a masked array?
            cutoff = nz_percentile(targets, 80)
            pd_mask = np.bitwise_or(targets < cutoff, img.mask).filled(1)
            percent_calculated = (pd_mask.size - pd_mask.sum()) / pd_mask.size

            if verbose:
                print(f"finding PD's for {percent_calculated:.2%} of image"
                      f"anything above vesselness score {cutoff:.6f}"
```

```
                    )
            t1, t2 = principal_directions(img, sigma=sigma, H=this_scale['H'],
                                          mask=pd_mask)

            # add them to this scale's output
            this_scale['t1'] = t1
            this_scale['t2'] = t2

        else:
            if verbose:
                print('skipping principal direction calculation')

        # store results as a list of dictionaries
        multiscale.append(this_scale)

    print()
    return multiscale


def extract_pcsvn(img, filename, scales, beta=0.5, gamma=0.5, c=None,
                  dark_bg=True, dilate_per_scale=True, verbose=True,
                  generate_json=True, output_dir=None, kernel=None,
                  signed_frangi=False, rescale_frangi=False,
                  gradient_filter=False):
    """Run PCSVN extraction on the sample given in the file.

    Despite the name, this simply returns the Frangi filter responses at
    each provided scale without explicitly making any decisions about what
    is or is not part of the PCSVN.

    As a matter of fact, this function currently just is a wrapper for
    make_multiscale that logs some output
    The original main use of this function has kind of bled into
    extract_NCS_pcsvn.py. that needs fixing. You should load the image
    outside of this function, do post processing there, pass it inside here
    with a dictionary of things to add to the json file

    """

    # Multiscale Frangi Filter#################################################

    # output is a dictionary of relevant info at each scale
    multiscale = make_multiscale(img, scales, beta=beta, gamma=gamma, c=None,
                                 find_principal_directions=False,
                                 dilate_per_scale=dilate_per_scale,
                                 kernel=kernel, signed_frangi=signed_frangi,
                                 dark_bg=dark_bg, verbose=verbose,
                                 rescale_frangi=rescale_frangi,
                                 gradient_filter=gradient_filter)

    # extract these for logging
    c = [scale['c'] for scale in multiscale]
    border_radii = [scale['border_radius'] for scale in multiscale]

    # ignore targets too close to edge of plate
     # wait are we doing this twice?
    if dilate_per_scale:
        if verbose:
            print('trimming collars of plates (per scale)')

        for i in range(len(multiscale)):
            f = multiscale[i]['F']
            # twice the buffer (be conservative!)
            radius = int(multiscale[i]['sigma']*2)
```

```
            if verbose:
                print('dilating plate for radius={}'.format(radius))
            f = dilate_boundary(f, radius=radius, mask=img.mask)
            # get rid of mask
            multiscale[i]['F'] = f.filled(0)
    else:
        for i in range(len(multiscale)):
            # get rid of mask
            multiscale[i]['F'] = multiscale[i]['F'].filled(0)
    # Make Composite##########################################

    # get a M x N x n_scales array of Frangi targets at each level
    F_all = np.dstack([scale['F'] for scale in multiscale])

    if generate_json:

        time_of_run = datetime.datetime.now()
        timestring = time_of_run.strftime("%y%m%d_%H%M")

        # numpy arrays have to be turned into lists first
        vectorize = lambda x: x if x is None or np.isscalar(x) else list(x)

        logdata = {'time': timestring,
                   'filename': filename,
                   'betas': vectorize(beta),
                   'gammas': vectorize(gamma),
                   'c': vectorize(c),
                   'sigmas': list(scales)
                   }

        if dilate_per_scale:
            logdata['border_radii'] = border_radii

        if output_dir is None:
            output_dir = 'output'

        base = os.path.basename(filename)
        *base, suffix = base.split('.')
        dumpfile = os.path.join(output_dir,
                                ''.join(base) + '_' + str(timestring)
                                + '.json')

        with open(dumpfile, 'w') as f:
            json.dump(logdata, f, indent=True)

    return F_all, dumpfile


def get_outname_lambda(filename, output_dir=None, timestring=None):
    """
    return a lambda function which can build output filenames
    """

    if output_dir is None:
        output_dir = 'output'

    base = os.path.basename(filename)
    *base, suffix = base.split('.')

    if timestring is None:
        time_of_run = datetime.datetime.now()
        timestring = time_of_run.strftime("%y%m%d_%H%M")

    outputstub = ''.join(base) +'_' + timestring +  '_{}.'+ suffix
```

```
    return lambda s: os.path.join(output_dir, outputstub.format(s))


def _build_scale_colormap(N_scales, base_colormap, basecolor=(0,0,0,1)):
    """
    returns a mpl.colors.ListedColormap with N samples,
    based on the colormap named "default_colormap" (a string)

    the N colors are given by the default colormap, and
    basecolor (default black) is added to map to 0.
    (you could change this, for example, to (1,1,1,1) for white)

    reversed colormaps often work better if the basecolor is black
    you should make sure there's good contrast between the basecolor
    and the first color in the colormap
    """

    map_range = np.linspace(0, 1, num=N_scales)

    colormap = plt.get_cmap(base_colormap)

    colorlist = colormap(map_range)

    # add basecolor as the first entry
    colorlist = np.vstack((basecolor, colorlist))

    return mpl.colors.ListedColormap(colorlist)


def scale_label_figure(wheres, scales, savefilename=None,
                       crop=None, show_only=False, image_only=False,
                       base_cmap='viridis_r', save_colorbar_separate=False,
                       savecolorbarfile=None, output_dir=None):
    """
    crop is a slice object.
    if show_only, then just plt.show (interactive).
    if image_only, then this will *not* be printed with the colorbar

    if save_colormap_separate, then the colormap will be saved as a separate
    file
    """
    if crop is not None:
        wheres = wheres[crop]

    fig, ax = plt.subplots()  # not sure about figsize
    N = len(scales)  # number of scales / labels

    tabemap = _build_scale_colormap(N, base_cmap)

    if image_only:
        plt.imsave(savefilename, wheres, cmap=tabemap, vmin=0, vmax=N)
        plt.close()
    else:
        imgplot = ax.imshow(wheres, cmap=tabemap, vmin=0, vmax=N)
        # discrete colorbar
        cbar = plt.colorbar(imgplot)

        # this is apparently hackish, beats me
        tick_locs = (np.arange(N+1) + 0.5)*(N-1)/N

        cbar.set_ticks(tick_locs)
        # label each tick with the sigma value
        scalelabels = [r"$\sigma = {:.2f}$".format(s) for s in scales]
        scalelabels.insert(0, "(no match)")
```

```
        # label with their sigma value
        cbar.set_ticklabels(scalelabels)
        # ax.set_title(r"Scale ($\sigma$) of maximum vesselness ")
        plt.tight_layout()
        # plt.savefig(outname('labeled'), dpi=300)
        if show_only or (savefilename is None):
            plt.show()
        else:
            plt.savefig(savefilename, dpi=300)

        plt.close()

    if save_colorbar_separate:
        if savecolorbarfile is None:
            savecolorbarfile = os.path.join(output_dir, "scale_colorbar.png")
        fig = plt.figure(figsize=(1, 8))
        ax1 = fig.add_axes([0.05, 0.05, 0.15, 0.9])
        tick_locs = (np.arange(N+1) + 0.5)*(N-1)/N
        scalelabels = [r"$\sigma = {:.2f}$".format(s) for s in scales]
        scalelabels.insert(0, "n/a")
        cbar = mpl.colorbar.ColorbarBase(ax1, cmap=tabemap,
                                         norm=mpl.colors.Normalize(vmin=0,
                                                                   vmax=N),
                                         orientation='vertical',
                                         ticks=tick_locs)
        cbar.set_ticklabels(scalelabels)
        plt.savefig(savecolorbarfile, dpi=300)
```

listings/placenta.py

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

"""
Get registered, unpreprocessed placental images.  No automatic registration
(i.e. segmentation of placental plate) takes place here. The background,
however, *is* masked.

Again, there is no support for unregistered placental pictures.
A mask file must be provided.

There is currently no support for color images.
"""

import numpy as np
import numpy.ma as ma
from skimage import segmentation, morphology
import os.path
import os
import json
from scipy.ndimage import imread

from numpy.ma import is_masked
from skimage.color import gray2rgb
import matplotlib.pyplot as plt


def open_typefile(filename, filetype, sample_dir=None, mode=None):
    """
    filetype is either 'mask' or 'trace'
    mask -> 'L' mode
    trace -> 'RGB' mode
    use mode keyword to override this behavior (for example if you
```

```
    want a binary trace)

    typefiles that aren't the above will be treated as 'L'
    """
    # try to open what the mask *should* be named
    # this should be done less hackishly
    # for example, if filename is 'ncs.1029.jpg' then
    # this would set the maskfile as 'ncs.1029.mask.jpg'

    #if filetype not in ("mask", "trace"):
    #    raise NotImplementedError("Can only deal with mask or trace files.")

    # get the base of filename and build the type filename
    *base, suffix = filename.split('.')
    base = ''.join(base)
    typefile = '.'.join((base, filetype, suffix))

    if sample_dir is None:
        sample_dir = 'samples'

    typefile = os.path.join(sample_dir, typefile)

    if mode is not None:
        if filetype == 'mask':
            mode = 'L'
        elif filetype in ('ctrace', 'veins', 'arteries'):
            mode = 'RGB'
        else:
            # handle this if you need to?
            mode = 'L'
    try:
        img = imread(typefile, mode=mode)

    except FileNotFoundError:
        print('Could not find file', typefile)
        return None

    return img


def open_tracefile(base_filename, as_binary=True,
                   sample_dir=None):

    """

    ###width parsing is no longer done here. instead, this function
    should handle the venous/arterial difference.

    this currently only serves to open the RGB traces as binary
    files instead of RGB, which is processed later

    #TODO: expand this later to handle arterial traces and venous traces
    INPUT:
        base_filename: the name of the base file, not the tracefile itself
        as_binary: if True
    """

    if as_binary:
        mode = 'L'
    else:
        mode = 'RGB'

    T = open_typefile(base_filename, 'trace', sample_dir=sample_dir, mode=mode)

```

```
    if as_binary:

        return np.invert(T != 0)

    else:
        return T

def mimg_as_float(mimg):

    if not ma.is_masked(mimg):

        return img_as_float(ming)

    else:
        return ma.masked_array(img_as_float(mimg.data.filled(0)),
                               mask=mimg.mask)

def get_named_placenta(filename, sample_dir=None, masked=True,
                       maskfile=None, mode='L'):
    """
    This function is to be replaced by a more ingenious/natural
    way of accessing a database of unregistered and/or registered
    placental samples.

    Parameters
    ----------

    filename: name of file (including suffix?) but NOT directory
    masked: return it masked.
    maskfile: if supplied, this use the file will use a supplied 1-channel
            mask (where 1 represents an invalid/masked pixel, and 0
            represents a valid/unmasked pixel. the supplied image must be
            the same shape as the image. if not provided, the mask is
            calculated (unless masked=False)
            the file must be located within the sample directory

            If maskfile is 'None' then this function will look for
            a default maskname with the following  pattern:

                test.jpg -> test.mask.jpg
                ncs.1029.jpg  -> ncs.1029.mask.jpg

    sample_directory: Relative path where sample (and mask file) is located.
            defaults to './samples'

    if masked is true (default), this returns a masked array.

    NOTE: A previous logical incongruity has been corrected. Masks should have
    1 as the invalid/background/mask value (to mask), and 0 as the
    valid/plate/foreground value (to not mask)
    """
    if sample_dir is None:
        sample_dir = 'samples'

    full_filename = os.path.join(sample_dir, filename)

    if mode.lower() in ('g', 'green'):
        # first channel of RGBA (or RGBA!)
        raw_img = imread(full_filename)[...,1]

    else:
        raw_img = imread(full_filename, mode=mode)

    if maskfile is None:
```

```
        # try to open what the mask *should* be named
        # this should be done less hackishly
        # for example, if filename is 'ncs.1029.jpg' then
        # this would set the maskfile as 'ncs.1029.mask.jpg'
        *base, suffix = filename.split('.')
        test_maskfile = ''.join(base) + '.mask.' + suffix
        test_maskfile = os.path.join(sample_dir, test_maskfile)
        try:
            mask = imread(test_maskfile, mode='L')
        except FileNotFoundError:
            print('Could not find maskfile', test_maskfile)
            print('Please supply a maskfile. Autogeneration of mask',
                  'files is slow and buggy and therefore not supported.')
            raise
            #return mask_background(raw_img)
    else:
        # set maskfile name relative to path
        maskfile = os.path.join(sample_dir, maskfile)
        mask = imread(maskfile, mode='L')

    return ma.masked_array(raw_img, mask=mask)


def list_by_quality(quality=0, N=None, json_file=None, return_empty=False):
    """
    returns a list of filenames that are of quality ``quality''

    quality is either "good" or 0
                      "OK" or 1
                      "fair" or 2
                      "poor" or 3

    N is the number of placentas to return (will return # of placentas
    of that quality or N, whichever is smaller)

    if json_name is not None just use that filename directly

    if return_empty then silenty failing is OK
    """

    quality_keys = ('good', 'okay', 'fair', 'poor')

    if quality in quality_keys:
        pass
    elif quality in (0, 1, 2, 3):
        quality = quality_keys[quality]
    else:
        try:
            quality = quality.lower()
        except AttributeError:
            if return_empty:
                return list()
            else:
                print(f'unknown quality {quality}')
                raise
        else:
            # if no json file is provided, and quality is a string,
            # just assume it follows a template format
            if json_file is None:
                json_file = f"{quality}-mccs.json"

    # if it's still not provided in the main file, it's in the main file
    if json_file is None:
        json_file = 'sample-qualities.json'
```

```
225
226     try:
227         with open(json_file, 'r') as f:
228             D = json.load(f)
229     except FileNotFoundError:
230         if return_empty:
231             return list()
232         else:
233             print('cannot find', json_file)
234             raise FileNotFoundError
235
236     if json_file == 'sample-qualities.json':
237         # go one level deep
238         placentas = [k for k in D[quality].keys()]
239     else:
240         placentas = [k for k in D.keys()]
241
242     if N is not None:
243         return placentas[:N]
244     else:
245         return placentas
246
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':
307                 placentas.append(f)
308
309     return sorted(placentas)
310
311
312 def show_mask(img, mask=None, interactive=False, mask_color=None):
313     """
314     rename this color_mask since showing the mask is just a secondary feature
315     show a masked grayscale image with a dark blue masked region
316
317     custom version of imshow that shows grayscale images with the right
318     colormap and, if they're masked arrays, sets makes the mask a dark blue) a
319     better function might make the grayscale value dark blue (so there's no
320     confusion)
321
322     if interactive, this operates like "plt.imshow"
323     if interactive==False, return the RGB matrix
324
325     if mask provided, add it to the image. (pass img.data instead if you don't
326     want to use the original mask)
327     """
328
329     if mask_color is None:
330         mask_color = (0, 0, 60)
331
332     # if there's no mask at all
333     if (mask is None) and (not is_masked(img)):
334         if interactive:
335             plt.imshow(img, cmap=plt.cm.gray)
336             return  # we're done
337         else:
338             # return as an rgb image so output is uniform
339             return gray2rgb(img)
340
341     elif not is_masked(img):
342         # add mask to the image / add to existing mask
343         # if i just rewrite img will it change outside this function?
344         new_img = ma.masked_array(img, mask=mask)
345     else:
346         new_img = img.copy()
347
348     # otherwise, get an RGB array, black where the mask is
349     mimg = gray2rgb(new_img.filled(0))
350
351     # fill masked regions with the mask color
352     mimg[new_img.mask, :] = mask_color
```

```
353
354     if interactive:
355         plt.imshow(mimg)
356     else:
357         return mimg
358
359
360 def _cropped_bounds(img, mask=None):
361
362     if mask is not None:
363
364         img = ma.masked_array(img, mask=mask)
365
366     X, Y = (np.argwhere(np.invert(img.mask).any(axis=k)).squeeze()
367             for k in (0, 1)
368             )
369
370     if X.size == 0:
371         X = [None, None]  # these will slice correctly
372     if Y.size == 0:
373         Y = [None, None]
374
375     return Y[0], Y[-1], X[0], X[-1]
376
377
378 def cropped_args(img, mask=None):
379     """
380     get a slice that would crop image
381     i.e. img[cropped_args(img)] would be a cropped view
382     """
383
384     x0, x1, y0, y1 = _cropped_bounds(img, mask=None)
385
386     return np.s_[x0:x1, y0:y1]
387
388
389 def cropped_view(img, mask=None):
390     """
391     removes entire masked rows and columns from the borders of a masked array.
392     will return a masked array of smaller size
393
394     don't ask me about data
395
396     the name sucks too
397     """
398
399     # find first and last row with content
400     x0, x1, y0, y1 = _cropped_bounds(img, mask=mask)
401
402     return img[x0:x1, y0:y1]
403
404
405 CYAN = [0, 255, 255]
406 YELLOW = [255, 255, 0]
407
408
409 def measure_ncs_markings(ucip_img=None, filename=None, verbose=True):
410     """
411     find location of ucip and resolution of image based on input
412     (similar to perimeter layer in original NCS data set
413
414     Parameters
415     ----------
416
```

```
    ucip_img: an RGB ndarray or None
        The perimeter layer of an NCS sample (colorations according to the
        tracing protocol). if None, filename must be included. Default is None.
    filename:
        the filename of the SAMPLE (not the ucip image file itself)

    Returns
    -------
    m : tuple of ints
        the coordinates of (the center of) of the umbilical cord point
        (depicted as a yellow dot) in the original image.
    resolution: a float
        measured distance between the two cyan dots
    """

    if ucip_img is None:
        ucip_img = open_typefile(filename, 'ucip')

    if ucip_img is None:
        # if it's still none (no file), return None
        return None, None

    # just in case it's got an alpha channel, remove it
    img = ucip_img[:, :, 0:3]

    # given the image img (make sure no alpha channel)
    # find all cyan pixels (there are two boxes of 3 pixels each and we
    # just want to extract the middle of each
    if verbose:
        print('the image size is {}x{}'.format(img.shape[0], img.shape[1]))

    rulemarks = np.all(img == CYAN, axis=-1)

    # turn into two pixels (these should each be shape (18,))
    X, Y = np.where(rulemarks)

    assert X.shape == Y.shape

    # if they followed the protocol correctly...
    if X.size == 18:
        # get the two pixels at the center of each box
        A, B = (X[4], Y[4]), (X[13], Y[13])
    else:
        # dots are a nonstandard size for some reason. this works too.
        thinned = morphology.thin(rulemarks)
        X, Y = np.where(thinned)
        assert(thinned.sum() == 2)  # there should be just two pixels now.
        A, B = (X[0], Y[0]), (X[1], Y[1])

    ruler_distance = np.sqrt((A[0] - B[0])**2 + (A[1] - B[1])**2)
    if verbose:
        print(f'one cm equals {ruler_distance} pixels')

    # the umbillical cord insertion point (UCIP) is a yellow circle, radius 19
    ucipmarks = np.all(img == YELLOW, axis=-1)
    X, Y = np.where(ucipmarks)

    # find midpoint of the x & y cooridnates
    assert X.max() - X.min() == Y.max() - Y.min()
    radius = (X.max() - X.min()) // 2

    mid = (X.min() + radius, Y.min() + radius)

    if verbose:
```

```
        print('the middle of the UCIP location is', mid)
        print('the radius outward is', radius)
        print('the total measurable diameter is', radius*2 + 1)

    return mid, ruler_distance


def add_ucip_to_mask(m, radius=100, mask=None, size_like=None):
    """
    - m is a tuple (2x1) representing the (coordinate) midpoint of the UCIP
    - radius around which to dilate the UCIP is the dilation radius as it
    works in morphology--this is passed directly to skimage.morphology.disk.
    thus a circle centered at point m with diameter 2*radius + 1
    - if no mask is supplied, dilate the point in an array of zeros the shape
    of `size_like` (would be the same as passing mask=np.zeros_like(size_like))

    Note: this behaves much faster than binary dilation on the point
    """
    if mask is None:
        if size_like is not None:
            mask = np.zeros_like(size_like)
        else:
            raise ValueError("No mask info supplied!")

    # an empty mask (since we need to merge--we don't want to copy the
    # zeros of the dilated UCIP -- just the ones!)
    to_add = np.zeros_like(mask)

    # this is way faster than dilating the point in the matrix,
    # just set this at the centered point

    # doesn't check for out of bounds stuff. use at your own peril
    D = morphology.disk(radius)
    to_add[m[0]-radius:m[0]+radius+1, m[1]-radius:m[1]+radius+1] = D

    # merge with supplied mask
    return mask | to_add


if __name__ == "__main__":

    """test that this works on an easy image."""

    test_filename = 'barium1.png'

    img = get_named_placenta(test_filename, maskfile=None)

    print('showing the mask of', test_filename)
    print('run plt.show() to see masked output')

    show_mask(img, interactive=True)
```

listings/plate_morphology.py

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

from skimage.morphology import (disk, binary_erosion, binary_dilation,
                                convex_hull_image, thin)
from skimage.segmentation import find_boundaries, watershed

from placenta import open_typefile, get_named_placenta

```

```
import numpy as np
import numpy.ma as ma

def dilate_boundary(img, radius=10, mask=None):
    """
    grows the mask by a specified radius of a masked 2D array
    Manually remove (erode) the outside boundary of a plate.
    The goal is remove any influence of the zeroed background
    on reporting derivative information.

    There is varying functionality here (maybe should be multiple functions
    instead?)

    If img is a masked array and mask=None, the mask will be dilated and a
    masked array is outputted.

    If img is any 2D array (masked or unmasked), if mask is specified, then
    the mask will be dilated and the original image will be returned as a
    masked array with a new mask.

    If the img is None, then the specified mask will be dilated and returned
    as a regular 2D array.

    """

    if mask is None:
        # grab the mask from input image
        # if img is None this will break too but not handled
        try:
            mask = img.mask
        except AttributeError:
            raise('Need to supply mask information')

    perimeter = find_boundaries(mask, mode='inner')

    maskpad = np.zeros_like(perimeter)

    M,N = maskpad.shape
    for i,j in np.argwhere(perimeter):
        # just make a cross shape on each of those points
        # these will silently fail if slice is OOB thus ranges are limited.
        maskpad[max(i-radius,0):min(i+radius,M),j] = 1
        maskpad[i,max(j-radius,0):min(j+radius,N)] = 1

    new_mask = np.bitwise_or(maskpad, mask)

    if img is None:
        return new_mask # return a 2D array
    else:
        # replace the original mask or create a new masked array
        return ma.masked_array(img, mask=new_mask)


def l2_dist(p,q):
    return int(np.round(np.sqrt((p[0]-q[0])**2 + (p[1]-q[1])**2)))


def mask_cuts_simple(img, ucip, mask_only=False, in_place=False,
                     return_success=False):
    """
    this covers up the cut with a disc originating at the perimeter of
    significant radius
    """

```

```
    cutmarks = np.all(ucip==(0,0,255), axis=-1)
    B = np.all(ucip==(0,0,255), axis=-1)
    dilcut = img.copy()

    if not np.any(cutmarks):

        #print("no cutmarks found on image")

        if return_success:
            return img, False
        else:
            return img
    else:
        #print("found a cutmark!")
        pass

    cutmarks = np.nonzero(cutmarks)
    # get the first pixel of it (we don't need to be too precise here)
    G = np.all(ucip==(0,255,0), axis=-1) # perimeter elements
    cutmarks = np.nonzero(thin(B))
    perimeter = np.nonzero(G)

    cutinds = np.stack(cutmarks).T

    for P in cutinds:

        # consider larger and larger window sizes
        for W in [100,200,300]:
            # consider all perimeter elements within these bounds

            rmin, rmax = max(0, P[0]-W), min(img.shape[0], P[0]+W)
            cmin, cmax = max(0, P[1]-W), min(img.shape[1], P[1]+W)
            #window = np.s_[rmin:rmax, cmin:cmax]

            # perimeter indices within the window
            pinds = [(x,y) for x, y in zip(*perimeter)
                        if x > rmin and x < rmax and y > cmin and y < cmax
                        ]
            if pinds:
                break #otherwise increase the size of the window
    if pinds:

        # max distance to boundary point in the window
        # we really only need to keep the largest; deque?
        dists = sorted([(pp, l2_dist(P,pp)) for pp in pinds],
                       key=lambda t: t[1])
        r = 2*int(dists[0][1]) + 1 # get largest radius but closest point
        P = dists[0][0]
        B = np.zeros_like(img.mask)

        B[cutmarks] = True

        # center a disk of found radius there
        D = disk(r)
        winx = max(P[0]-r,0), min(P[0]+r+1,B.shape[0])
        winy = max(P[1]-r,0), min(P[1]+r+1,B.shape[1])
        try:
            B[winx[0]:winx[1] , winy[0]:winy[1]] = D
        except ValueError:
            # they're out of bounds so it's a size mismatch. fix it
            # by starting/ending D index with opposite sign of the initial
            # p +/- radius that was out of bounds
            # for example P[0]-r was -9 and everything else was fine
            # so you just need to set left side to D[9:,:]
```

```
137             # but you should  wrap this up in a function so the three times
138             # you do it here and the one time in ucip all gets the same
139             # code
140             print("too close to the boundary or size mismatch?")
141             success = False
142         else:
143             dilcut[B] = ma.masked
144             success = True
145     else:
146         print("we completely failed to mask the cut. too close to the",
147               "boundary to fit an unmodified disk in. fix this")
148         success = False
149 
150     return dilcut, success
151 
152 
153 def mask_cuts_watershed(img, ucip, mask_only=False, in_place=False,
154                         return_success=False):
155     """
156 
157     this doesn't handle any image, io. just provide the ucip img and the
158     base (masked) image and we'll fix the mask
159 
160     ucip is the actual RGB array, not the file. do io elsewhere.
161 
162     if mask_only, this will simply return the new mask as a 2D boolean array.
163     Otherwise, it returns a masked_array.
164     The cut region will be added to the img's mask. If you really want just the
165     difference, you'll have to to run
166     >>>(cut_mask & ~img.mask) youself.
167 
168     yourself.
169 
170     If in_place, this changes the mask of the image directly (but still returns
171     a masked array. If mask_only is True, in_place will automatically be set to
172     False to prevent hideous side effects
173 
174     if return_success, this function returns True if there was a cutmark found,
175     otherwise false as a second output
176     """
177     # get indices where the blue square indicating center of a cut apprears
178     cutmarks = np.all(ucip==(0,0,255), axis=-1)
179 
180     if not np.any(cutmarks):
181 
182         #print("no cutmarks found on image")
183 
184         if return_success:
185             return img, False
186         else:
187             return img
188     else:
189         #print("found a cutmark!")
190         pass
191 
192     cutmarks = np.nonzero(cutmarks)
193     # get the first pixel of it (we don't need to be too precise here)
194     X, Y = cutmarks[0][0], cutmarks[1][0]
195 
196     # get a value somewhat lower than the value of bg in the cut
197     # (this should be a high number before we take 85%)
198     # sometimes this is in a shadowy region which fucks everything up though
199     #threshold = max(img[cutmarks].mean() * .85, 175)
200     # get the brightest value in a smallish window around the cut * .85
```

```
    threshold = np.max(img[X-10:X+10,Y-10:Y+10])

    rmin, rmax = max(0, X-100), min(img.shape[0], X+100)
    cmin, cmax = max(0, Y-100), min(img.shape[1], Y+100)
    cutregion = np.s_[rmin:rmax, cmin:cmax] # get a window around the mark

    # mark inside of the placenta with label 2, original mask and cutmarks with
    # label 1, and the rest with 0 (i dunno)
    markers = np.zeros(img.shape, dtype='int32')
    markers[img.filled(255) < threshold] = 2
    markers[img.mask] = 1
    markers[cutmarks] = 1

    # perform watershedding on the thresholded image to fill in the cut with
    # label 1
    cutfix = watershed(img.filled(255) < threshold, markers=markers)

    # this is a waste considering the in_place, but eh
    new_mask = img.mask.copy()

    new_mask[cutregion] = (cutfix[cutregion] == 1)

    if mask_only:

        out = new_mask

    elif not in_place:

        out = ma.masked_array(img, mask=new_mask)

    else:

        # will this work?
        img[new_mask] = ma.masked

        out = img

    # now return succeed if asked to
    if return_success:
        return out, True

    else:
        return out


if __name__ == "__main__":

    # DEMO FOR SHOWING OFF DILATE_BOUNDARY EFFECT

    from placenta import get_named_placenta
    from frangi import frangi_from_image
    import matplotlib.pyplot as plt

    import os.path

    dest_dir = 'demo_output'
    img = get_named_placenta('T-BN0164923.png')

    sigma = 3
    radius = 25

    inset = np.s_[800:1000, 500:890]

    D = dilate_boundary(img, radius=radius)
```

```
    Fimg = frangi_from_image(img, sigma, dark_bg=False, dilation_radius=None)
    FD = frangi_from_image(D, sigma, dark_bg=False)
    FDinv = frangi_from_image(D, sigma, dark_bg=True)
    Finv = frangi_from_image(img, sigma, dark_bg=True, dilation_radius=None)

    fig, axes = plt.subplots(ncols=2, nrows=3)

    axes[0,0].imshow(img[inset].filled(0), cmap=plt.cm.gray)
    axes[0,1].imshow(D[inset].filled(0), cmap=plt.cm.gray)
    axes[1,0].imshow(Fimg[inset].filled(0), cmap=plt.cm.nipy_spectral)
    axes[1,1].imshow(FD[inset].filled(0), cmap=plt.cm.nipy_spectral)
    axes[2,0].imshow(Finv[inset].filled(0), cmap=plt.cm.nipy_spectral)
    axes[2,1].imshow(FDinv[inset].filled(0), cmap=plt.cm.nipy_spectral)

    for a in axes.ravel():
        # get rid of all the labels
        plt.setp(a.get_xticklabels(), visible=False)
        plt.setp(a.get_yticklabels(), visible=False)

    # lol matlab
    for i in range(5):
        fig.tight_layout()

    plt.savefig(os.path.join(dest_dir, "boundary_dilation_demo.png"), dpi=300)
```

listings/postprocessing.py

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

"""
doing things to the Frangi targets, i.e. feeding them into other algorithms
"""

from skimage.filters import sobel
from skimage.morphology import remove_small_holes, remove_small_objects, thin
from frangi import frangi_from_image
from merging import apply_threshold, nz_percentile
from plate_morphology import dilate_boundary
from skimage.segmentation import random_walker
import numpy as np

def random_walk_fill(img, Fmax, high_thresh, low_thresh, dark_bg):
    """
    there are a lot of decisions to make here but it's just a demo
    so who cares
    """

    s = sobel(img)
    s = dilate_boundary(s, mask=img.mask, radius=20)

    finv = frangi_from_image(img, sigma=0.8, beta=0.5, dark_bg=(not dark_bg),
                             dilation_radius=20)

    finv_thresh = (finv > nz_percentile(finv, 50)).filled(0)
    margins = remove_small_objects(finv_thresh, min_size=32)

    markers = np.zeros(img.shape, dtype=np.int32)
    markers[Fmax < low_thresh] = 1

    margins_added = (margins | (Fmax > high_thresh))
    #margins_added = remove_small_holes(margins_added, area_threshold=50)
```

```
35
36      markers[Fmax < low_thresh] = 1
37
38      markers[margins_added] = 2
39
40      rw = random_walker(1-Fmax, markers, beta=1000)
41
42      approx_rw = (rw == 2)
43
44      return approx_rw, markers, margins_added
45
46  def random_walk_scalewise(F, high_thresh, return_labels=False):
47
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          W[n] = (random_walker(1-v, markers) == 2)
58      print()
59      if return_labels:
60          return W.any(axis=0), W.argmax(axis=0)
61      else:
62          return W.any(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
```

```
    B = ma.masked_array(img, mask=glared)  # masked background *and* glare
    new_img = img.copy()  # copy values of original image (will rewrite)
    d = int(window_size)

    for j, k in zip(*np.where(glared)):
        # rewrite all glared pixels with the mean of nonmasked elements
        # in a window_size window. (this doesn't check OoB, be careful!)
        new_img[j, k] = B[j-d:j+d, k-d:k+d].compressed().mean()

    return new_img


def inpaint_with_boundary_median(img, threshold=175, mask=None):
    """
    mask glare pixels, then replace by the median value on the mask's boundary
    """
    if mask is None:
        glared = mask_glare(img, threshold=threshold, mask_only=True)
    else:
        glared = mask

    B = ma.masked_array(img, mask=glared)

    new_img = img.copy()  # copy values of original image (will rewrite)
    bounds = find_boundaries(glared)
    lb, _ = label(bounds)
    fill_vals = np.zeros_like(img.data)

    # for each boundary of masked region, find the median value of the img
    for lab in range(1, lb.max()+1):
        inds = np.where(lb == lab)
        fill_vals[inds] = nz_median(B[inds])

    # label masked regions together with their boundaries (they'll be
    # connected)
    lm, _ = label(np.logical_or(glared, lb != 0))

    # fill the masked areas with the corresponding fill value
    for lab in range(1, lm.max()+1):
        inds = np.where(lm == lab)
        # find locations of filled values corresponding to this label
        # median in case there's overlapped regions? (sloppy)
        replace_value = nz_median(fill_vals[inds])

        if replace_value == 0:
            raise

        fill_vals[inds] = replace_value

    # now fill in the values
    new_img[glared] = fill_vals[glared]

    return new_img

def nz_median(A):

    if ma.is_masked(A):
        relevant = A[A > 0].compressed()
    else:
        relevant = A[A > 0]

    return np.median(relevant)


```

```
def inpaint_hybrid(img, threshold=175, min_size=64, boundary_radius=10):
    """
    use biharmonic inpainting in larger, inner areas (important stuff)
    and median inpainting in smaller areas and along boundary
    """

    glare = mask_glare(img, threshold=threshold, mask_only=True)

    glare_inside = dilate_boundary(glare, mask=img.mask,
                                   radius=boundary_radius).filled(0)

    large_glare = remove_small_objects(glare_inside, min_size=min_size,
                                       connectivity=2)
    small_glare = np.logical_and(glare, np.invert(large_glare))

    # inpaint smaller and less important values with less expensive method
    inpainted = inpaint_with_boundary_median(img, mask=small_glare)
    hybrid = img_as_float(inpainted) # scale 0 to 1

    # inpaint larger regions with biharmonic inpainting
    large_inpainted = inpaint_biharmonic(img.filled(0), mask=large_glare)

    # now overwrite with these values
    hybrid[large_glare] = large_inpainted[large_glare]

    # put on old image mask
    return ma.masked_array(hybrid, mask=img.mask)

def inpaint_with_biharmonic(img, threshold=175):
    """
    use biharmonic inpainting *all* glare
    """
    glare = mask_glare(img, threshold=threshold, mask_only=True)
    inpainted = inpaint_biharmonic(img_as_float(img.filled(0)), mask=glare)

    if ma.is_masked(img):
        return ma.masked_array(inpainted, mask=img.mask)
    else:
        return inpainted

def mask_glare(img, threshold=175, mask_only=False):
    """
    for demoing purposes, with placenta.show_mask

    if mask_only, just return the mask. Otherwise return a copy of img with
    that added to the mask. If you want the original mask to be ignored,
    just pass img.filled(0) ya doofus

    threshold is expected to be of the same dtype as img *unless# it assumes
    its default value, in which case the threshold will be converted to a float

    """
    # if img.dtype is floating but threshold value is still the default
    # this could be generalized
    if np.issubdtype(img.dtype, np.floating) and (threshold == 175):
        threshold = 175 / 255
    # region to inpaint
    inp = (img > threshold)

    # get a larger area around the specks
    inp = binary_dilation(inp, selem=disk(2))

    # remove anything large
    #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):
```

```
        fig.tight_layout()

    IMGS = np.vstack((
        np.hstack((img_view, masked_view, inpainted_view)),
        np.hstack((minpainted_view, binpainted_view, hinpainted_view))))

    # THEN IMSAVE

    # plt.imsave('preprocessing_comparison_cropped.png',  IMGS)
    # plt.imsave('preprocessing_comparison_zoomed.png',  IMGS)

    # if it's zoomed, then rescale the output in GIMP to 4x
```

listings/process_NCS_xcfs.py

```
#!/usr/bin/env python

"""
This should be a plugin to take images from the folder NCS_vessel_GIMP_xcf
and create trace, mask, and backgrounded images from each xcf file.

to use:
chmod +x and then copy or link to  ~/gimp-2.x/plug-ins/
"""

from gimpfu import *
import os.path
from functools import partial

#basefile, ext = os.path.splitext(xcffile)

def _outname(base, s=None):

    #base = base.split("_", maxsplit=1)[0]
    if s is None:
        stubs = (base, 'png')
    else:
        stubs = (base, s, 'png')
    file
    filename = '.'.join(stubs)

    return os.path.join(os.getcwd(), filename)

# get active image
def process_NCS_xcf(timg,tdrawable):
    img = timg
    basename, _ = os.path.splitext(img.name) # split off extension .xcf
    basename = basename.split("_")[0] # only get T-BN-kjlksf part
    print "*"*80
    print '\n\n'

    print "Processing " , img.name
    # generate output names easier
    outname = partial(_outname, base=basename)

    # get coordinates of the center
    cx, cy = img.height // 2 , img.width // 2

    # disable the undo buffer
    img.disable_undo()

    #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,0,0,255,0,0,0,1,1,1)
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     # now with these two visible, merge them and add layer
120     trace = pdb.gimp_layer_new_from_visible(img,img,'trace')
121     img.add_layer(trace,0)
122
123     pdb.gimp_layer_flatten(trace) # remove alpha channel
124
125     # 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/scaledecay.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
```

```
plt.imshow(img)
pls.show()
plt.show()
filename =  list_by_quality(0)[0]
img = get_named_placenta(filename)
from placenta import cropped_args
crop = cropped_args(img)
img[crop]
plt.imshow(img[crop])
plt.show()
from hfft import fft_gaussian
get_ipython().run_line_magic('pinfo', 'fft_gaussian')
C = fft_gaussian(img, 32, 'discrete')
B = fft_gaussian(img, 5, 'discrete')
A = fft_gaussian(img, .12, 'discrete')
plt.imshow(A)
plt.show()
A = fft_gaussian(img, .25, 'discrete')
plt.imshow(A)
plt.show()
plt.imshow(B)
plt.show()
plt.imshow(C)
plt.show()
gA = np.gradient(A)
gA
gB = np.gradient(B)
gC = np.gradient(C)
gA.shape
gA[0].shape
aa = lambda g: np.sqrt((1+g[0]*g[0] + g[0]*g[0]))
plt.imshow(aa(gA))
plt.show()
from plate_morphology import dilate_boundary
from functools import partial
dilate = partial(dilate_boundary, mask=img.mask)
dilate(aa(gA), 20)
plt.imshow(_)
plt.show()
dilate(aa(gA), 20).filled(0)
plt.show()
plt.imshow(_)
plt.show()
Aaa = dilate(aa(gA), 20).filled(0)
Aaa.max()
Aaa.min()
Aaa[~img.mask].min()
Aaa[img.mask].min()
Aaa[img.mask].max()
Aaa[~img.mask].max()
Baa = dilate(aa(gB), 20).filled(0)
Caa = dilate(aa(gC), 20).filled(0)
plt.imshow(Baa)
plt.show()
plt.imshow(Caa)
plt.show()
Caa.min()
Caa[~img.mask].min()
Caa == 0
plt.imshow(_)
plt.show()
Caa[~img.mask].max()
Caa[~img.mask].min()
Caa[~img.mask].argmin()
```

```
dilate_boundary(img.mask, 20)
dilate_boundary(img.mask, 20, mask_only=True)
get_ipython().run_line_magic('pinfo', 'dilate_boundary')
dilate_boundary(img, radius=20)
dil = _.mask.copy()
dil
plt.imshow(dil)
plt.show()
Caa[~dil].argmin()
Caa[~dil]
Caa[~dil].min()
Caa[~dil].max()
Baa[~dil].max()
Baa[~dil].min()
Aaa[~dil].min()
Aaa[~dil].max()
plt.imshow(Caa)
plt.show()
plt.imshow(Aaa)
plt.show()
#for sigma in np.logspace(-3, 8, base=2, num=20):
#    D = fft_gaussian(img, sigma, 'discrete')
#    gD = np.gradient(D)
#    Daa = dilate(aa(dG), 20).filled(1)
#    print(Daa[~dil].min(), Daa[~dil].max()
aas = list()
for sigma in np.logspace(-3, 8, base=2, num=20):
    D = fft_gaussian(img, sigma, 'discrete')
    gD = np.gradient(D)
    Daa = dilate(aa(dG), 20).filled(1)
    aas.append(Daa)
    print(f"sigma={sigma:.3f}", "min: {:6f}, max:{:6f}".format(
          Daa[~dil].min(), Daa[~dil].max())
          )

for sigma in np.logspace(-3, 8, base=2, num=20):
    D = fft_gaussian(img, sigma, 'discrete')
    gD = np.gradient(D)
    Daa = dilate(aa(gD), 20).filled(1)
    aas.append(Daa)
    print(f"sigma={sigma:.3f}", "min: {:6f}, max:{:6f}".format(
          Daa[~dil].min(), Daa[~dil].max())
          )

for sigma in np.logspace(-4, 8, base=2, num=50):
    D = fft_gaussian(img, sigma, 'discrete')
    gD = np.gradient(D)
    Daa = dilate(aa(gD), 20).filled(1)
    aas.append(Daa)
    print(f"sigma={sigma:.3f}", "min: {:6f}, max:{:6f}".format(
          Daa[~dil].min(), Daa[~dil].max())
          )

bb lambda g: np.linalg.norm(np.array(
        [[1+g[1]**2, -g[0]*g[1]],
         [-g[0]*g[1], 1 + g[0]**2]]))
bb = lambda g: np.linalg.norm(np.array(
        [[1+g[1]**2, -g[0]*g[1]],
         [-g[0]*g[1], 1 + g[0]**2]]))
bb(gA)
get_ipython().set_next_input('man np.linalg.norm');get_ipython().run_line_magic('pinfo', 'n
ginv = lambda g: np.array(
        [[1+g[1]**2, -g[0]*g[1]],
         [-g[0]*g[1], 1 + g[0]**2]])
```

```
ginv(gA)
_.shape
G[:,:,34,289]
ginvA = _101
ginvA[:,:,340,289]
bb = lambda g: np.sqrt((1+g[1]**2)**2 + 2*(g[0]*g[1])**2 + (1+g[0]**2)**2)
bb(gA)
_.shape
plt.imshow(bb)
_.shape
bb(gA)
plt.imshow(_)
plt.show()
bb(gA) / aa(gA)
plt.imshow(_)
plt.show()
dilate(bb(gA) / aa(gA))
plt.imshow(dilate(bb(gA) / aa(gA)).filled(0))
plt.show()
bb = lambda g: np.sqrt((1+g[1]**2)**2 + 2*(g[0]*g[1])**2 + (1+g[0]**2)**2)
plt.imshow(dilate(bb(gA),20))
plt.show()
bb(gA)[~dil].min()
bb(gA)[~dil].max()
(bb(gA) / aa(gA))[~dil].min()
(bb(gA) / aa(gA))[~dil].max()
(bb(gA) / aa(gA))
plt.imshow(dilate(_,20).filled(1.414))
plt.show()
for sigma in np.logspace(-4, 8, base=2, num=50):
    D = fft_gaussian(img, sigma, 'discrete')
    gD = np.gradient(D)
    Daa, Dbb = aa(gD), bb(gD)
    Dcc = Daa / Dbb
    aas = Daa[~dil].min(), Daa[~dil].max()
    bbs = Dbb[~dil].min(), Dbb[~dil].max()
    ccs = Dcc[~dil].min(), Dcc[~dil].max()
    print(f"sigma={sigma:.3f}",
          "\tmin: {:.6f},\tmax:{:.6f}".format(aas),
          "\tmin: {:.6f},\tmax:{:.6f}".format(bbs),
          "\tmin: {:.6f},\tmax:{:.6f}".format(ccs), sep='\n')


for sigma in np.logspace(-4, 8, base=2, num=50):
    D = fft_gaussian(img, sigma, 'discrete')
    gD = np.gradient(D)
    Daa, Dbb = aa(gD), bb(gD)
    Dcc = Daa / Dbb
    aas = Daa[~dil].min(), Daa[~dil].max()
    bbs = Dbb[~dil].min(), Dbb[~dil].max()
    ccs = Dcc[~dil].min(), Dcc[~dil].max()
    print(f"sigma={sigma:.3f}",
          "\tmin: {:.6f},\tmax:{:.6f}".format(*aas),
          "\tmin: {:.6f},\tmax:{:.6f}".format(*bbs),
          "\tmin: {:.6f},\tmax:{:.6f}".format(*ccs), sep='\n')


for sigma in np.logspace(-4, 8, base=2, num=50):
    D = fft_gaussian(img, sigma, 'discrete')
    gD = np.gradient(D)
    Daa, Dbb = aa(gD), bb(gD)
    Dcc = Dbb / Daa
    aas = Daa[~dil].min(), Daa[~dil].max()
```

```
    bbs = Dbb[~dil].min(), Dbb[~dil].max()
    ccs = Dcc[~dil].min(), Dcc[~dil].max()
    print(f"sigma={sigma:.3f}",
           "\tmin: {:.6f},\tmax:{:.6f}".format(*aas),
           "\tmin: {:.6f},\tmax:{:.6f}".format(*bbs),
           "\tmin: {:.6f},\tmax:{:.6f}".format(*ccs), sep='\n')

data = _
data = list()
for sigma in np.logspace(-4, 8, base=2, num=50):
    D = fft_gaussian(img, sigma, 'discrete')
    gD = np.gradient(D)
    Daa, Dbb = aa(gD), bb(gD)
    Dcc = Dbb / Daa
    aas = Daa[~dil].min(), Daa[~dil].max()
    bbs = Dbb[~dil].min(), Dbb[~dil].max()
    ccs = Dcc[~dil].min(), Dcc[~dil].max()
    print(f"sigma={sigma:.3f}",
           "\tmin: {:.6f},\tmax:{:.6f}".format(*aas),
           "\tmin: {:.6f},\tmax:{:.6f}".format(*bbs),
           "\tmin: {:.6f},\tmax:{:.6f}".format(*ccs), sep='\n')
    data.append(
        [sigma, *aas, *bbs, *ccs])

import pandas
table = pandas.DataFrame(data)
print(table)
from hfft import fft_hessian
get_ipython().run_line_magic('pinfo', 'fft_hessian')
helems = fft_hessian(img, sigma=1, kernel='discrete')
np.sqrt(helems[0]**2 + 2*helems[1]**2 + helems[2]**2)
_.shape
plt.imshow(np.sqrt(helems[0]**2 + 2*helems[1]**2 + helems[2]**2))
plt.show()
data = list()
for sigma in np.logspace(-4, 8, base=2, num=50):
    D = fft_gaussian(img, sigma, 'discrete')
    gD = np.gradient(D)
    Daa, Dbb = aa(gD), bb(gD)
    Dcc = Dbb / Daa
    h = fft_hessian(img,sigma, 'discrete')
    hnorm = np.sqrt(h[0]**2 + 2*h[1]**2 + h[2]**2)
    Lnorm = hnorm*Dcc
    aas = Daa[~dil].min(), Daa[~dil].max()
    bbs = Dbb[~dil].min(), Dbb[~dil].max()
    ccs = Dcc[~dil].min(), Dcc[~dil].max()
    dds = hnorm[~dil].min(), hnorm[~dil].max()
    lls = Lnorm[~dil].min(), Lnorm[~dil].max()
    print(f"sigma={sigma:.3f}",
           "\tmin: {:.6f},\tmax:{:.6f}".format(*aas),
           "\tmin: {:.6f},\tmax:{:.6f}".format(*bbs),
           "\tmin: {:.6f},\tmax:{:.6f}".format(*ccs),
           "\tmin: {:.6f},\tmax:{:.6f}".format(*dds),
           "\tmin: {:.6f},\tmax:{:.6f}".format(*lls), sep='\n')
    data.append(
        [sigma, *aas, *bbs, *ccs, *dds, *lls])


data
table = pandas.DataFrame(data)
table
table.columns
help(table.columns)
```

```
plt.imshow(Lnorm)
plt.show()
Ls = list()
for sigma in np.logspace(-4, 8, base=2, num=50):
    D = fft_gaussian(img, sigma, 'discrete')
    gD = np.gradient(D)
    Daa, Dbb = aa(gD), bb(gD)
    Dcc = Dbb / Daa
    h = fft_hessian(img,sigma, 'discrete')
    hnorm = np.sqrt(h[0]**2 + 2*h[1]**2 + h[2]**2)
    Lnorm = hnorm*Dcc
    Ls.append(Lnorm)
    aas = Daa[~dil].min(), Daa[~dil].max()
    bbs = Dbb[~dil].min(), Dbb[~dil].max()
    ccs = Dcc[~dil].min(), Dcc[~dil].max()
    dds = hnorm[~dil].min(), hnorm[~dil].max()
    lls = Lnorm[~dil].min(), Lnorm[~dil].max()
    print(f"sigma={sigma:.3f}",
          "\tmin: {:.6f},\tmax:{:.6f}".format(*aas),
          "\tmin: {:.6f},\tmax:{:.6f}".format(*bbs),
          "\tmin: {:.6f},\tmax:{:.6f}".format(*ccs),
          "\tmin: {:.6f},\tmax:{:.6f}".format(*dds),
          "\tmin: {:.6f},\tmax:{:.6f}".format(*lls), sep='\n')
    #data.append(
    #    [sigma, *aas, *bbs, *ccs, *dds, *lls])

L[0]
Ls[0]
plt.imshow(_)
plt.show()
for Lnorm, sigma in zip(Ls, np.logspace(-4,8, base=2,num=50)):
    plt.imshow(Lnorm[crop], cmap='nipy_spectral')
    mng = plt.get_current_fig_manager()
    mng.window.showMaximized()
    plt.colorbar()
    plt.title(r'Lnorm $\sigma={:.3f}$'.format(sigma))
    plt.axis('off')
    plt.tight_layout()
    plt.show()
    plt.close('all')

for Lnorm, sigma in zip(Ls, np.logspace(-4,8, base=2,num=50)):
    L = dilate(Lnorm, min(20,int(sigma))).filled(0)
    plt.imshow(Lnorm[crop], cmap='nipy_spectral')
    mng = plt.get_current_fig_manager()
    mng.window.showMaximized()
    plt.colorbar()
    plt.title(r'Lnorm $\sigma={:.3f}$'.format(sigma))
    plt.axis('off')
    plt.tight_layout()
    plt.show()
    plt.close('all')

for Lnorm, sigma in zip(Ls, np.logspace(-4,8, base=2,num=50)):
    L = dilate(Lnorm, min(20,int(sigma))).filled(0)
    plt.imshow(L[crop], cmap='nipy_spectral')
    mng = plt.get_current_fig_manager()
    mng.window.showMaximized()
    plt.colorbar()
    plt.title(r'Lnorm $\sigma={:.3f}$'.format(sigma))
    plt.axis('off')
    plt.tight_layout()
    plt.show()
    plt.close('all')
```

```
327
328 for Lnorm, sigma in zip(Ls, np.logspace(-4,8, base=2,num=50)):
329     L = dilate(Lnorm, max(20,int(sigma))).filled(0)
330     plt.imshow(L[crop], cmap='nipy_spectral')
331     mng = plt.get_current_fig_manager()
332     mng.window.showMaximized()
333     plt.colorbar()
334     plt.title(r'Lnorm $\sigma={:.3f}$'.format(sigma))
335     plt.axis('off')
336     plt.tight_layout()
337     plt.show()
338     plt.close('all')
339
340 for Lnorm, sigma in zip(Ls, np.logspace(-4,8, base=2,num=50)):
341     L = dilate(Lnorm, max(20,int(sigma))).filled(0)
342     plt.imshow(L[crop], cmap='nipy_spectral')
343     mng = plt.get_current_fig_manager()
344     mng.window.showMaximized()
345     plt.colorbar()
346     plt.title(r'Lnorm $\sigma={:.3f}$'.format(sigma))
347     plt.axis('off')
348     plt.tight_layout()
349     plt.show()
350     plt.close('all')
351
352 for Lnorm, sigma in zip(Ls, np.logspace(-4,8, base=2,num=50)):
353     L = dilate(Lnorm, max(20,int(2*sigma))).filled(0)
354     plt.imshow(L[crop], cmap='nipy_spectral')
355     mng = plt.get_current_fig_manager()
356     mng.window.showMaximized()
357     plt.colorbar()
358     plt.title(r'Lnorm $\sigma={:.3f}$'.format(sigma))
359     plt.axis('off')
360     plt.tight_layout()
361     plt.show()
362     plt.close('all')
363
364 print(table)
365 table
366 table + 2
367 table[:,0]
368 table[0]
369 table / table[0]
370 T = np.array(table)
371 T
372 T.shape
373 T.dtype
374 T / T[:,0]
375 T / T[...,0]
376 T[...,-1] / T[...,0]
377 T[...,-1] / np.sqrt(T[...,0])
378 T[...,-1] * np.sqrt(T[...,0])
379 T[...,-1] * T[...,0]
380 T[...,-1] * T[...,0]**2
381 table
382 T[...,-3] * T[...,0]**2
383 T[...,-3] * T[...,0]
384 T[...,-4] * T[...,0]
385 T[...,-4] / T[...,0]
386 T[...,-4] / T[...,0] > .01
387 which = _
388 T[...,0][which]
389 (T[...,-4] / T[...,0]) > .001
390 scales
```

```
scales = np.logspace(-4,8,num=50,base=2)
scales
(T[...,-3] / T[...,0]) > .001
(T[...,-3] / T[...,0]) > .005
scales[_]
(T[...,-3] / T[...,0]) > .001
scales
scales
(T[...,-3] / T[...,0]) > .001
scales[_]
(T[...,-3] / T[...,0]) > .05
T[...,-3]
(T[...,-3] / T[...,0])
(T[...,-3] / T[...,0]**2)
(T[...,-3] *np.sqrt(1/T[...,0]))
(T[...,-4] / T[...,0]) > .05
table
from frangi import frangi_from_image
g[0]g[1]
g[0]*g[1]
gA[0]*gA[1]
plt.imshow(_)
plt.show()
```

listings/scale_sweep_demo.py

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

from placenta import (get_named_placenta, list_placentas, _cropped_bounds,
                      cropped_view, cropped_args, show_mask)
from frangi import frangi_from_image

import numpy as np
import numpy.ma as ma

from plate_morphology import dilate_boundary

import os.path
import matplotlib.pyplot as plt
import matplotlib as mpl
from itertools import product

# pick two samples and two insets (should be the same size)
demo1 = 'BN2315363', np.s_[370:670, 530:930]
demo2 = 'BN5280796', np.s_[150:450, 530:930]

make_individual = False

for sample_name, inset_slice in (demo1, demo2):
    img = get_named_placenta(f'T-{sample_name}.png')

    crop = cropped_args(img)

    F, fi = list(), list() # make some empty lists to store for inspection

    scales = [0.2, 0.8, 1.0, 2.0, 4.0, 6.0, 8.0, 16.0]
    CMAP = plt.cm.nipy_spectral
    cmin, cmax = (0, 0.4)

    for n, sigma in enumerate(scales):
        R = max(int(sigma*3), 10) # only really necessary for signed
        target = frangi_from_image(img, sigma, dark_bg=False,
```

```
                                    signed_frangi=False, dilation_radius=R)
        plate = target[crop].filled(0)
        inset = target[inset_slice].filled(0)
        F.append(plate)
        fi.append(inset)

        if not make_individual:
            continue

        # else this might be nice for the actual thesis defense
        for label in ['plate', 'inset']:
            if label == 'inset':
                printable = inset
            else:
                printable = plate

            plt.imshow(printable, cmap=CMAP)
            plt.title(r'$\sigma={:.2f}$'.format(sigma))
            plt.tight_layout()
            c = plt.colorbar()
            c.set_ticks = np.linspace(cmin, cmax, num=len(scales)+1)
            plt.clim(cmin, cmax)
            plt.axis('off')
            outname = f'demo_output/scalesweep_{sample_name}_{label}_{n}.png'
            plt.savefig(outname, dpi=300, bbox_inches='tight')
            print('saved', outname)
            plt.close()
    # now make a stitched together version
    for label in ['plate', 'inset']:
        if label == 'inset':
            L = fi
            imgview = img[inset_slice].filled(0)
            figsize = (12, 6)

        else:
            L = F
            imgview = img[crop].filled(0)
            figsize = (12, 9)
        #adjust this manually depending on how many scales you end up using!

        nrows, ncols = 2, 4
        fig, axes = plt.subplots(nrows=nrows, ncols=ncols, figsize=figsize)

        for n, (i, j) in enumerate(product(range(nrows), range(ncols))):

            if n == 0:
                axes[i,j].imshow(imgview, cmap=plt.cm.gray)
                axes[i,j].set_title('raw')
            else:
                im = axes[i,j].imshow(L[n], cmap=CMAP, vmin=cmin, vmax=cmax)
                axes[i,j].set_title(r'$\sigma={:.2f}$'.format(scales[n]))

            plt.setp(axes[i,j].get_xticklabels(), visible=False)
            plt.setp(axes[i,j].get_yticklabels(), visible=False)

        fig.subplots_adjust(top=0.954, bottom=0.025, left=0.010,
                            right=0.989, hspace=0.0, wspace=0.0)

        plt.savefig(f'demo_output/scalesweep_stitch_{sample_name}_{label}.png',
                    dpi=300)

        cfile = 'demo_output/scalesweep_colorbar.png'
        if os.path.isfile(cfile):
            continue # no need to make another
```

```
101
102         fig = plt.figure(figsize=(figsize[0],2))
103         ax1 = fig.add_axes([0.15, 0.25, 0.75, 0.5])
104         cbar = mpl.colorbar.ColorbarBase(ax1, cmap=CMAP,
105                                          norm=mpl.colors.Normalize(cmin,cmax),
106                                          orientation='horizontal')
107         plt.savefig(cfile) # don't set dpi maybe it won't be so small and weird
```

listings/scoring.py

```
1  #!/usr/bin/env python3
2
3  import numpy as np
4  from placenta import open_typefile, open_tracefile
5  from skimage.morphology import thin
6
7  import itertools
8  from collections import deque
9
10 def rgb_to_widths(T):
11     """
12     this will take an RGB trace image (MxNx3) and return a 2D (MxN)
13     "labeled" trace corresponding to the traced pixel length.
14     there is no distinguishing between arteries and vessels
15
16     it's preferrable to do this in real-time so only one tracefile
17     needs to be stored (making the sample folder less cluttered)
18     although obviously at the expense of storing a larger image
19     which is only needed for visualization purposes.
20
21     Input:
22         T: a MxNx3 RGB (uint8) array, where the colorations are
23         assumed as described in NOTES below.
24
25     Output:
26         widthtrace: a MxN array whose inputs describe the width of the
27         vessel (in pixels), see NOTES.
28
29     Notes:
30
31         The correspondence is as follows:
32         3 pixels: "#ff006f",  # magenta
33         5 pixels: "#a80000",  # dark red
34         7 pixels: "#a800ff",  # purple
35         9 pixels: "#ff00ff",  # light pink
36         11 pixels: "#008aff",  # blue
37         13 pixels: "#8aff00",  # green
38         15 pixels: "#ffc800",  # dark yellow
39         17 pixels: "#ff8a00",  # orange
40         19 pixels: "#ff0015"   # bright red
41
42     According to the original tracing protocol, the traced vessels are
43     binned into these 9 sizes. Vessels with a diameter smaller than 3px
44     are not traced (unless they're binned into 3px).
45
46     Note: this does *not* deal with collisions. If you pass anything
47     with addition (blended colors) as the ctraces are, you will have
48     trouble, as those will not be registered as any of the colors above
49     and will thus be ignored. If you want to handle data from both
50     arterial *and* venous layers, you should do so outside of this
51     function.
52     """
```

```
53
54      # a 2D picture to fix in with the pixel widths
55      W = np.zeros_like(T[:,:,0])
56
57      for pix, color in TRACE_COLORS.items():
58
59          #ignore pixelwidths outside the specified range
60          # get the 2D indices that are that color
61          idx = np.where(np.all(T == color, axis=-1))
62          W[idx] = pix
63
64
65      return W
66
67  def merge_widths_from_traces(A_trace, V_trace, strategy='minimum'):
68      """
69      combine the widths from two RGB-traces A_trace and V_trace
70      and return one width matrix according to `strategy`
71
72      Parameters
73      ----------
74      A_trace: ndarray
75          an MxNx3 matrix, where each pixel (along the
76          last dimension) is an RGB triplet (i.e. each entry
77          is an integer between [0,256). The colors each
78          correspond to those in TRACE_COLORS, and (255,255,255)
79          signifies "no vessel". This will normally correspond to
80          the sample's arterial trace.
81      V_trace: ndarray
82          an MxNx3 matrix the same shape and other
83          requirements as A_trace (see above). This will normally
84          correspond to the sample's venous trace.
85      strategy: keyword string
86          when A_trace and V_trace coincide at some entry,
87          this is the merging strategy. It should be a keyword
88          of one of the following choices:
89
90          "minimum": take the minimum width of the two traces
91              (default). this is the sensible option if you
92              are filtering out larger widths.
93          "maximum": take the maximum width of the two traces
94          "artery" or "A" or "top": take the width from A_trace
95          "vein" or "V" or "bottom": take the width from V_trace
96
97      Returns
98      -------
99          W : ndarray
100         a width-matrix where each entry is a number 0 (no vessel), 3,5,7,...19
101
102     Notes
103     -----
104     Since arteries grow over the veins on the PCSVN and are generally easier
105     to extract, it might be preferable to indicate "arteries". In reality,
106     each strategy is a compromise, and only by keeping track of both would
107     you get the complete picture.
108
109     No filtering out widths is done here.
110     """
111     assert A_trace.shape == V_trace.shape
112
113     A = rgb_to_widths(A_trace)
114     V = rgb_to_widths(V_trace)
115
116     # collisions (where are widths both reported)
```

```
    c = (A!=0)& (V!=0)

    W = np.maximum(A,V)  # get the nonzero value
    if strategy == 'maximum':
        pass # already done, else rewrite the collisions
    elif strategy in ('arteries', 'A', 'top'):
        W[c] = A[c]
    elif strategy in ('veins', 'V', 'bottom'):
        W[c] = V[c]
    else:
        if strategy != 'minimum':
            print(f"Warning: unknown merge strategy: {strategy}")
            print("Defaulting to minimum strategy")

        W[c] = np.minimum(A[c], V[c])

    return W

def filter_widths(W, widths=None, min_width=3, max_width=19):
    """
    Filter a width matrix, removing widths according to rules.

    This function will take a 2D matrix of vessel widths and
    remove any widths outside a particular range (or alternatively,
    that are not included in a particular list)

    Should be roughly as easy as doing it by hand, except that you
    won't have to rewrite the code each time.

    Inputs:

    W:  a width matrix (2D matrix with elements 0,3,5,7,...19

    min_width: widths below this will be excluded (default is
                3, the min recorded width). assuming these
                are ints

    max_width: widths above this will be excluded (default is
                19, the max recorded width)

    widths: an explicit list of widths that should be returned.
            in this case the above min & max are ignored.
            this way you could include widths = [3, 17, 19] only
            """

    Wout = W.copy()
    if widths is None:
        Wout[W < min_width] = 0
        Wout[W > max_width] = 0

    else:
        # use numpy.isin(T, widths) but that's only in version 1.13 and up
        # of numpy this is basically the code for that though
        to_keep = np.in1d(W, widths, assume_unique=True).reshape(W.shape)
        Wout[~to_keep] = 0
    return Wout


TRACE_COLORS = {
    3: (255, 0, 111),
    5: (168, 0, 0),
    7: (168, 0, 255),
    9: (255, 0, 255),
    11: (0, 138, 255),
```

```
    13: (138, 255, 0),
    15: (255, 200, 0),
    17: (255, 138, 0),
    19: (255, 0, 21)
}


def widths_to_rgb(w, show_non_matches=False):
    """Convert width matrix back to RGB values.

    For display purposes/convenience. Return an RGB matrix
    converting back from [3,5,7, ... , 19] -> TRACE_COLORS

    this doesn't do any rounding (i.e. it ignores anything outside of
    the default widths), but maybe you'd want to?
    """
    B = np.zeros((w.shape[0], w.shape[1], 3))

    for px, rgb_triplet in TRACE_COLORS.items():
        B[w == px, : ] = rgb_triplet

    if show_non_matches:
        # everything in w not found in TRACE_COLORS will be black
        B[w == 0, : ] = (255, 255, 255)
    else:
        non_filled = (B == 0).all(axis=-1)

        B[non_filled,:] = (255,255,255) # make everything white

    # matplotlib likes the colors as [0,1], so....
    return B / 255.


def _hex_to_rgb(hexstring):
    """
    there's a function that does this in matplotlib.colors
    but its scaled between 0 and 1 but not even as an
    array so this is just as much work

    ##TODO rewrite everything so this is useful if it's not been
    rewritten already.
    """
    triple = hexstring.strip("#")
    return tuple(int(x, 16) for x in (triple[:2], triple[2:4], triple[4:]))


def skeletonize_trace(T, T2=None):
    """
    if T is a boolean matrix representing a trace, then thin it

    if T is an RGB trace, then register it according to the
    tracing protocol then thin it

    if T2 is provided, do the same thing to T2 and then merge the two
    """
    if T.ndim == 3:
        trace = (rgb_to_widths(T) > 0)  # booleanize it
    else:
        trace = T.astype('bool')

    thinned = thin(trace)

    if T2 is None:
        return thinned
```

```
245
246     else:
247         # do the same thing to second trace and merge it
248         if T2.ndim == 3:
249             trace_2 = (rgb_to_widths(T2) > 0)  # booleanize it
250         thinned_2 = thin(trace_2)
251
252         return np.logical_or(thinned, thinned_2)
253
254
255 def confusion(test, truth, bg_mask=None, colordict=None, tint_mask=True):
256     """
257     distinct coloration of false positives and negatives.
258
259     colors output matrix with
260         true_pos if test[-] == truth[-] == 1
261         true_neg if test[-] == truth[-] == 0
262         false_neg if test[-] == 0 and truth[-] == 1
263         false_pos if test[-] == 1 and truth[-] == 0
264
265     if colordict is supplied: you supply a dictionary of how to
266     color the four cases. Spec given by the default below:
267
268     if tint mask, then the mask is overlaid on the image, not replacing totally
269     colordict = {
270         'TN': (247, 247, 247), # true negative
271         'TP': (0, 0, 0) # true positive
272         'FN': (241, 163, 64), # false negative
273         'FP': (153, 142, 195), # false positive
274         'mask': (247, 200, 200) # mask color (not used in MCC calculation)
275         }
276     """
277
278     if colordict is None:
279 #         colordict = {
280 #             'TN': (247, 247, 247),  # true negative# 'f7f7f7'
281 #             'TP': (0, 0, 0),  # true positive  # '000000'
282 #             'FN': (241, 163, 64),  # false negative # 'f1a340' orange
283 #             'FP': (153, 142, 195),  # false positive # '998ec4' purple
284 #             'mask': (247, 200, 200)  # mask color (not used in MCC calculation)
285 #             }
286 #
287         colordict = {
288             'TN': (49,49,49),  # true negative# 'f7f7f7'
289             'TP': (0, 0, 0),  # true positive  # '000000'
290             'FN': (201,53,108),  # false negative # 'f1a340' orange
291             'FP': (0,112,163),  # false positive # '998ec4' purple
292             'mask': (247, 200, 200)  # mask color (not used in MCC calculation)
293             }
294     #TODO: else check if mask is specified and add it as color of TN otherwise
295
296     true_neg_color = np.array(colordict['TN'], dtype='f')/255
297     true_pos_color = np.array(colordict['TP'], dtype='f')/255
298     false_neg_color = np.array(colordict['FN'], dtype='f') /255
299     false_pos_color = np.array(colordict['FP'], dtype='f')/255
300     mask_color = np.array(colordict['mask'], dtype='f') /255
301
302     assert test.shape == truth.shape
303
304     # convert to bool
305     test, truth = test.astype('bool'), truth.astype('bool')
306
307     # RGB array size of test and truth for output
308     output = np.zeros((test.shape[0], test.shape[1], 3), dtype='f')
```

```
309
310     # truth conditions
311     true_pos = (test==truth & truth)
312     true_neg = (test==truth & ~truth)
313     false_neg = (truth & ~test)
314     false_pos = (test & ~truth)
315
316     output[true_pos,:] = true_pos_color
317     output[true_neg,:] = true_neg_color
318     output[false_pos,:] = false_pos_color
319     output[false_neg,:] = false_neg_color
320
321     # try to find a mask
322     if bg_mask is None:
323         try:
324             bg_mask =  test.mask
325         except AttributeError:
326             # no mask is specified, we're done.
327             return output
328
329     # color the mask
330     if tint_mask:
331         output[bg_mask,:] += mask_color
332         output[bg_mask,:] /= 2
333     else:
334         output[bg_mask,:] = mask_color
335
336     return output
337
338
339 def compare_trace(approx, trace=None, filename=None,
340                   sample_dir=None, colordict=None):
341     """
342     compare approx matrix to trace matrix and output a confusion matrix.
343     if trace is not supplied, open the image from the tracefile.
344     if tracefile is not supplied, filename must be supplied, and
345     tracefile will be opened according to the standard pattern
346
347     colordict are parameters to pass to confusion()
348
349     returns a matrix
350     """
351
352     # load the tracefile if not supplied
353     if trace is None:
354         if filename is not None:
355             try:
356                 trace = open_typefile(filename, 'trace')
357             except FileNotFoundError:
358                 print("No trace file found matching ", filename)
359                 print("no trace found. generating dummy trace.")
360                 trace = np.zeros_like(approx)
361         else:
362             print("no trace supplied/found. generating dummy trace.")
363             trace = np.zeros_like(approx)
364
365     C = confusion(approx, trace, colordict=colordict)
366
367     return C
368
369
370 def mcc(test, truth, bg_mask=None, score_bg=False, return_counts=False):
371     """
372     Matthews correlation coefficient
```

```
    returns a float between -1 and 1
    -1 is total disagreement between test & truth
    0 is "no better than random guessing"
    1 is perfect prediction

    bg_mask is a mask of pixels to ignore from the statistics
    for example, things outside the placental plate will be counted
    as "TRUE NEGATIVES" when there wasn't any chance of them not being
    scored as negative. therefore, it's not really a measure of the
    test's accuracy, but instead artificially pads the score higher.

    setting bg_mask to None when test and truth are not masked
    arrays should give you this artificially inflated score.
    Passing score_bg=True makes this decision explicit, i.e.
    any masks (even if supplied) will be ignored, and your count of
    false positives will be inflated.

    """

    true_pos = ((test == truth) & truth)
    true_neg = ((test == truth) & ~truth)
    false_neg = (truth & ~test)
    false_pos = (test & ~truth)

    if score_bg:
        # take the classifications above as they are (nothing is masked)
        pass
    else:
        # if no specified mask, check the test array itself?
        if bg_mask is None:
            try:
                bg_mask = test.mask
            except AttributeError:
                # no mask is specified, we're done.
                bg_mask = np.zeros_like(test)

        # only get stats in the plate
        true_pos[bg_mask] = 0
        true_neg[bg_mask] = 0
        false_pos[bg_mask] = 0
        false_neg[bg_mask] = 0

    # now tally
    TP = true_pos.sum()
    TN = true_neg.sum()
    FP = false_pos.sum()
    FN = false_neg.sum()

    if not score_bg:
        total = np.sum(~bg_mask)
    else:
        total = test.size

    #print('TP: {}\t TN: {}\nFP: {}\tFN: {}'.format(TP,TN,FP,FN))
    #print('TP+TN+FN+FP={}\ntotal pixels={}'.format(TP+TN+FP+TN,total))
    # prevent potential overflow
    denom = np.sqrt(TP+FP)*np.sqrt(TP+FN)*np.sqrt(TN+FP)*np.sqrt(TN+FN)

    if denom == 0:
        # set MCC to zero if any are zero
        m_score =  0
    else:
        m_score = ((TP*TN) - (FP*FN)) / denom

```

```
437     if return_counts:
438         return m_score, (TP,TN,FP,FN)
439     else:
440         return m_score
441 
442 
443 def mean_squared_error(A,B):
444     """
445     get mean squared error between two matrices of the same size
446 
447     input:
448         A, B : two ndarrays of the same size.
449 
450     output:
451 
452         mse:   a single number.
453     """
454 
455     try:
456         mse = ((A-B)**2).sum() / A.size
457 
458     except ValueError:
459         print("inputs must be of the same size")
460         raise
461 
462     return mse
463 
464 def chain_lengths(iterable):
465 
466     pos, s = 0, 0
467 
468     for b, g in itertools.groupby(iterable):
469 
470         if not b:
471             # alternative if the bottom doesn't work or something
472             #d = deque(enumerate(g,1), maxlen=1)
473             #pos += d[0][0] if d else 0
474 
475             pos += sum((1 for i in g if not i))
476 
477         else:
478 
479             s = sum(g)
480 
481             yield pos, s
482 
483             pos += s
484 
485     if not s:
486         # so it will return something even if iterable is empty
487         yield 0, 0
488 
489 
490 def _longest_chain_1d(iterable):
491     """ will return a tuple of ind, length
492     where ind is the position in the iterable the chain starts and length is the
493     length of the chain
494     """
495     return max(chain_lengths(iterable), key=lambda x: x[1])
496 
497 
498 def longest_chain(arr, axis):
499     """Find where the longest chain of boolean values and occurs across an array
500     and also return its length
```

```
    """

    C = np.apply_along_axis(_longest_chain_1d, axis, arr.astype('bool'))

    start_inds, chain_lens =  np.split(C, 2, axis)

    return np.squeeze(start_inds), np.squeeze(chain_lens)


if __name__ == "__main__":

    import matplotlib.pyplot as plt
    from skimage.data import binary_blobs

    A = binary_blobs()
    B = binary_blobs()

    true_neg_color = np.array([247,247,247], dtype='f') # 'f7f7f7'
    true_pos_color = np.array([0, 0, 0] , dtype='f')  # '000000'
    false_neg_color = np.array([241,163,64], dtype='f')# 'f1a340'
    false_pos_color = np.array([153,142,195], dtype='f') # '998ec4'

    C = confusion(A,B)

    fig, (ax0, ax1, ax2) = plt.subplots(nrows=1,
                                        ncols=3,
                                        figsize=(8, 2.5),
                                        sharex=True,
                                        sharey=True)

    ax0.imshow(A, cmap='gray')
    ax0.set_title('A')
    ax0.axis('off')
    ax0.set_adjustable('box-forced')

    ax1.imshow(B, cmap='gray')
    ax1.set_title('B')
    ax1.axis('off')
    ax1.set_adjustable('box-forced')

    ax2.imshow(C)
    ax2.set_title('confusion matrix of A and B')
    ax2.axis('off')
    ax2.set_adjustable('box-forced')

    fig.tight_layout()
```

listings/signed_sweep_demo.py

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

from placenta import (get_named_placenta, list_placentas, _cropped_bounds,
                      cropped_view, cropped_args, show_mask)
from frangi import frangi_from_image

import numpy as np
import numpy.ma as ma

from plate_morphology import dilate_boundary

import os.path
import matplotlib.pyplot as plt
```

```
import matplotlib as mpl
from itertools import product

# pick two samples and two insets (should be the same size)
demo1 = 'BN2315363', np.s_[370:670, 530:930]
demo2 = 'BN5280796', np.s_[150:450, 530:930]

for sample_name, inset_slice in (demo1, demo2):
    img = get_named_placenta(f'T-{sample_name}.png')

    crop = cropped_args(img)

    F, fi = list(), list() # make some empty lists to store for inspection

    #scales = np.logspace(-3, 4, num=8, base=2)
    scales = [0.2, 0.8, 1.0, 2.0, 4.0, 6.0, 8.0, 16.0]
    CMAP = plt.cm.Spectral
    cmin, cmax = (-0.4, 0.4)

    for n, sigma in enumerate(scales):
        R = max(int(sigma*3), 10)
        target = frangi_from_image(img, sigma, dark_bg=False,
                                   signed_frangi=True, dilation_radius=R)
        plate = target[crop].filled(0)
        inset = target[inset_slice].filled(0)
        F.append(plate)
        fi.append(inset)
        #for label in ['plate', 'inset']:
        #    if label == 'inset':
        #        printable = inset
        #    else:
        #        printable = plate

        #    plt.imshow(printable, cmap=CMAP)
        #    plt.title(r'$\sigma={:.2f}$'.format(sigma))
        #    plt.tight_layout()
        #    c = plt.colorbar()
        #    c.set_ticks = np.linspace(cmin, cmax, num=len(scales)+1)
        #    plt.clim(cmin, cmax)
        #    plt.axis('off')
        #    outname = f'demo_output/signsweep_{sample_name}_{label}_{n}.png'
        #    #plt.savefig(outname, dpi=300, bbox_inches='tight')
        #    print('saved', outname)
        #    plt.close()

    # now make a stitched together version
    for label in ['plate', 'inset']:
        if label == 'inset':
            L = fi
            imgview = img[inset_slice].filled(0)
            figsize = (12, 6)

        else:
            L = F
            imgview = img[crop].filled(0)
            figsize = (12, 9)
        #adjust this manually depending on how many scales you end up using!

        nrows, ncols = 2, 4
        fig, axes = plt.subplots(nrows=nrows, ncols=ncols, figsize=figsize)

        for n, (i, j) in enumerate(product(range(nrows), range(ncols))):

            if n == 0:
```

```
                axes[i,j].imshow(imgview, cmap=plt.cm.gray)
                axes[i,j].set_title('raw')
            else:
                im = axes[i,j].imshow(L[n], cmap=CMAP, vmin=cmin, vmax=cmax)
                axes[i,j].set_title(r'$\sigma={:.2f}$'.format(scales[n]))

            plt.setp(axes[i,j].get_xticklabels(), visible=False)
            plt.setp(axes[i,j].get_yticklabels(), visible=False)

        #for i in range(5):
        #    fig.tight_layout()

        #fig.subplots_adjust(right=0.8)
        #cax = fig.add_axes([.85,.15,.05,.7])
        #c = fig.colorbar(im, ax=cax)

        fig.subplots_adjust(top=0.954, bottom=0.025, left=0.010,
                            right=0.989, hspace=0.0, wspace=0.0)

        plt.savefig(f'demo_output/signsweep_stitch_{sample_name}_{label}.png',
                    dpi=300)

        cfile = 'demo_output/signsweep_colorbar.png'
        if os.path.isfile(cfile):
            continue # no need to make another

        fig = plt.figure(figsize=(figsize[0],2))
        ax1 = fig.add_axes([0.15, 0.25, 0.75, 0.5])
        cbar = mpl.colorbar.ColorbarBase(ax1, cmap=CMAP,
                                         norm=mpl.colors.Normalize(cmin,cmax),
                                         orientation='horizontal')
        plt.savefig(cfile, dpi=300)
        #top = np.concatenate(L[:4],axis=1)
        #bottom = np.concatenate(L[4:],axis=1)
        #stitched = np.concatenate((top,bottom),axis=0)
        #imga = plt.imshow(stitched, cmap=CMAP)
        #plt.imsave(f'demo_output/signsweep_stitch_{sample_name}_{label}.png',
        #        stitched, cmap=CMAP, vmin=cmin, vmax=cmax)

        # also save the original pic
        #plt.imsave(f'demo_output/signsweep_{sample_name}_{label}_raw',
        #        imgview, cmap=plt.cm.gray)
```

APPENDIX B

3D VISUALIZATION OF THE FRANGI FILTER

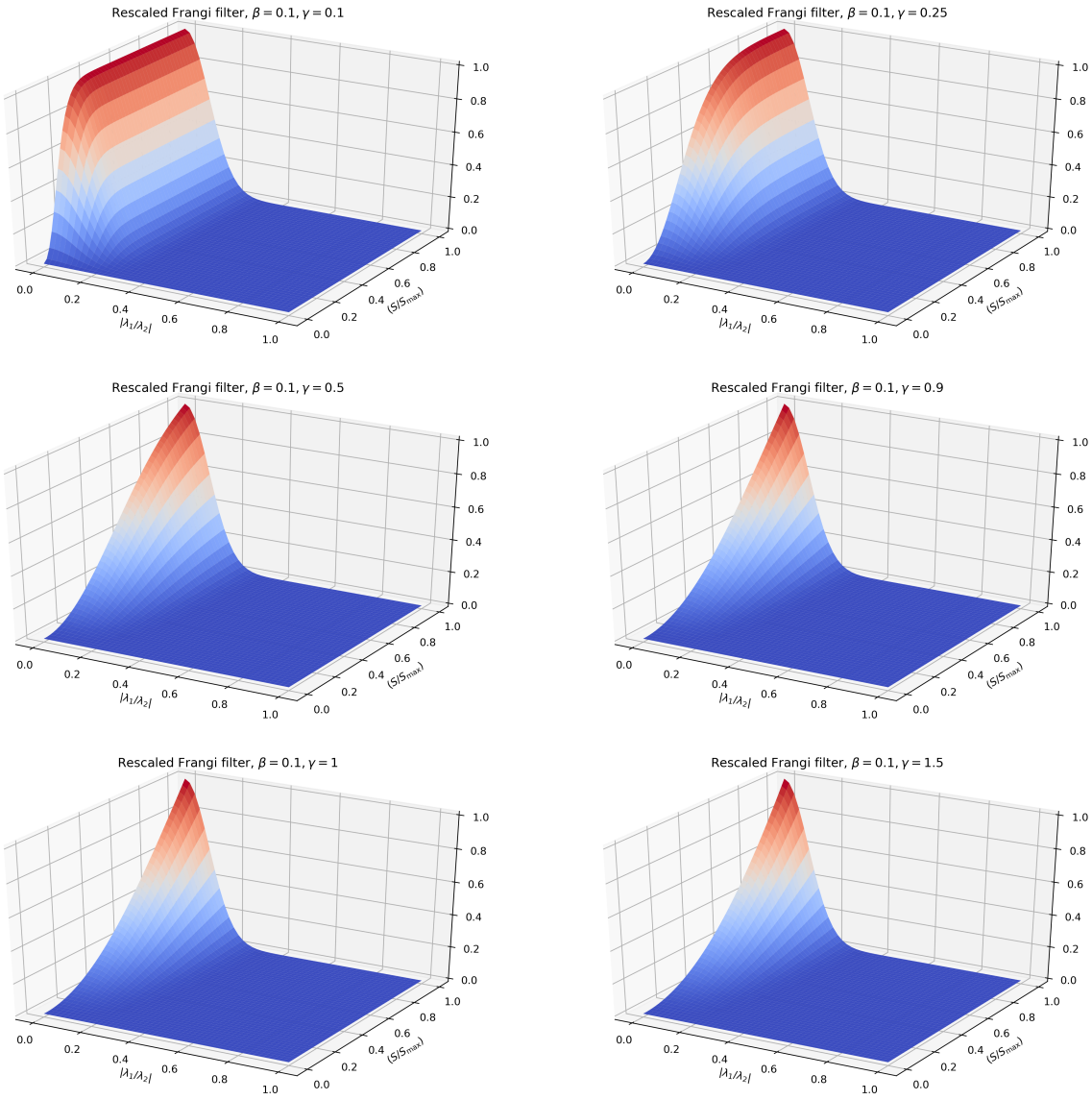


FIGURE 27: 3D graph of the Frangi Vesselness Measure, variable γ, $\beta = 0.1$

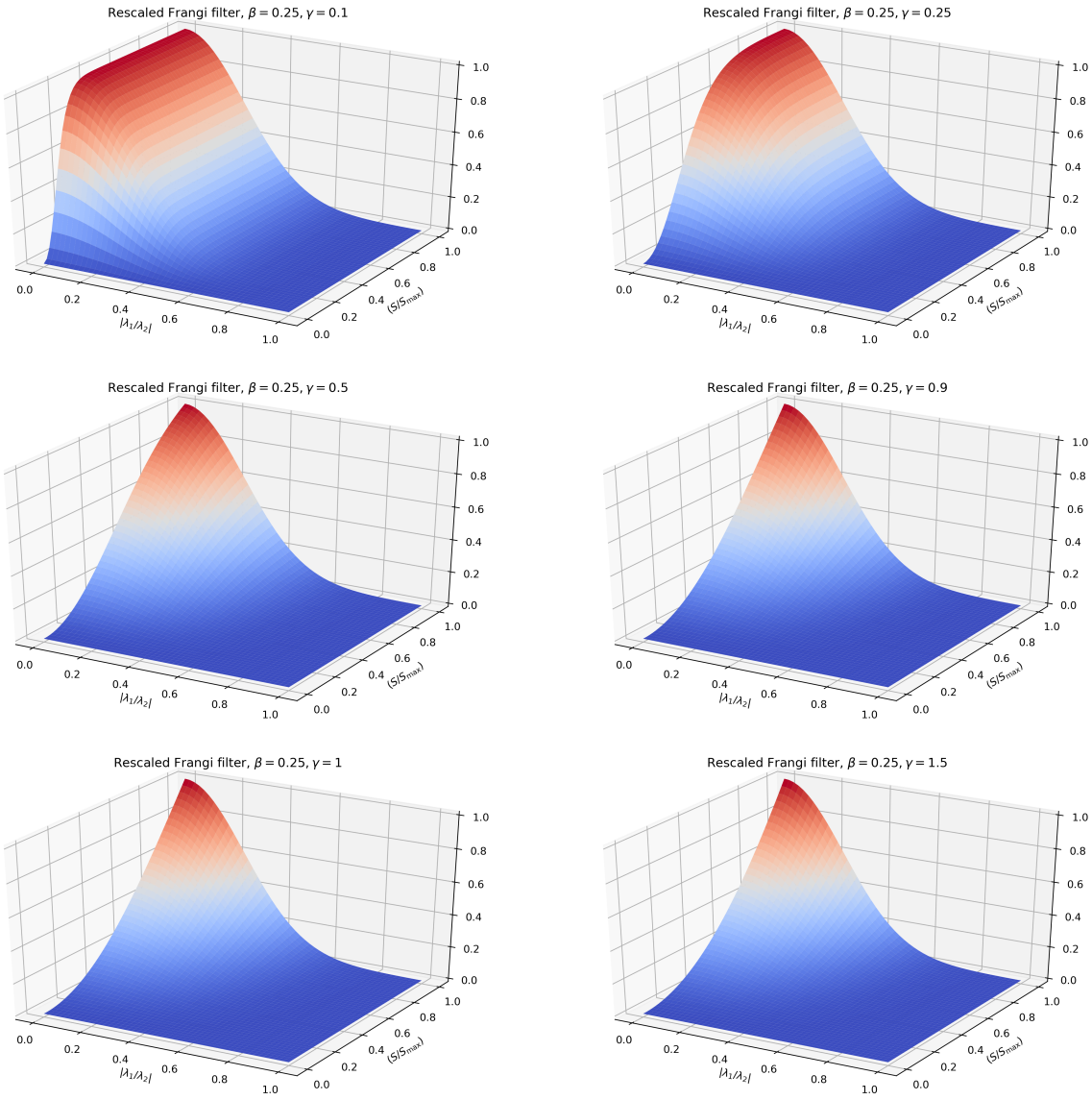


FIGURE 28: 3D graph of the Frangi Vesselness Measure, variable γ, $\beta = 0.25$

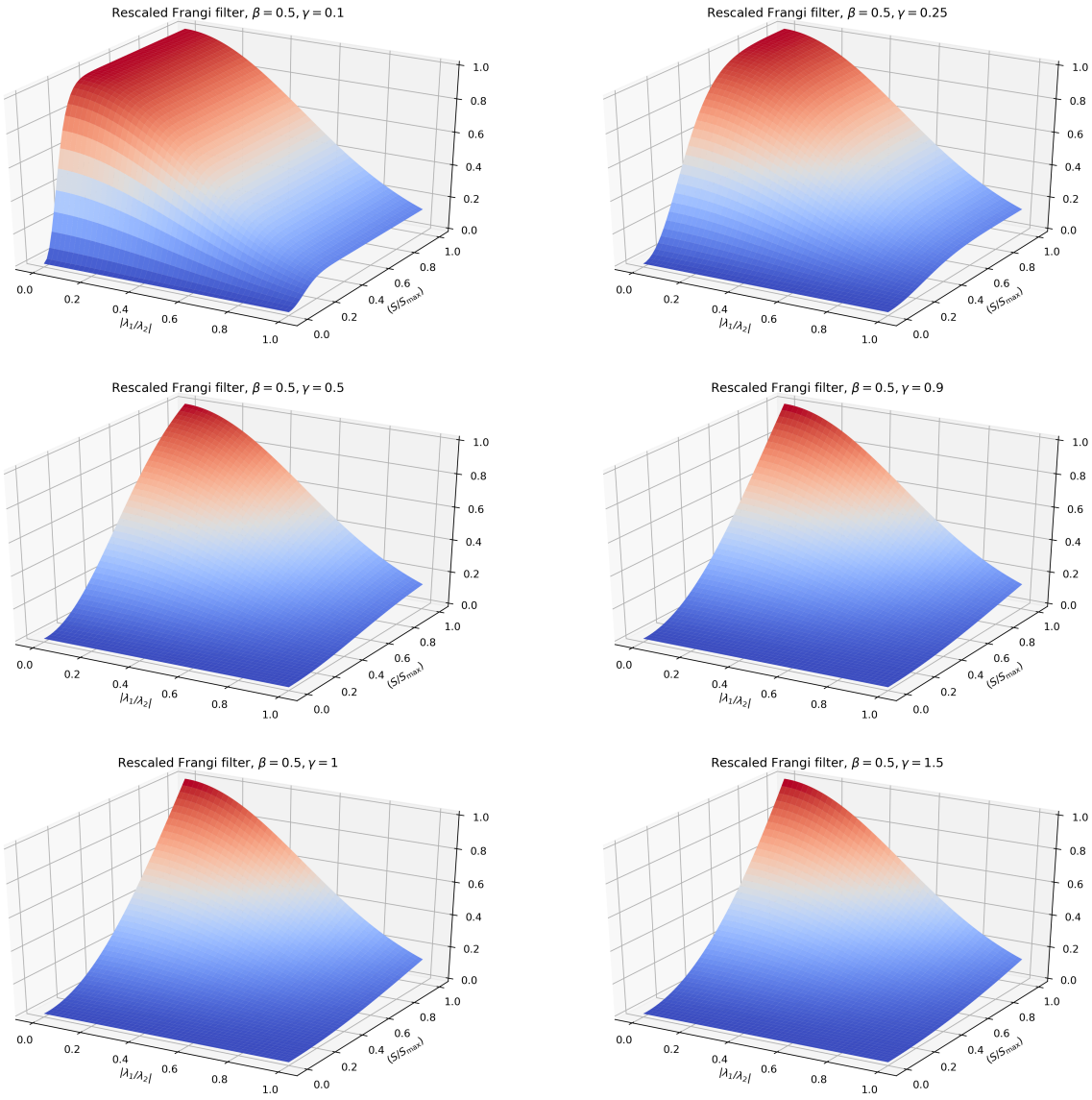


FIGURE 29: 3D graph of the Frangi Vesselness Measure, variable γ, $\beta = 0.5$

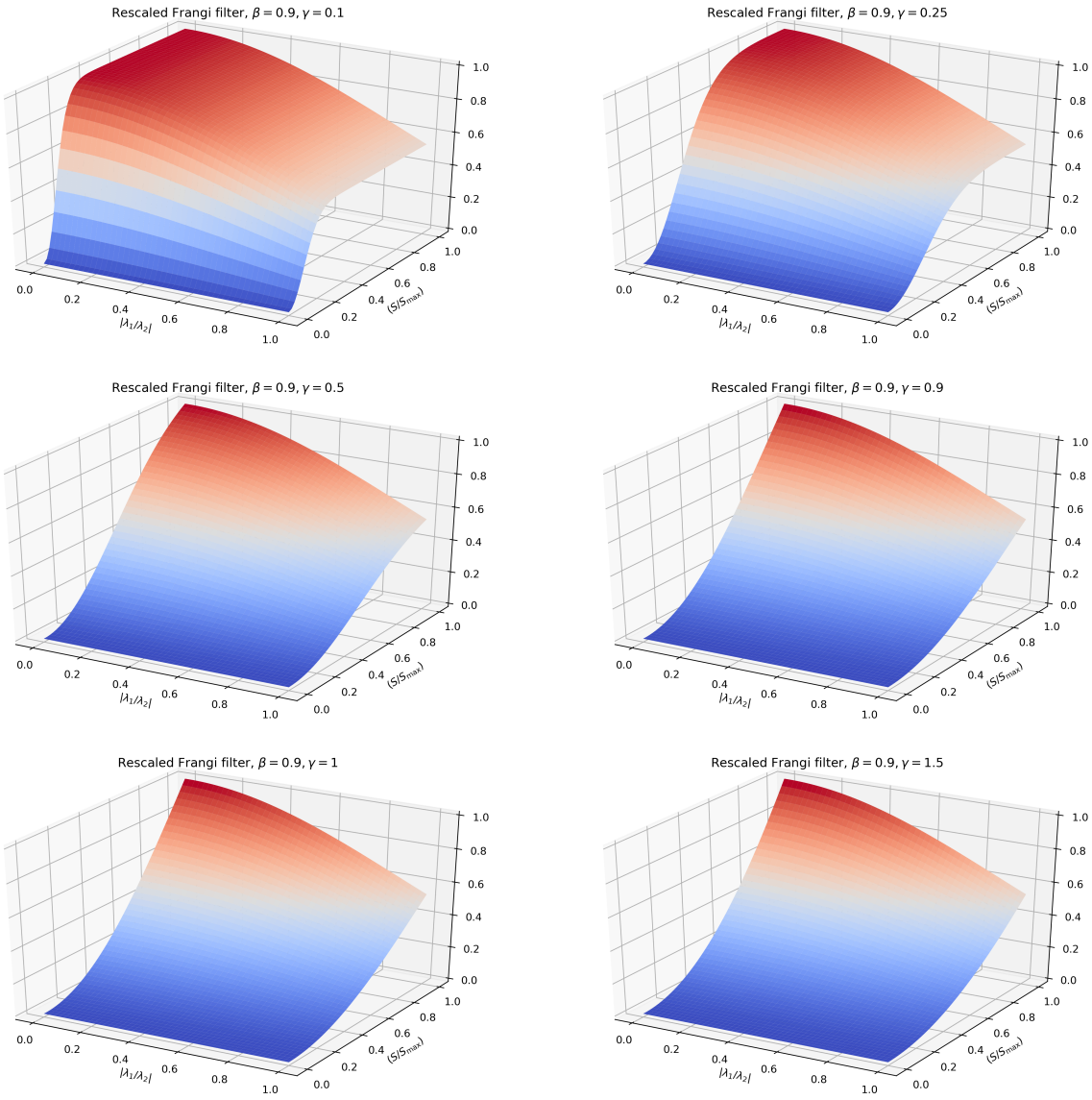


FIGURE 30: 3D graph of the Frangi Vesselness Measure, variable γ, $\beta = 0.9$

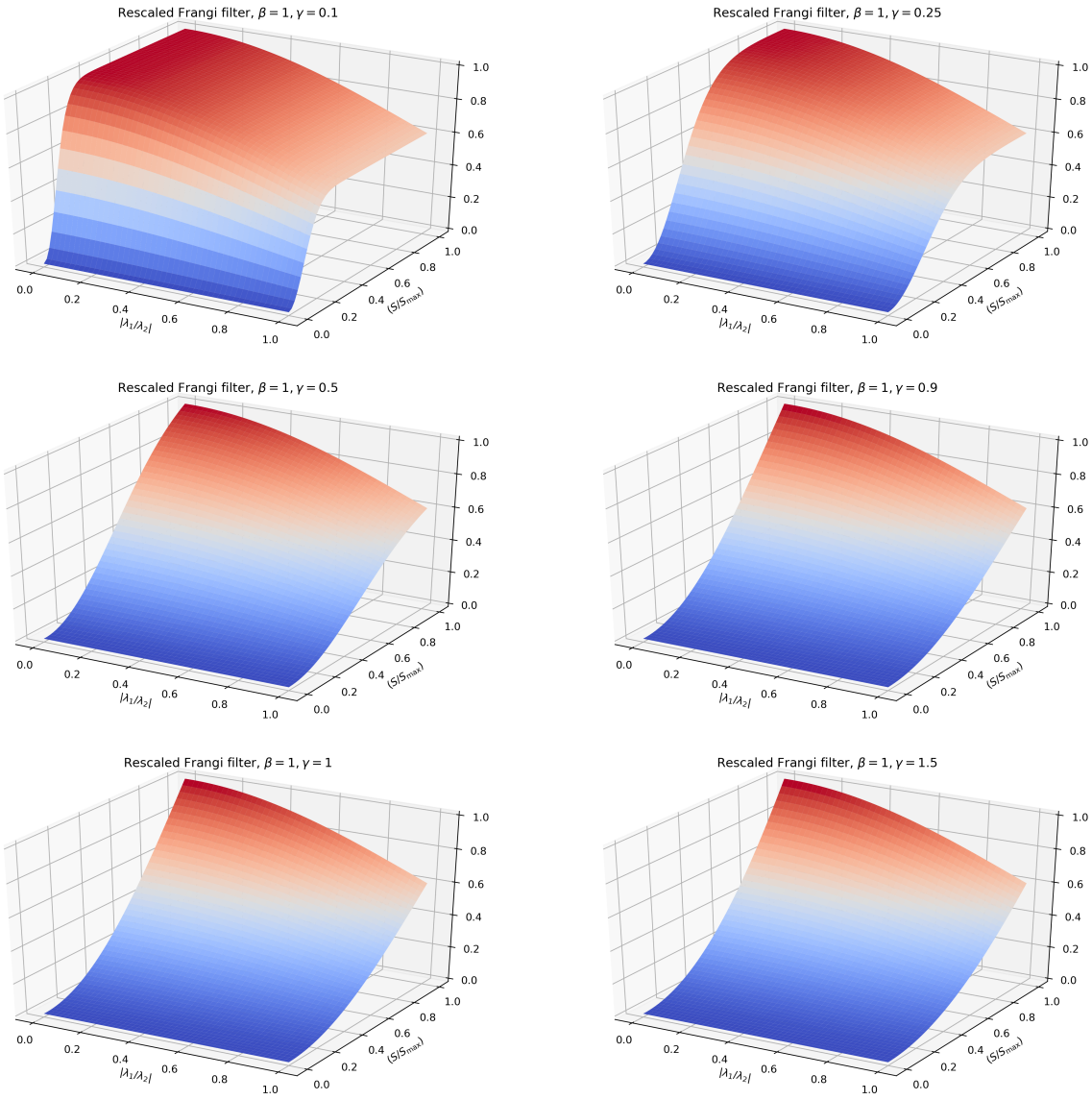


FIGURE 31: 3D graph of the Frangi Vesselness Measure, variable γ, $\beta = 1$

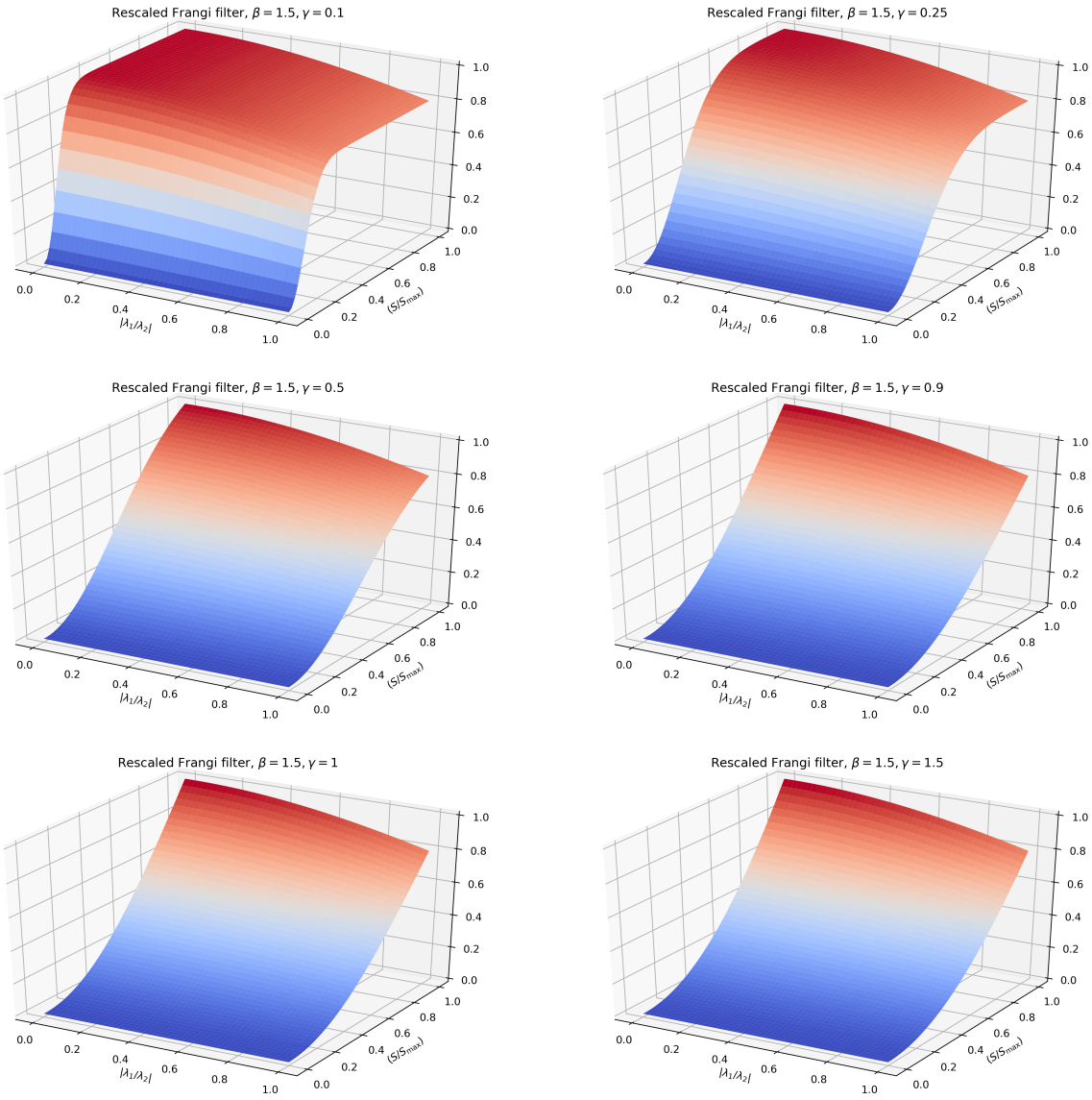


FIGURE 32: 3D graph of the Frangi Vesselness Measure, variable γ, $\beta = 1.5$

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BIBLIOGRAPHY

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