Realistic Skin Model (RSM)

BIO Toolkit interactive script for ASAP

This technical publication describes how to use the tissue phantom, Realistic Skin Model™ (RSM™), a BIO Toolkit™ interactive script for the Advanced Systems Analysis Program (ASAP®) from Breault Research Organization (BRO). The RSM is used to create realistic tissue phantoms for analysis in an optical system.

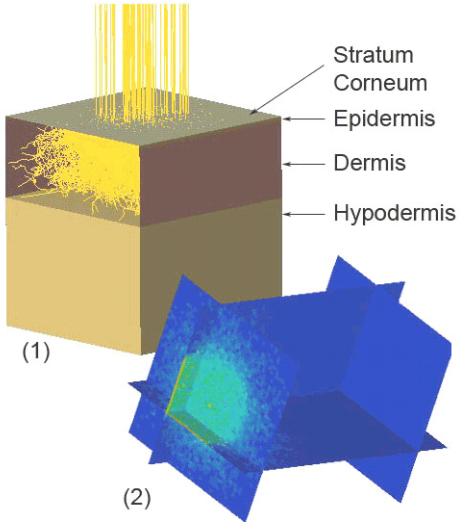

Figure 1 Examples of 3D trace rendering (1), and voxel representation of fluence (2) in the Realistic Skin Model (RSM) in ASAP, at a wavelength of 550nm.

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Using a proprietary scatter and absorption model developed by BRO, the RSM accurately replicates the absorption and scattering properties of human skin. The major chromophores of skin—melanin, hemoglobin, and water—are all represented within the model, along with lesser contributors such as bilirubin and beta carotene. The absorption and scatter characteristics of each layer of tissue are calculated independently, taking into account the different chromophore concentrations in each layer. The flexibility of being able to vary the concentrations for different chromophores allows you to model a vast array of skin conditions.

The RSM program is dialog-driven, allowing as much or as little control over the modeling process as you want. A single tissue phantom can be created and placed within an existing optical system with ease, or the entire trace and analysis process can be accomplished from the RSM dialogs.

This publication details the features inherent in the design of the RSM, including background information and relevant default characteristics of the model, and dialog options.

BACKGROUND

The skin is one of the most complex and dynamic organs of the human body. It is our environmental barrier, thermal regulator, and water retention system. Skin can be weathered by age, transformed by disease, and marred by genetics. Modeling of the skin in any accurate manner is necessarily complex, and no model can completely encompass all factors involved. The RSM takes into account as many biologically relevant aspects of the human skin as is feasible. The result is to produce a model that is both comprehensive and time-efficient for ray tracing.

RSM volume scatter model

To model the scattering properties of the skin, the RSM uses the built-in volumetric scattering model in ASAP that adopts the Henyey-Greenstein approximation for the angular distribution of scattered light. Four parameters are required to create this model: the anisotropy factor (g), the scattering coefficient (μ_s), the absorption coefficient (μ_a), and the fractional obscuration per unit area (f). In general, the anisotropy factor (g), the scattering coefficient (μ_s), and the absorption coefficient (μ_a) are wavelength (λ) dependent.

Anisotropic Factor (g)

The anisotropy factor (g) is the average directional cosine of the scattered light in the random medium, and varies from -1 (complete backscatter) to 1 (complete forward scatter). Most biological tissues have g values in the range of 0.7 to 0.9.

Scatter Coefficient (μ_s)

The scatter coefficient for tissue is a measure of the probability that a scatter event occurs. This value has units of inverse length. The RSM uses bulk scatter coefficients to describe the scattering properties of the skin tissues. The wavelength-dependent scatter coefficient in RSM is extracted using published data on skin tissue scattering properties.

Absorption Coefficient (μ_a)

Similar to the scatter coefficient, the absorption coefficient defines the probability of a photon absorption event, and has units of inverse length.

Fractional Obscuration per Unit Area (f)

If we consider the scattering medium as an aggregate of particles, the fractional obscuration per unit area (*f*) is defined as the product of the particle number density (number of particles per unit volume) and the average particle cross-sectional area. The *f* value is approximately equal to the inverse mean free path length of the medium. Conversely, if we are concerned with only the bulk optical properties of the medium, and use the bulk absorption and scattering coefficients to describe such optical properties, the *f* value is normalized to be one (see the topic, "VOLUME (ASAP Command)" in ASAP Help for a better understanding of this subject). In the RSM, since the bulk absorption and scattering coefficients are used, the *f* value is set to one.

Modeled chromophores

Chromophores that were modeled within the RSM are listed in Table 1, along with corresponding layers that contain these chromophores.

Table 1 Chromophores modeled with the RSM

Chromophore	Sub-category	Stratum Corneum	Epidermis	Dermis
Water		X	X	X
Melanin				
	Eumelanin		X	
	Pheomelanin		X	
Hemoglobin				
	Deoxyhemoglobin			X
	Oxyhemoglobin			X
Beta Carotene		X	X	X
Bilirubin			X	X
Protein		X	X	X

The absorption curves for the different chromophores are presented in Figure 2.

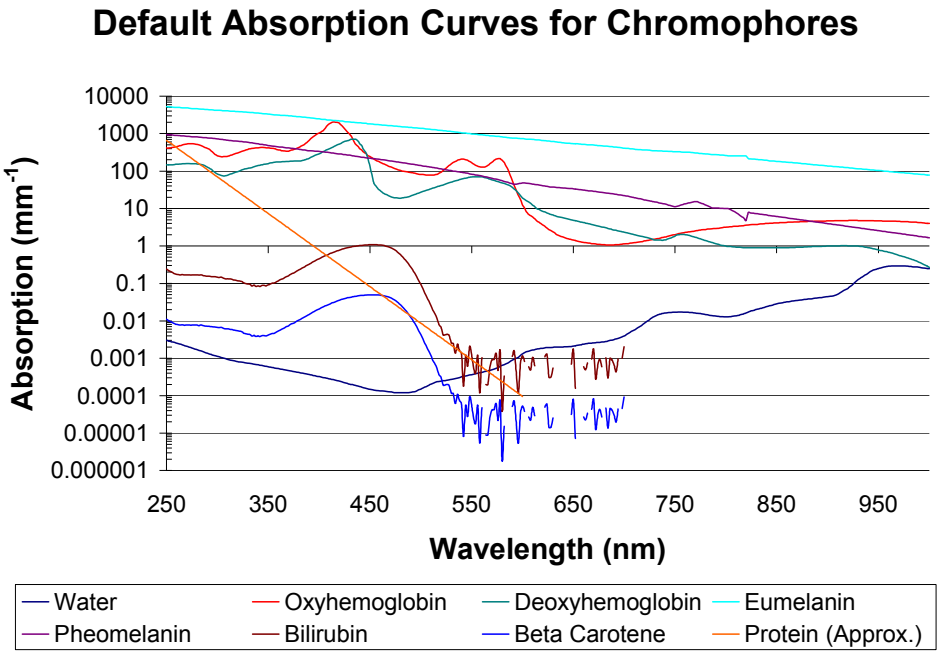


Figure 2 Absorption for chromophores (Protein absorption is approximate)

GETTING STARTED

Installing RSM

To install the Realistic Skin Model in ASAP, you must have ASAP and the BIO Toolkit.

1. Install ASAP on your machine if you have not already done so. Do not open ASAP.
2. Install the BIO Toolkit from the BIO Toolkit installation disc, and enter the provided password if requested. *The BIO Toolkit installer also adds links to the Knowledge Base for documentation under Start> Programs>ASAP BIO Toolkit> Documentation> RSM.*
3. Open ASAP from the Start menu under Programs> ASAP or from the desktop icon.
4. See "Running an interactive script" on page 6.

The Quick Start toolbar is usually on the right of the ASAP window (Figure 3). If it is not in view, select **Quick Start Bar** from the View menu. For descriptions of the ASAP interface, see ASAP Help (Help> Contents).

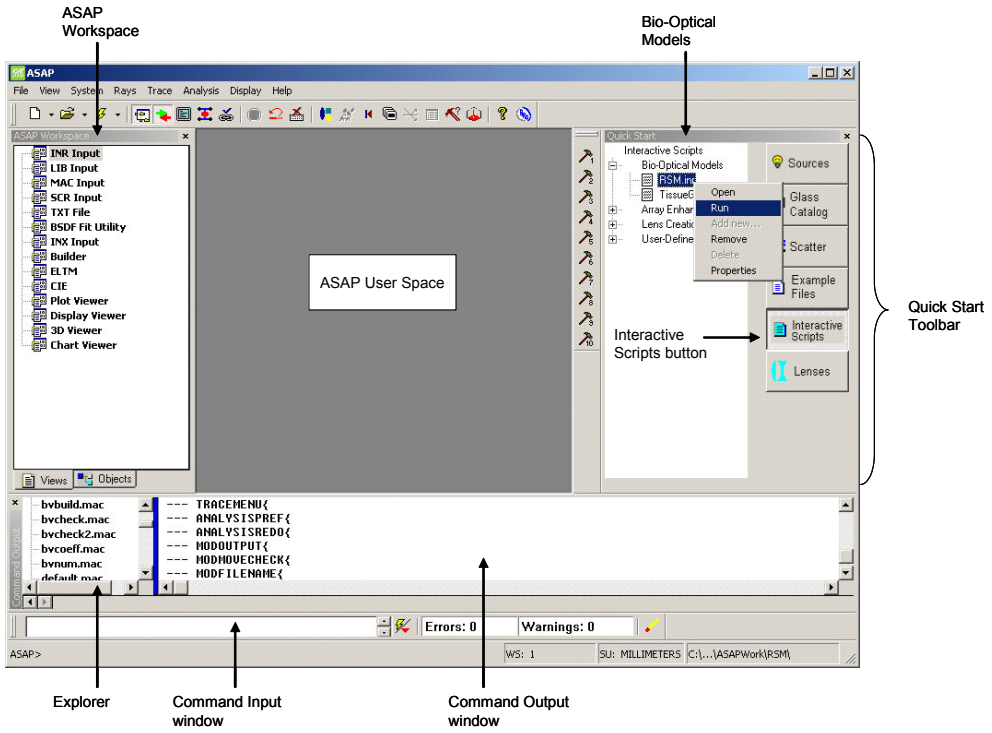


Figure 3 ASAP Window with open Quick Start toolbar on right

Running an interactive script

1. Select the script file, **rsm.inr** from the tree view of the Interactive Scripts page, under Bio-Optical Models.
2. Double-click the script file, or right-click the file and select **Run** on the menu.

The file opens and runs in the ASAP Editor window in the user space area of ASAP.

Uninstalling the ASAP BIO Toolkit

- To uninstall the ASAP BIO Toolkit, open the Start menu and select Programs> ASAP BIO Toolkit> Uninstall BIO Toolkit.

CAUTION ***Whenever you upgrade ASAP, the BIO Toolkit must be re-installed. Upgrading ASAP or uninstalling the BIO Toolkit for ASAP deletes any user-defined script files specific to the RSM. Before you upgrade or uninstall, move these files to a different folder if you want to save them. Uninstalling the BIO Toolkit also removes* Bio-Optical Models *from the Interactive Scripts page on the Quick Start toolbar in ASAP.***

SKIN MODELING

Now you can start defining your model by selecting options in the RSM dialogs. Each dialog includes a set of buttons (Table 2) in the lower section: **OK**, **Cancel**, **Restore**, **Help**, and **Print**. Some of the figures shown in this technical publication omit these buttons.

Table 2 RSM Dialog Buttons

OK	Select to accept your selections and continue.
Cancel	Close the RSM without saving selections.
Restore	Re-apply default settings to the dialog.
Help	Opens help topic for the active dialog, and describes the purpose of each option. NOTE: While ASAP Help does not include topics specific to the BIO Toolkit, it does include topics on all aspects of the ASAP user interface and ASAP commands.
Print	Prints the dialog.

In the Model Initiation dialog (Figure 4), you select the Sample, Source, and Analysis options for the modeling process. See Table 3 for descriptions of the settings.

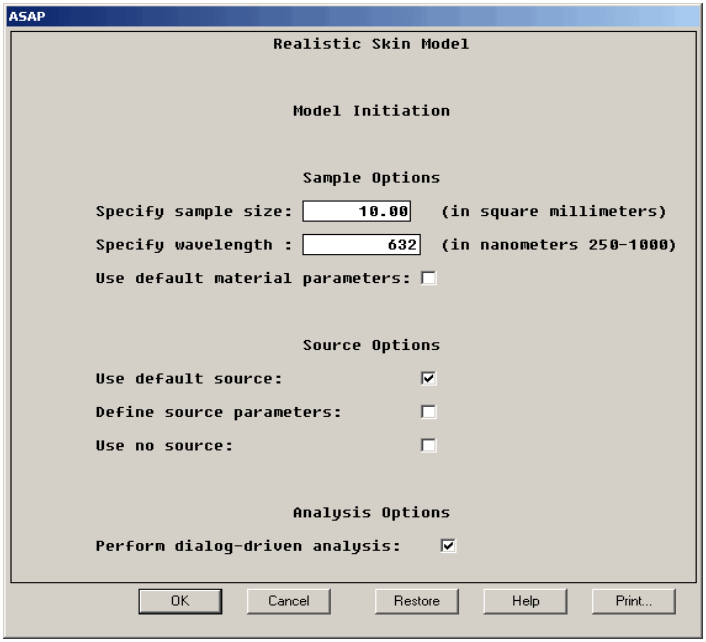


Figure 4 Model Initiation dialog—specify sample, source, and analysis options.

Table 3 Initiation Settings

Sample Options:	
Specify sample size	The sample size must be non-zero (default: 10mm^2) and in square millimeters. The sample created always has a square surface area, with length and width equal to the square root of the sample size.
Specify wavelength	Enter a source wavelength between 250 and 1000nm (default: 633nm), which is essential to the creation of the skin model. The RSM calculates the scatter and absorption characteristics for each skin layer based on wavelength-dependent chromophore properties. Even if a source created outside of the RSM interface is used, the desired source wavelength must be entered.
Use default material parameters	Select this option if the desired characteristics of the skin model are unknown. Select Help to view the defaults. This option creates an “average” skin model, using baseline chromophore concentrations as quantified in detail in published literature. If selected, the skin model is created using default parameters that represent the average skin. Deselect this option to define the tissue properties manually. If it is deselected, the RSM displays the dialog, Model Creation, as shown in Figure 5.
Source Options:	

Table 3 Initiation Settings

Use default source	When this option is selected, the dialog for specifying source parameters is displayed for number of rays and total flux.
Define source parameters	Provides greater control over the source creation process. You can specify the geometrical shape of the source, the radiant emittance profile, incident angle of the radiation, and other source parameters.
Use no source	If this option is selected, the RSM skips the remaining source and analysis process. You can output the sample model and incorporate it into other ASAP optical analysis code to perform further raytracing and analysis. Note: the wavelength of the intended source must be input or the model will not function correctly.
Analysis Options:	
Perform menu driven analysis	When the ray tracing is complete, the RSM provides dialogs for you to specify parameters for analysis.

Sample

Overview on parameter input for skin sample modeling

As shown in Figure 4 on page 8, the third entry under the Sample Options section asks if you want to use the default parameters for your sample. If this option is selected, the skin model is created using default parameters that represent average skin. If this option is deselected, the RSM displays the Sample Creation dialog (Figure 5), which gives you three ways to specify parameters for the skin model.

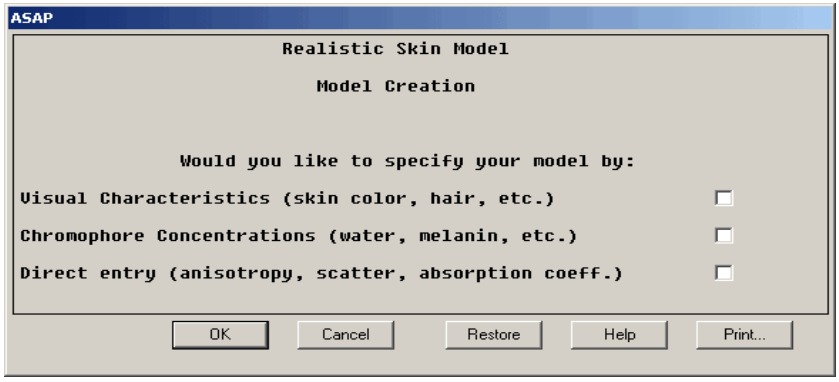


Figure 5 Model Creation dialog—specify the RSM using visual characteristics, chromophore concentrations, or direct entry of coefficients

Visual characteristics: When general characteristics of the skin are known, the visual characteristics option is recommended. The Skin Type Selection dialog (Figure 6) provides options for the skin color of the sample, so that a more realistic model can be created without detailed information.

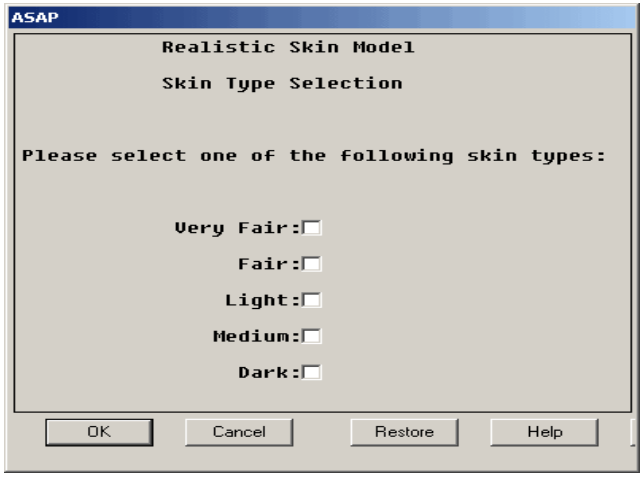


Figure 6 Skin Type Selection—select skin color of the sample

Chromophore concentrations: If you selected **Chromophore Concentrations** in the Model Creation dialog (Figure 5 on page 9), you can alter nearly every aspect of the optical properties of the skin model by changing the amount of chromophores present in the skin. When this option is selected, a series of dialogs are displayed for your input of parameters of different layers selected to model. This method is discussed in "Detailed description on parameter input options—Chromophore Concentrations and Direct Entry" on page 20.

Direct entry: This option allows you to specify the model parameters using the bulk optical properties of the skin tissues— the bulk absorption coefficient, bulk scattering coefficient, and anisotropy factor. For a more detailed explanation on this method, see "Direct entry" on page 29.

Layer Selection

After specifying the preferred method for parameter input, the RSM displays the dialog to select layer or layers to model (Figure 7). You can model individual layers as well as multi-layered tissue. For multiple layers, all tissue layers must be continuous. For example, to model the stratum corneum and dermis, the epidermis must be modeled. The model automatically adjusts so that the surface of the first modeled layer is located at the origin.

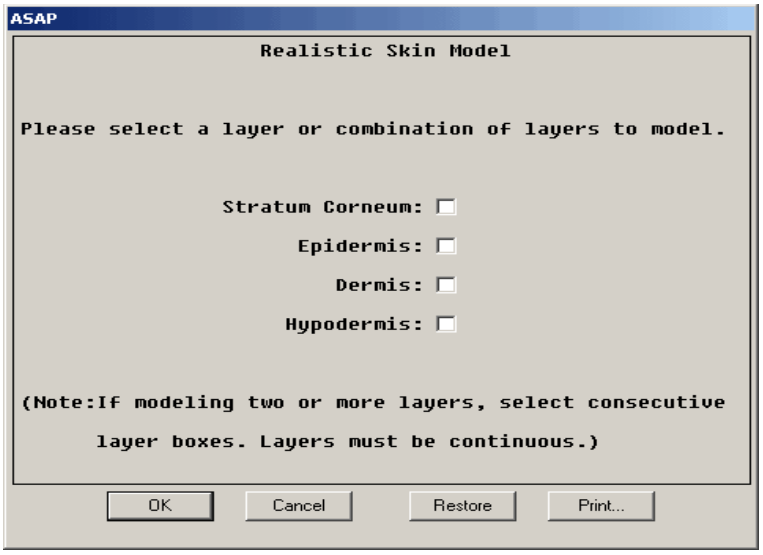


Figure 7 Layer dialog—select one or more layers to model

Dermal Modeling

The RSM provides two methods for modeling the dermis:

- Two-layer dermis: the dermis is sub-divided into the papillary and reticular dermis, which is a more detailed dermis model.
- Single-layer dermis: a bulk approximation of the dermis.

The two-layer model—available only if the epidermis is also modeled—also provides modeling of the dermal papillae, or interdigitation between the epidermis and papillary dermis. If the epidermis and dermis were selected in the Layer Selection dialog (Figure 7), the Dermal Modeling dialog (Figure 8) is displayed.

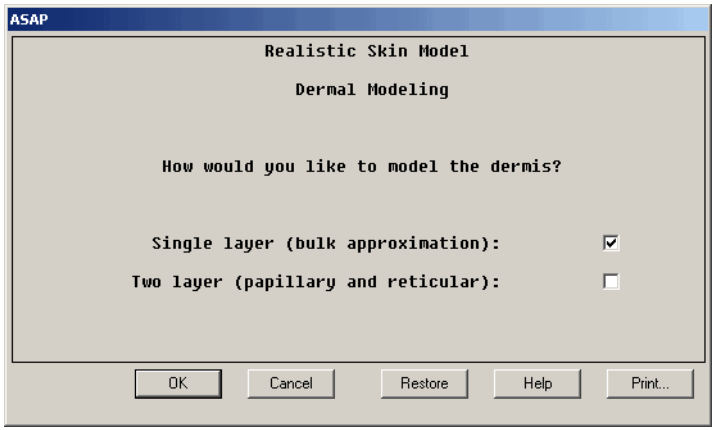


Figure 8 Dermal Modeling dialog—model the dermis as either a single layer or two separate layers

Currently, the dermal papillae, hair, and blood vessel models in the RSM modeling system cannot be combined. If the single layer option is selected, the Hair Modeling dialog (Figure 9) is displayed. If the two-layer model is selected, the hair and blood vessel modeling dialogs are not displayed. See “Appendix” on page 56 for allowed combinations on modeling hair, blood vessel, or dermal papillae according to layer selection.

Hair Modeling

The hair modeling option (Figure 9) is another feature in the RSM that can be integrated with the skin model. In general, the absorption properties of hair are determined by the concentrations of chromophores, such as eumelanin and pheomelanin in the hair, and are therefore dependent on hair color. In the current version of the RSM, only the contribution of eumelanin to hair absorption is considered, while the effect of other chromophores, such as pheomelanin, is ignored. The default eumelanin concentrations for hair of different colors are set to be the mid-value of the possible ranges of concentration, as published in literature. Also, the scatter model applied to each hair in the current version of the RSM is an approximation.

Figure 9 Hair Modeling dialog—select whether or not to model hair with your skin sample

Select **No** if no hair exists. If you select **Yes**, the Hair Model Creation Settings dialog (Figure 10) is displayed. See Table 4 for descriptions of the settings.

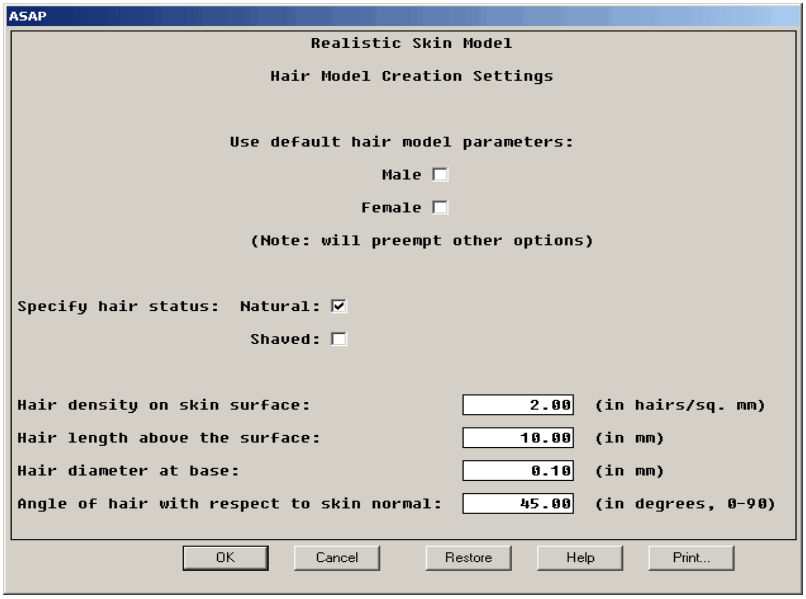


Figure 10 Hair Model Creation Settings dialog—select settings for hair model creation

Table 4 Hair Model Creation Settings

Male/Female hair option	When choosing this option, the hair is modeled using default values for all parameters, except hair length, for both sexes. Vellus hair—the hair found over most of the human body—is, on average, longer for males than females. Hair length for either sex defaults to the mid-value of the possible ranges for the two sexes found in published literature. The default values of other parameters—hair density, hair diameter, and angle of hair—are shown in the lower part of the dialog. Once the Male/Female hair option is selected, the RSM ignores any changes made to these three parameters.
Specify hair status: Natural/Shaved	This option allows the selection of modeling the hairs as either naturally protruding above the skin surface, or shaved off at the surface of the stratum corneum. Usually, light-based treatments are used on an area of skin that has been shaved to reduce scattering from hairs above the skin surface.
Hair density on skin surface	Enter the number of hairs per square millimeter. The actual number of hairs created in your skin model depends on the sample size.
Hair length above the surface	Enter the length (in millimeters) as measured from the surface of the stratum corneum. Hair length may differ from the height of the hair above the surface if the hair is tilted at an oblique angle with respect to the skin normal.

Table 4 Hair Model Creation Settings

Hair diameter at base	Enter the base diameter of the hair (in millimeters). Hairs are considered as cones, tapered to a point at a constant rate from base to tip. Thickness is determined by hair diameter at the base.
Angle of hair with respect to skin normal	The RSM allows for a wide range of hair growth angles, although some of them may not be biologically relevant. Cautiously set this parameter to an angle that makes sense. All hair does not grow straight out of the skin—it grows at an oblique angle with respect to the skin normal.

After setting the modeling parameters, you must select a hair color (Figure 11), which determines the level of light absorption in the hair shaft.

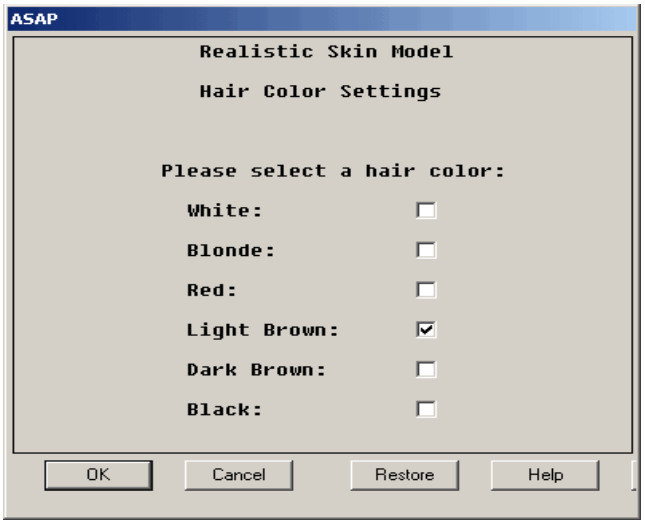


Figure 11 Hair Color Settings dialog—select hair color

BLOOD VESSEL MODELING

The blood vessel model is another feature supported by the RSM, which can be activated in the Blood Vessel Modeling dialog (Figure 12). The RSM provides a basic modeling of blood vessels as layers of blood-filled tubes just under the dermo-epidermal junction. The number of vessels can be specified using the subsequent Blood Vessel Modeling dialog (Figure 13). The RSM automatically scales the diameter of the vessels to fit within the geometrical constraint of the model. The maximum blood vessel length and diameter are displayed on the Blood Vessel Design dialog (Figure 14).

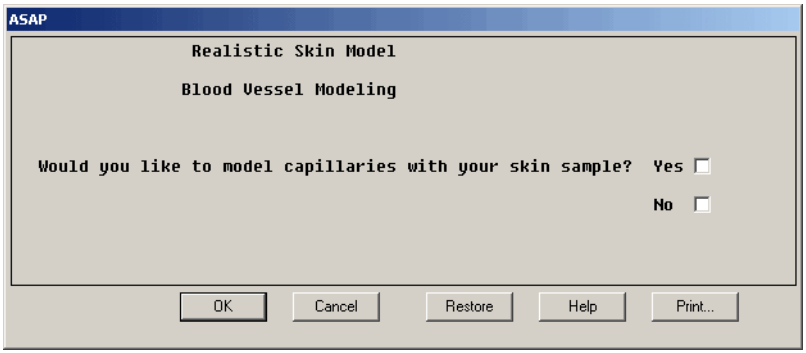


Figure 12 Blood Vessel Modeling dialog—activate to model capillaries with your skin model

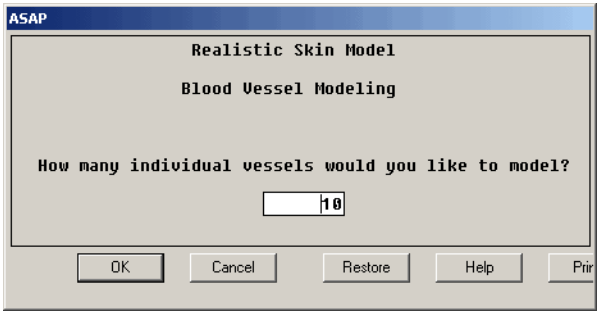


Figure 13 Blood Vessel Modeling—enter number of vessels to model

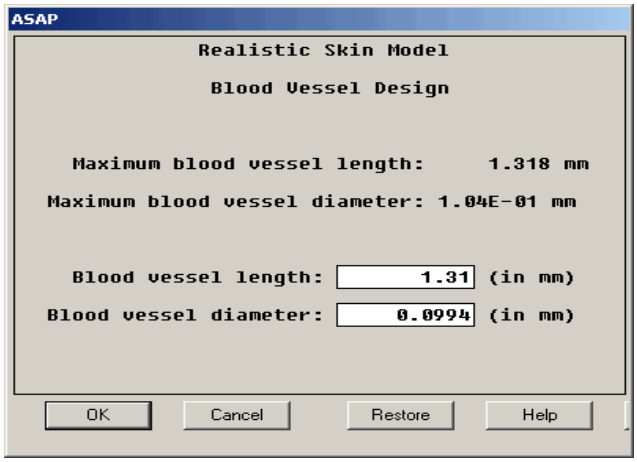


Figure 14 Blood Vessel Design dialog—enter blood vessel length and diameter

Both length and diameter must be non-zero, and kept below the maximum. According to the dimension of the blood vessel, ASAP informs you of the minimum number of voxels required to resolve the blood vessels across their shortest dimension (Figure 15). Select **Help** on this dialog for a description of voxels. You must select the check box to continue.

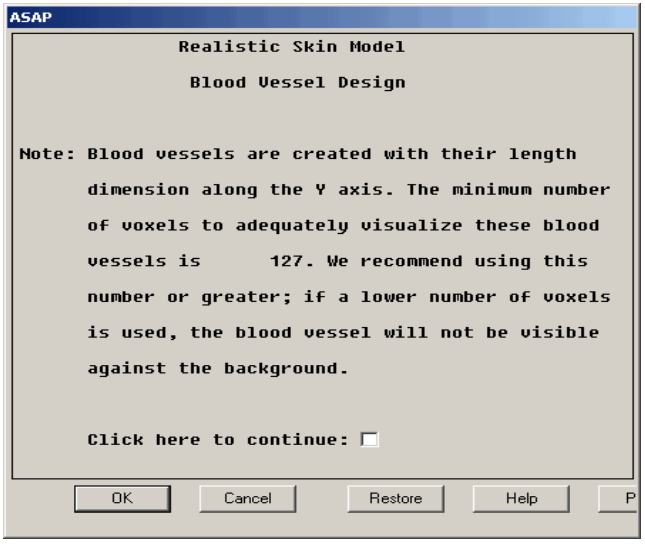


Figure 15 Blood Vessel Design dialog—minimum number of voxels needed to visualize blood vessels

In the final step of blood vessel creation, ASAP displays the Blood Volume Fraction dialog (Figure 16). The volume fraction of blood is calculated using the input values for blood vessel number and dimensions. This volume fraction is shown at the top of the dialog. If the fraction is acceptable, select **OK**. If you are more interested in modeling the correct amount of blood in the skin sample than in the number or size of vessels, select **Yes** and enter the desired blood volume fraction. The RSM rescales and increases the number of blood vessels in the sample to match the desired blood volume fraction. If the diameter of the vessels required to accomplish this exceeds the maximum diameter of the vessels, a second layer of blood vessel is created underneath the first layer, and the diameter of all vessels is rescaled to fit the blood volume fraction you specified. This process continues until the desired blood volume fraction is reached.

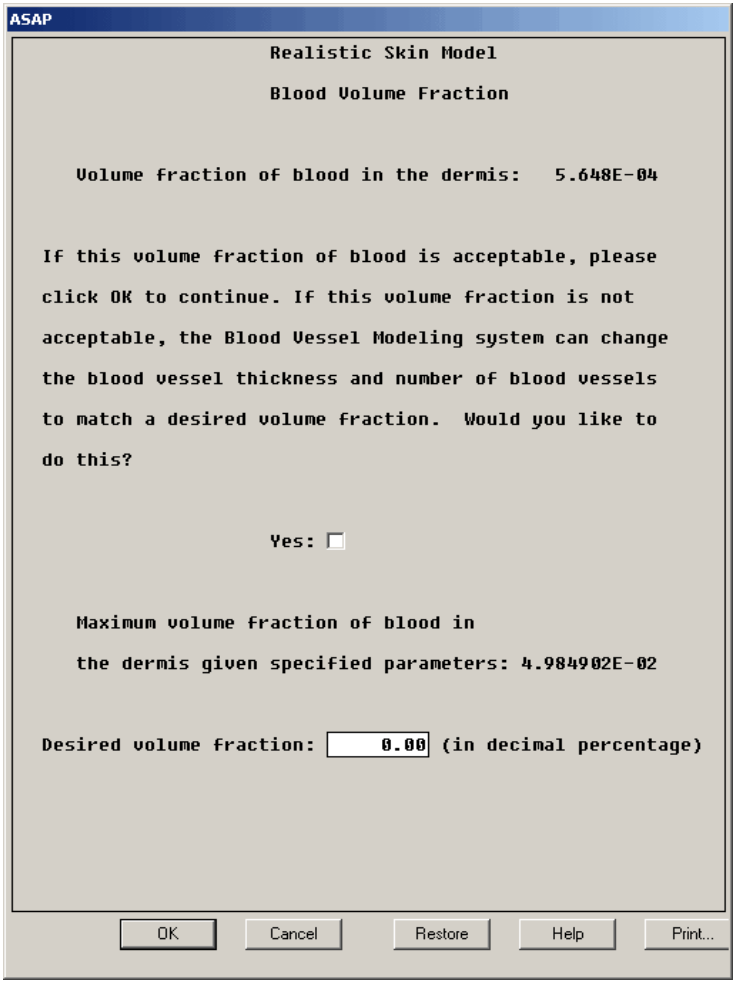


Figure 16 Blood Volume Fraction dialog—accept the default blood volume fraction, or change decimal percentage for the desired volume fraction

The modeling of blood vessels also fundamentally changes the absorption model of the dermis. Without blood vessel modeling, blood is assumed to be uniformly distributed within the dermis. If blood vessel modeling is selected, the contribution to the absorption coefficient due to hemoglobin in the dermis is removed. As a result, the option to change the blood volume fraction in the dermis is also removed from the dermis chromophore concentrations input dialog (Figure 19 on page 24).

NOTE: ***There is a limit to the blood volume fraction that can be modeled given the parameters for the skin model you entered previously. This maximum is displayed in the blood volume fraction dialog (Figure 16), and inputs beyond this value are not supported.***

Detailed description on parameter input options—Chromophore Concentrations and Direct Entry

In the section, "Overview on parameter input for skin sample modeling" on page 9, we explained the parameter input methods of "Using Default Parameters" and "Visual Characteristics". In the following sections, we explain in detail the other two parameter input methods—Chromophore Concentrations and Direct Entry.

Chromophore concentrations

When selecting **Chromophore Concentrations**, the input method for skin parameters, you can specify the concentrations of the different chromophores for the stratum corneum, epidermis, and dermis. Hypodermis is not included as it does not contain a significant amount of chromophores. However, optical properties of the hypodermis can be modified using **Direct Entry** as the input method.

> **Stratum corneum**: Construction of the stratum corneum is controlled through the Stratum Corneum dialog (Figure 17). The stratum corneum, a division of the epidermis, is the outermost layer of the skin. On average, it varies in thickness from 10 to 20 µm, and comprises layers of dead cells called corneocytes. The major chromophore in this layer is water, although small amounts of beta carotene are also present and contribute to the tan or yellowish appearance of the skin. See Table 5 for descriptions of the settings.

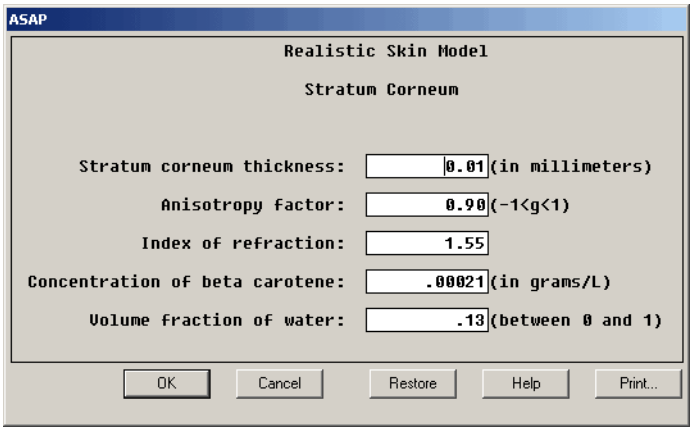


Figure 17 Stratum Corneum dialog—enter parameters

Table 5 Stratum Corneum Settings

Stratum corneum thickness	The RSM does not place a maximum thickness restriction on this layer—any non-zero value is accepted as a thickness. The default is recommended if exact thickness of the stratum corneum of the sample is unknown.
Anisotropy factor (g)	Describes the average directional cosine of the scattered light in the biological tissue. Most biological tissues are highly forward scattering (≥0.9), and 0.9 used as the default. If *g* is unknown, the default value is recommended.
Index of refraction	The RSM supports indices between 1 and 2. The index varies due to many factors, such as skin hydration and “oiliness”. Under normal conditions, the average stratum corneum refractivity is 1.55 (default).
Concentration of beta carotene	The RSM supports beta carotene levels up to an arbitrary maximum concentration of 5 grams/liter of skin (no precise data has been located on maximum concentration in living humans). Beta carotene levels in the outer layers of the skin are generally low except in certain medical conditions, such as hypervitaminosis A.
Volume fraction of water	Describes water concentration in the biological tissue. It varies from 10 to 15% on average. Limits for the acceptable volume fraction are from 0 (no water) to 1 (100% water).

Epidermis: The chromophore concentrations of the epidermis can be controlled through the Epidermis dialog (Figure 18). See Table 6 for descriptions of the settings. The epidermis contains several cell types, each with an essential role in maintaining homeostasis:

- Melanocytes—contain the pigment melanin that contributes to the overall appearance of our skin, and protects our bodies from harmful solar radiation.
- Langerhans' cells—provide the first line of immune defense against organisms attempting to invade the body through the skin.
- Merkel cells—also present in the epidermis, but their exact function has yet to be determined.

Despite containing all these cell types, the epidermis lacks a vascular system. Oxygen and nutrients are supplied through the dermo-epidermal junction from capillaries in the dermis. Melanin pigments are the major chromophore in the epidermis, although water does contribute to absorption at longer wavelengths.

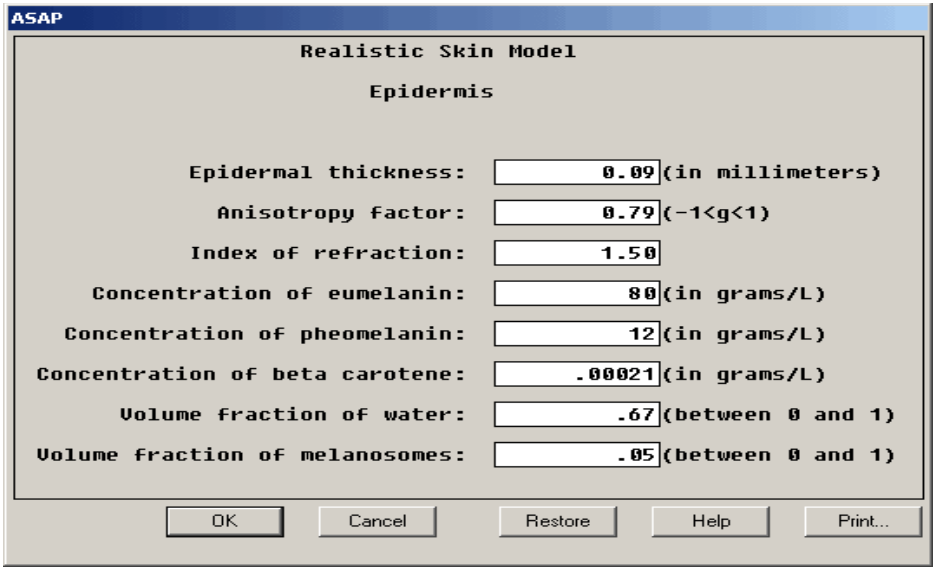


Figure 18 Epidermis dialog—enter chromophore concentration parameters

Table 6 Epidermis Settings

Epidermal thickness	Enter total thickness of epidermis in millimeters. The quantity must be non-zero, but has no maximum thickness. Depending on the area of the body, the epidermal layer can range from 0.05mm (eyelids) to 1.5mm (palm of hands).
Anisotropy factor (g)	Describes the average directional cosine of the scattered light in the biological tissue. Most biological tissues are highly forward scattering (≥0.9). The default anisotropy factor for the epidermis is 0.79. If *g* is unknown, the default value is recommended.
Index of refraction	Under normal conditions, the average index for the epidermis is 1.50 (default). Limits are between 1 and 2. The index varies due to many factors, such as skin hydration and “oiliness”.
Concentration of eumelanin	Limits are between 0 and 200g/L (arbitrary maximum). Eumelanin is a dark brown/black epidermal pigment. Darker-skinned individuals have a higher concentration of melanosomes and more eumelanin in their epidermis than individuals with lighter skin tones.
Concentration of pheomelanin	Limits are between 0 and 50g/L (arbitrary maximum). Pheomelanin is a yellowish skin pigment in the epidermis.
Concentration of beta carotene	Limits are between 0 and 5g/L (arbitrary maximum). A small amount of beta carotene is deposited in the epidermis.
Volume fraction of water	Limits are between 0 (no water) to 1 (100% water), and an average volume fraction of 65% for normal skin is recommended. A water volume fraction gradient is present in the epidermis—from nearly 80% water by volume at the dermo-epidermal interface, and decreasing to approximately 13% at the interface with the stratum corneum. Due to modeling constraints, the RSM uses an average value for water volume fraction in the epidermis.
Volume fraction of melanosomes	Melanosomes are regions in the malanocyte that contain the pigment molecules. Recommended fractions: Light-skinned adults: 0.013 to 0.063 Moderately pigmented adults: 0.11 to 0.16 Darkly pigmented adults: 0.18 to 0.43

Dermis: Chromophore concentrations of the dermis are defined using the Dermis dialog (Figure 19). The major chromophore in the dermal layer is hemoglobin, though water also contributes significantly to absorption at longer wavelengths (>1000nm).

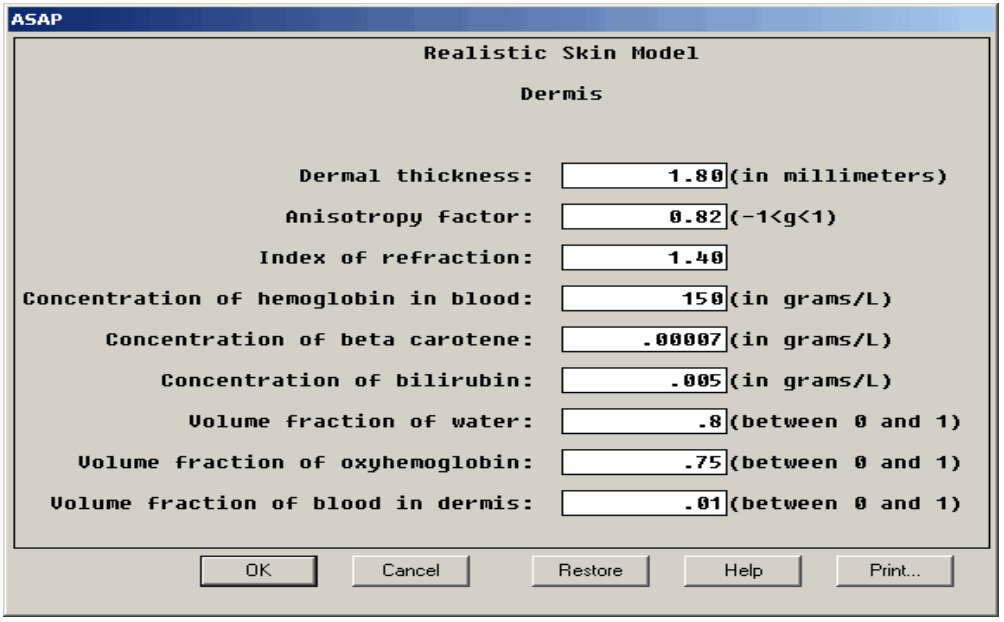


Figure 19 Dermis dialog—dermis chromophore concentrations

The thickness of the dermis ranges from 0.3mm on the eyelids up to 3mm on the back. The dermis contains many of the structures necessary for skin function, and can be divided into two sub-layers: papillary dermis and reticular dermis.

The papillary dermis is the upper layer of the dermis, and directly supplies the upper layers of skin with blood. The reticular dermis contains dense, irregular connective tissue, and is mainly responsible for giving skin its elasticity and strength. Capillaries in the dermis supply the skin with oxygen and nutrients, and sebaceous glands create oils essential for water conservation. Hair follicles can also be found in this layer.

The RSM assumes all blood constituents are the same for both the papillary and reticular dermis, with only the blood volume fraction varying by layer.

If the epidermis and dermis were both selected in the dialog for layer selection (see Figure 7 on page 11), and a two-layer dermal model was selected in the Dermal Modeling dialog (see Figure 8 on page 12), the Papillary Dermis dialog is displayed (Figure 20).

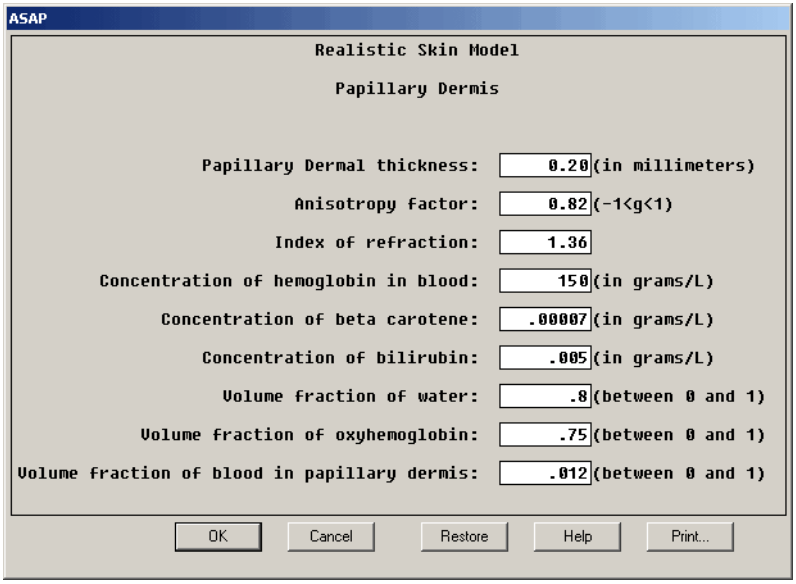


Figure 20 Papillary Dermis dialog—chromophore concentrations

After the settings for the papillary dermis are entered, the Reticular Dermis dialog is displayed (Figure 21).

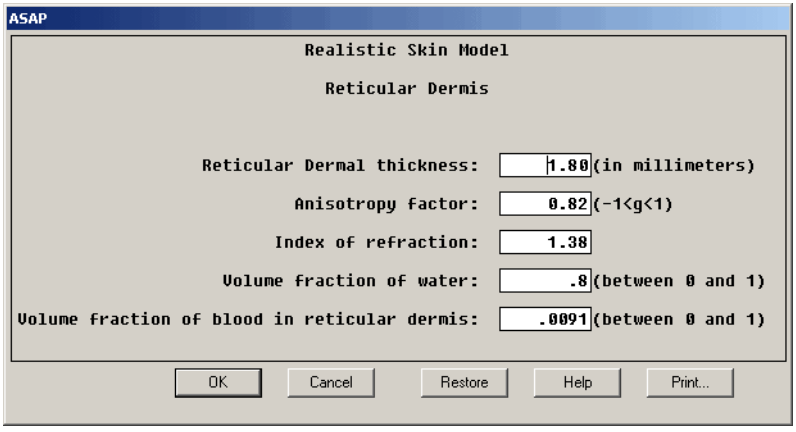


Figure 21 Reticular Dermis dialog—chromophore concentrations

The information in Table 7 applies to both single-layer and two-layer dermis models. If the two-layer dermis model was used, any mention of the dermis applies to the sub-layer of the dermis (papillary or reticular) as well.

Table 7 Dermis Settings

Dermal thickness	Enter total thickness in millimeters. The RSM supports any non-zero thickness. Depending on the area of the body, the dermis thickness can range from 0.3mm (eyelids) to 3mm (back). Keeping it within this range ensures biologically relevant results.
Anisotropy factor (*g*)	Describes the average directional cosine of the scattered light in the biological tissue. Most biological tissues are highly forward scattering. ($\geq$0.9). If *g* is unknown, the default value (*g*=0.82) is recommended.
Index of refraction	Limits are between 1 and 2. The default settings are n=1.4 for single-layer dermis model. For the two-layer model, default settings are n=1.36 for the papillary dermis and n=1.38 for the reticular dermis.
Concentration of hemoglobin in the blood	Specifies the total concentration within a range of 0 to 400 g/L (arbitrary maximum). The concentration of hemoglobin, the oxygen-carrying molecule in red blood cells, can vary over a wide range, depending upon the physical characteristics, altitude, and disease state of the individual. Males generally have a higher average concentration (138 to 172 g/L) than females (121 to 151 g/L).
Concentration of bilirubin	Defines total concentration, both blood-borne and deposited, in the dermal layer. Ranges are limited from 0 to 1 g/L (arbitrary maximum). Bilirubin is a yellow by-product of the breakdown of hemoglobin in dead red blood cells, and is found in the bloodstream and deposited in small quantities in the dermis. Abnormal increase in concentrations due to liver, kidney, or spleen problems can lead to a yellowing of the skin (a condition named jaundice, corresponding to a concentration of bilirubin $\geq$ 0.02 g/L).
Concentration of beta carotene	Limits are from 0 and 5 g/L (arbitrary maximum). This quantity includes beta carotene in both the blood and tissue.
Volume fraction of water	Limits are from 0 (no water) to 1 (100%) water. The dermis contains the highest concentration of water in the skin. An average volume fraction of 0.8 (80%) is advised for normal dermis.
Volume fraction of oxyhemoglobin	Limits are from 0 to 1. A setting closer to 1 denotes nearly 100% of the blood is oxygen enriched.
Volume fraction of blood in dermis	Limits range from 0.002 to 0.7, and may be elevated in certain skin conditions. You can vary total volume of blood in the skin as a fractional percentage of the whole dermal volume, ranging from 0 (no blood) to 1 (all blood). The dermis is the only portion of the skin that contains blood vessels.

***Dermal papillae**:* If you choose the two-layer dermis model, the Dermal Papillae Modeling dialog (Figure 22) is displayed, asking whether or not to model the dermal papillae. Reference Appendix 1 for possible feature modeling combinations according to skin layer selections.

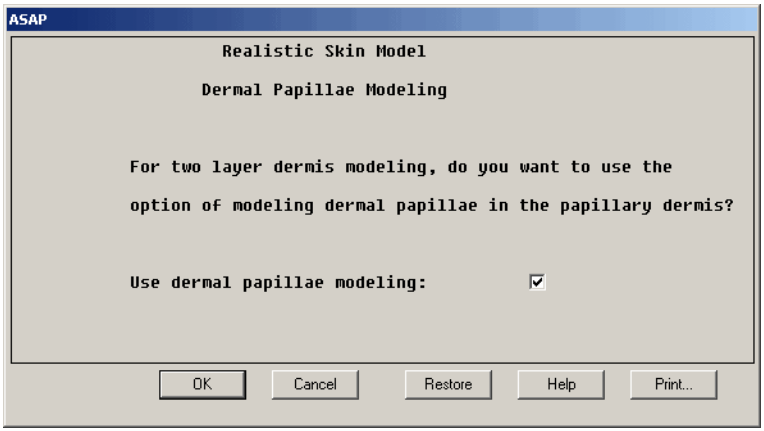


Figure 22 Dermal Papillae Modeling dialog—specify whether or not to model

If you choose to model the dermal papillae, the Dermal Papillae Input dialog (Figure 23) is displayed for entering the desired height and density of the dermal papillae. See Table 8 for descriptions of the settings.

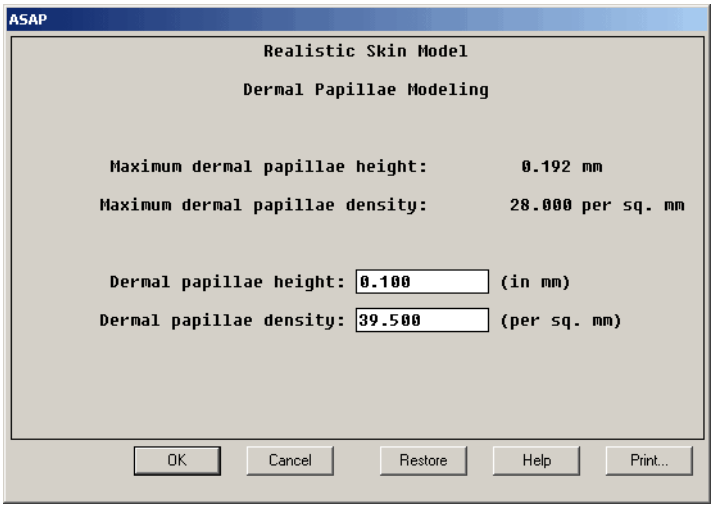


Figure 23 Dermal Papillae Input dialog—enter the desired height and density for the dermal papillae

Three parameters are needed for the modeling of the finger-like dermal papillae: radius, height, and density. In the current version of the RSM, the dermal papillae radius is set internally as the mean of the possible range (0.035mm-0.0925mm), according to published research. Using this dermal papillae radius, the RSM calculates the maximum dermal papillae density allowed for modeling, which is displayed the Dermal Papillae Input dialog (Figure 23). The maximum dermal papillae height is calculated as two-thirds of the sum of the epidermis and papillary dermis thicknesses. You can enter the desired height and density for your dermal papillae modeling in the dialog.

Table 8 Dermal Papillae Settings

Dermal papillae height	Specifies the height of the dermal papillae, which cannot be negative and must be larger than the dermal papillae radius, but smaller than the maximum height displayed at the top of the dialog.
Dermal papillae density	Specifies the desired density for dermal papillae modeling. Its value must be smaller than the maximum density displayed at the top of the dialog. Papillae are first created with a rectangular grid pattern along the dermo-epidermal interface, and then randomized locally around the individual grid points under the constraint that no two papillae intersect each other. NOTE: A high density of dermal papillae may dramatically increase the amount of time ASAP requires to plot the skin geometry.

DIRECT ENTRY

If you already possess a skin sample with well-defined optical properties, such as the absorption and scatter coefficients, the Direct Entry option allows you to customize your skin model using these values. Depending upon your selections in the Layer Selection dialog (see Figure 7 on page 11), any or all of the following dialogs may be displayed if the Direct Entry option was selected in the Model Creation dialog (see Figure 5 on page 9).

Stratum corneum (direct entry): If the stratum corneum layer is chosen in the model, the Stratum Corneum (direct entry) dialog (Figure 24) is displayed to enter optical parameters. See Table 9 for descriptions of the settings.

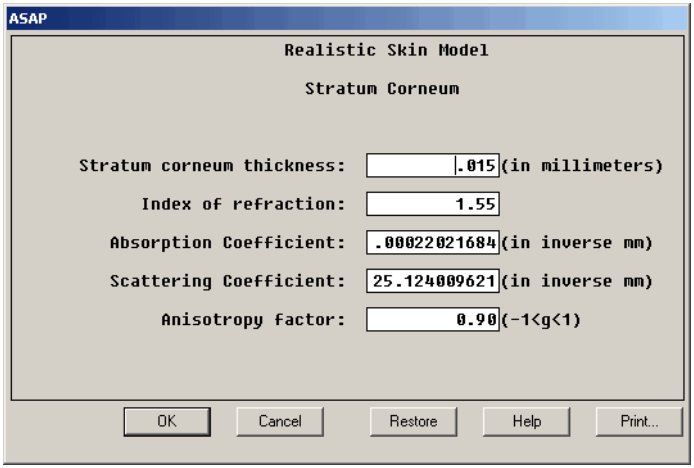


Figure 24 Stratum Corneum dialog (direct entry)—set the optical parameters

Table 9 Stratum Corneum Settings (direct entry)

Stratum corneum thickness	The RSM does not place a maximum thickness restriction on this layer. Any non-zero value is accepted as a thickness. The default is recommended if exact thickness of the stratum corneum for the sample is unknown.
Index of refraction	The RSM supports indices between 1 and 2. The index varies due to many factors, such as skin hydration and “oiliness”. Under normal conditions, the average stratum corneum index of refraction is 1.55 (default).
Absorption coefficient (μ_a)	This is a measure of the probability that an absorption event occurs per unit length within the tissue. It has the unit of inverse length. The number can vary greatly depending upon wavelength and concentrations of chromophores in the skin.
Scattering coefficient (μ_s)	This is a measure of the probability that a scattering event occurs per unit length within the tissue. It has the unit of inverse length. The number can vary greatly depending upon the wavelength and density of scattering structures, such as collagen in the skin.
Anisotropy factor (g)	This factor describes the average directional cosine of the scattered light in the tissue. It has a range of -1 to 1, where g=1 corresponds to completely forward scattering, g=0 corresponds to isotropic scatter, and g=-1 corresponds to completely backscattering. Most biological tissues are highly forward scattering ($\geq$ 0.9), and g=0.9 is used as the default value. If g is unknown, the default value is recommended.

Epidermis (direct entry): If the epidermis layer is selected in the model, the Epidermis dialog (Figure 25) is displayed to enter optical parameters. See Table 10 for descriptions of the settings.

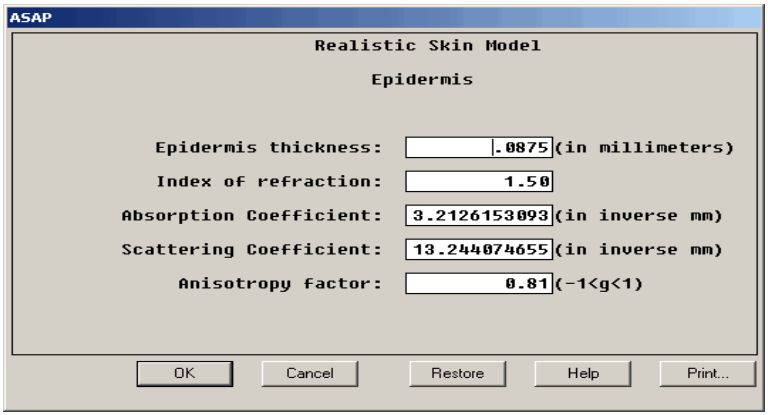


Figure 25 Epidermis dialog (direct entry)—set the optical parameters

Table 10 Epidermis Settings (direct entry)

Epidermis thickness	The RSM does not place a maximum thickness restriction on this layer. Any non-zero value is accepted as a thickness. The default is recommended if exact thickness of the epidermis for the sample is unknown.
Index of refraction	The RSM supports indices between 1 and 2. The index varies due to many factors, such as skin hydration and “oiliness”. Under normal condition, the average epidermis index of refraction is 1.5 (default).
Absorption coefficient (μ_a)	This is a measure of the probability that an absorption event occurs per unit length within the tissue. It has the unit of inverse length. This number can vary greatly depending upon the wavelength and the concentrations of chromophores in the skin.
Scattering coefficient (μ_s)	This is a measure of the probability that a scattering event occurs per unit length within the tissue. It has the unit of inverse length. This number can vary greatly depending upon the wavelength and the density of scattering structures, such as collagen, in the skin.

Table 10 Epidermis Settings (direct entry)

Anisotropy factor (g)	The anisotropy factor describes the average directional cosine of scattered light in the tissue. It has a range of -1 to 1, where *g*=1 corresponds to completely forward scattering, *g*=0 corresponds to isotropic scatter, and *g*=-1 corresponds to completely backscattering. Most biological tissues are highly forward scattering (*g*≥ 0.9). The default value for epidermis is set to *g*=0.81. If *g* is unknown, the default value is recommended.

Dermis (direct entry): If the dermis layer is chosen in the model, the Dermis dialog (direct entry) (Figure 26) is displayed for entering optical parameters. See Table 11 for descriptions of the settings.

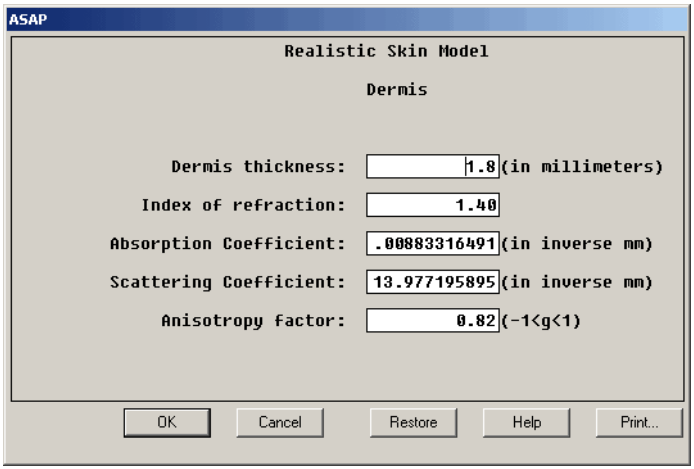


Figure 26 Dermis dialog (direct entry)—enter optical parameters

Table 11 Dermis Settings (direct entry)

Dermis thickness	The RSM does not place a maximum thickness restriction on this layer. Any non-zero value is accepted as a thickness. The default is recommended if exact thickness of the dermis for the sample is unknown.
Index of refraction	The RSM supports indices between 1 and 2. The index varies due to many factors, such as skin hydration and “oiliness”. Under normal conditions, the average dermis refractivity is 1.4 (default) for the single-layer dermis model. For the two-layer dermis model, the default refractivity is 1.36 for the papillary dermis, and 1.38 for the reticular dermis.
Absorption coefficient (μ_a)	This is a measure of the probability that an absorption event occurs per unit length within the tissue. It has unit of inverse length. This number can vary greatly depending upon the wavelength used and the concentrations of chromophores in the skin.
Scattering coefficient (μ_s)	This is a measure of the probability that a scattering event occurs per unit length within the tissue. It has units of inverse length. This number can vary greatly depending upon the wavelength and the density of scattering structures, such as collagen, in the skin.
Anisotropy factor (g)	The anisotropy factor describes the average directional cosine of scattered light in the tissue. It has a range of -1 to 1, where g=1 corresponds to completely forward scattering, g=0 corresponds to isotropic scatter, and g=-1 corresponds completely to backscattering. Most biological tissues are highly forward scattering ($g \geq 0.9$). The default value for the dermis is g=0.82. If g is unknown, the default value is recommended.

Two-layer dermis and dermal papillae: If the epidermis and dermis were both selected in the Layer dialog (Figure 7 on page 11), and a two-layer dermal model was selected in the Dermal Modeling dialog (Figure 8 on page 12), the Papillary Dermis dialog (direct entry) is displayed (Figure 27).

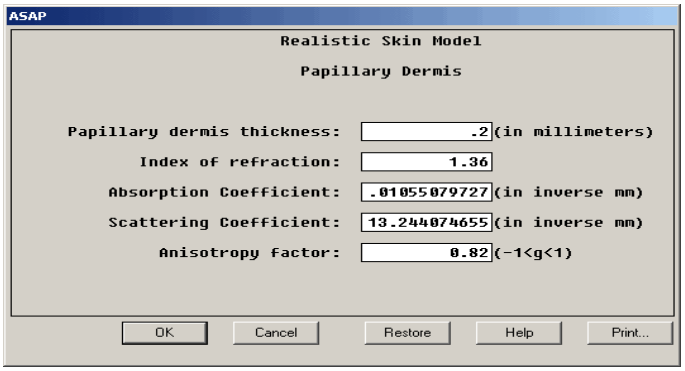


Figure 27 Papillary Dermis dialog (direct entry)—enter the parameters

After the settings for the papillary dermis, the Reticular Dermis dialog (direct entry) is displayed (Figure 28).

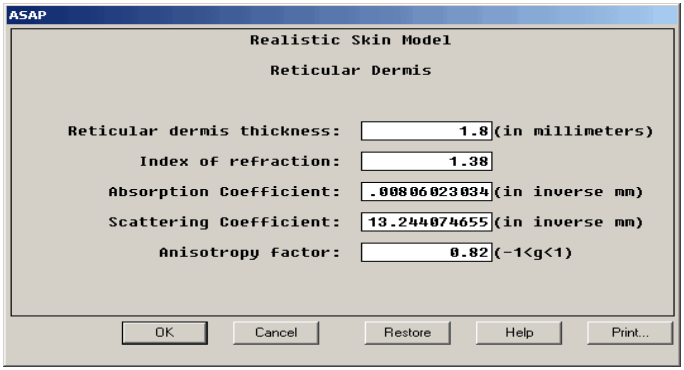


Figure 28 Reticular Dermis dialog (direct entry)—enter the parameters

If the two-layer dermis is modeled and the option to model dermal papillae was selected, the input dialog for dermal papillae height and density is displayed. See Figure 29 and Table 12 for descriptions of the settings.

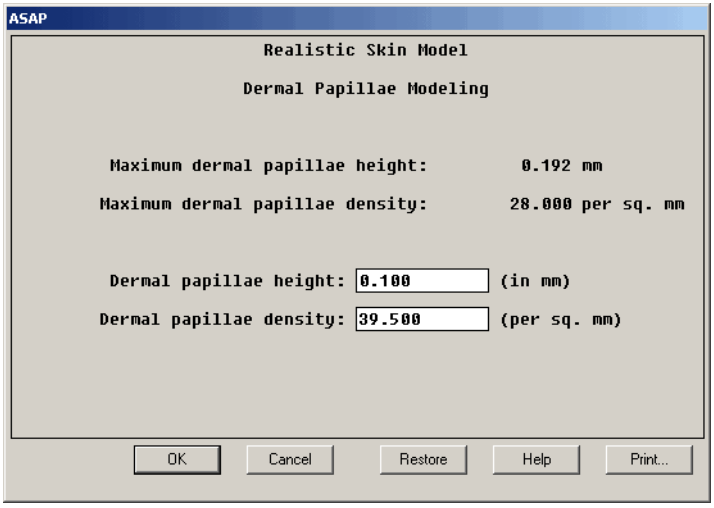


Figure 29 Dermal Papillae input dialog—enter the settings.

Table 12 Dermal Papillae Settings

Dermal papillae height	Specifies the height of the dermal papillae, which cannot be negative and must be larger than the dermal papillae radius, but smaller than the maximum height displayed at the top of the dialog.
Dermal papillae density	Specifies the desired density for dermal papillae modeling. Its value must be smaller than the maximum density displayed at the top of the dialog. Papillae are first created with a rectangular grid pattern along the dermo-epidermal interface, and then randomized locally around the individual grid points under the constraint that no two papillae intersect each other. NOTE: A high density of dermal papillae may dramatically increase the amount of time ASAP requires to plot the skin geometry.

Hypodermis (direct entry): If the hypodermis layer is selected in the model, the Hypodermis dialog (direct entry) (Figure 30) is displayed to enter optical parameters. See Table 13 for descriptions of the settings.

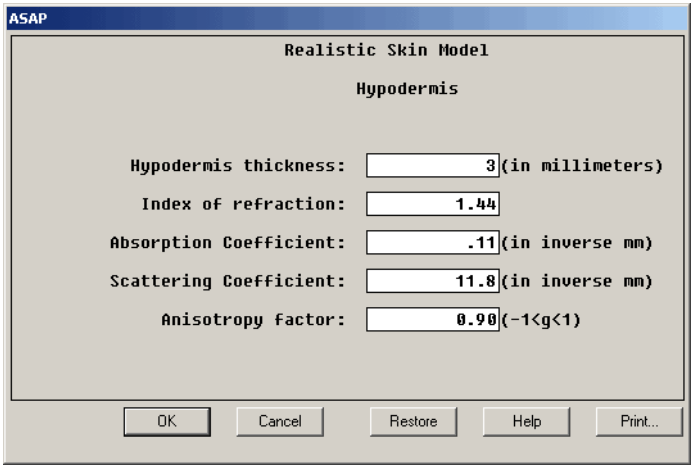


Figure 30 Hypodermis (direct entry)—enter the parameters

Table 13 Hypodermis Settings (direct entry)

Hypodermis thickness	The RSM does not place a maximum thickness restriction on this layer. Any non-zero value is accepted. The default is recommended if exact thickness of the hypodermis for the sample is unknown.
Index of refraction	The RSM supports indices between 1 and 2. The index varies due to many factors, such as skin hydration and “oiliness”. Under normal conditions, the average hypodermis refractivity is 1.44 (default).
Absorption coefficient (μ_a)	This is a measure of probability that an absorption event occurs per unit length within the tissue. It has the unit of inverse length. This number can vary greatly depending upon the wavelength used and the concentrations of chromophores in the skin.
Scattering coefficient (μ_s)	This is a measure of the probability that an scattering event occurred per unit length within the tissue. It has the unit of inverse length. This number can vary greatly depending upon the wavelength used and the chromophores in the skin.
Anisotropy factor (g)	The anisotropy factor describes the average directional cosine of scattered light in the tissue. It has a range of -1 to 1, where g=1 corresponds to completely forward scattering, g=0 corresponds to isotropic scatter, and g=-1 corresponds to completely backscattering. Most biological tissues are highly forward scattering ($g \geq 0.9$), and g=0.9 is used as the default value in RSM. If g is unknown, the default value is recommended.

Hair (direct entry): If you selected Hair Modeling on the Hair Modeling dialog (see Figure 10 on page 14), the Hair dialog (Figure 31) is displayed. See Table 14 for descriptions of the settings.

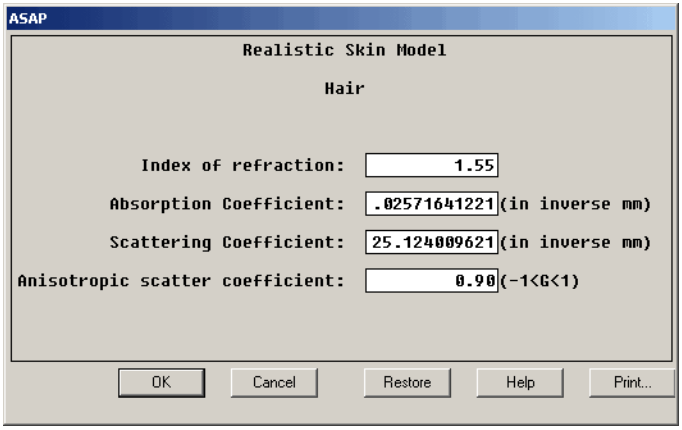


Figure 31 Hair dialog (direct entry)—set the parameters

Table 14 Hair Dialog Settings (direct entry

Index of refraction	The RSM supports indices between 1 and 2. In the current version of the RSM, the refractivity for hair is assumed to be 1.55.
Absorption coefficient (μ_a)	This is a measure of the probability that an absorption event occurs per unit length within the hair. It has the unit of inverse length. This number can vary greatly depending upon the wavelength and the concentrations of chromophores in the hair. For details on how the hair absorption coefficient is modeled in the RSM, see "Hair Modeling" on page 12.
Scattering coefficient (μ_s)	This is a measure of the probability that a scattering event occurs per unit length within the skin. It has the unit of inverse length. In the current version of the RSM, it is assumed that the hair shares the same scattering properties as the stratum corneum.
Anisotropy factor (g)	This factor describes the average directional cosine of the scattered light in the tissue. It has a range of -1 to 1, where *g*=1 corresponds to completely forward scattering, *g*=0 corresponds to isotropic scatter, and *g*=-1 corresponds to completely backscattering. Most biological tissues are highly forward scattering ($\geq$ 0.9), and 0.9 is used as the default value in the RSM. If *g* is unknown, the default value is recommended.

Blood vessel: If blood vessel modeling was selected in the Blood Vessel Modeling dialog (see Figure 14 on page 17), the direct entry input dialog (Figure 32) is displayed for entering optical parameters for the blood vessel.

***NOTE** Even though the term "blood vessel" is used here, it must be understood that the optical property entries (Table 15) actually correspond to the optical property of the blood, not the blood vessel walls. In effect, the RSM models the confined blood volume without modeling the blood vessel walls.*

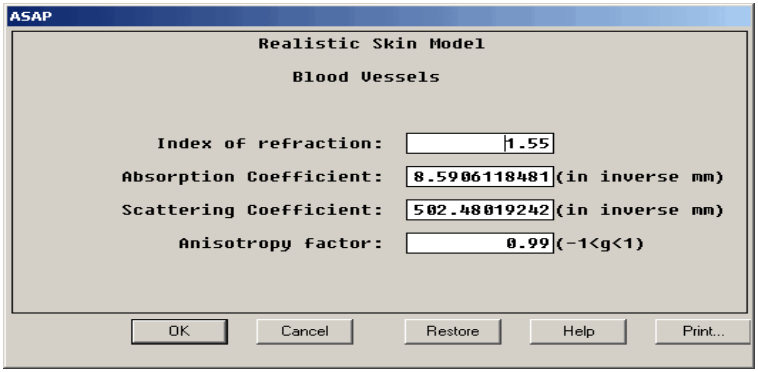


Figure 32 Direct Entry dialog—set the parameters for the blood vessel

Table 15 Blood Vessels Dialog Settings (direct entry)

Index of refraction	The RSM supports an indices between 1 and 2. The default of the blood refractivity is assumed at 1.55 (default).
Absorption coefficient (μ_a)	The absorption coefficient is a measure of the probability that an absorption event occurs per unit length within the blood. It has a unit of inverse length. This number can vary greatly depending upon the wavelength and properties of the blood.
Scattering coefficient (μ_s)	This is a measure of the probability that a scattering event occurred per unit length within the blood. It has the unit of inverse length. This number can vary greatly depending upon the wavelength and density of scattering centers in the blood.
Anisotropy factor (g)	This factor describes the average directional cosine of the scattered light in the tissue. It has a range of -1 to 1, where *g*=1 corresponds to completely forward scattering, *g*=0 corresponds to isotropic scatter, and *g*=-1 corresponds to completely backscattering. According to published literature, the anisotropy factor for blood ranges between 0.94 and 0.995. If *g* is unknown, the default value is recommended.

Creating the source

As displayed in the Model Initiation dialog (Figure 4 on page 8), the RSM includes three source options: **Use default sources**, **Define source parameters**, and **Use no source**. In this section, we describe details of the first two options.

DEFAULT SOURCE CREATION

The default source is an incoherent extended source with an elliptical geometry. The radiation emittance profile of the source is a Gaussian. This means the flux is stronger around the center of the source, and decays gradually according to a Gaussian function away from the center. The radius of the source is a quarter of the sample width. The $(1/e)^{-2}$ point for the Gaussian is $0.75x(\pi/2)^{1/2}$ by default of ASAP. The source is located at a distance of 5mm from the sample surface with the rays propagating parallel to the surface normal of the sample.

If you selected **Use default sources** on the Model Initiation dialog (Figure 4 on page 8), the RSM default source dialog (Figure 33) is displayed. See Table 16 for descriptions of the settings.

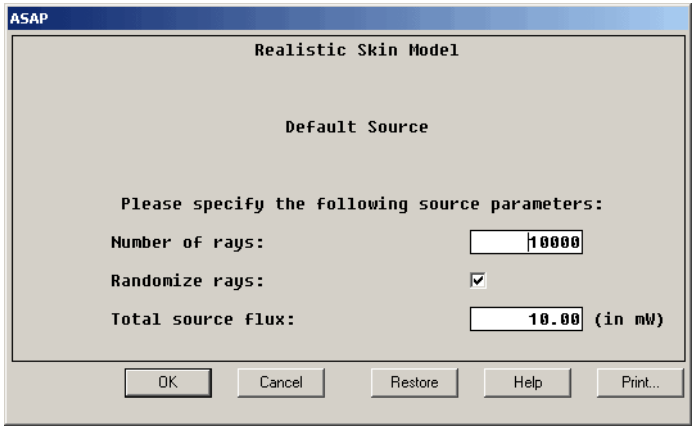


Figure 33 Default source dialog—specify source setting

Table 16 Default Source Settings

Number of rays	Specifies desired number of rays to be created, which may vary widely depending upon your application and degree of required accuracy. BRO recommends you do a test trace with a reasonable number of rays to ensure accurate and timely tracing. The actual number of rays created is different from the input value due to the way an elliptical source is created in ASAP: ASAP first creates a rectangular source with the width and length equal to the desired elliptical source diameter. This source has the correct number of rays, as specified in the input dialog. However, to create the desired elliptical source, an ellipse with the desired diameter is inscribed in the rectangle, and all rays outside this ellipse are clipped. Therefore, the actual number of rays created is always smaller than the input value.
Randomize rays	If this option is selected, locations of each individual ray are perturbed randomly within one unit of the local grid spacing to produce a more realistic ray distribution of the source.
Total source flux	Specify total flux of the source in milliwatts.

DEFINE SOURCE CREATION

If **Define source parameters** was selected in the Model Initiation dialog (see Figure 4 on page 8), use the Source Definition dialog (Figure 34) to create your source. See Table 17 for descriptions of the settings.

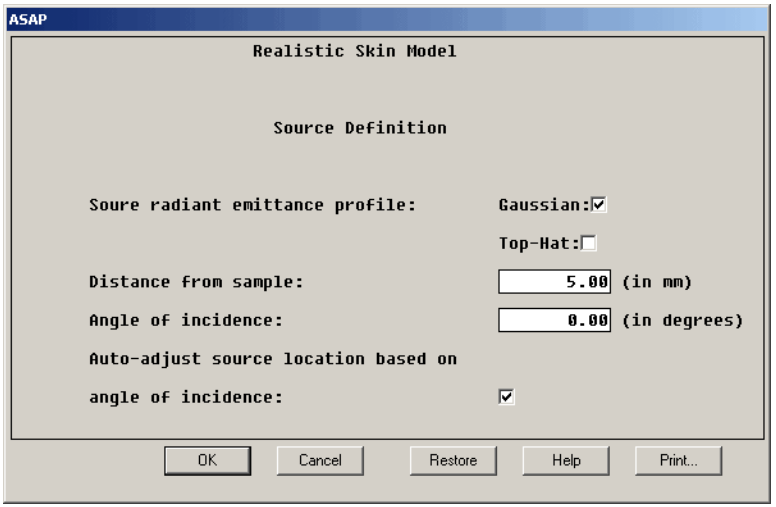


Figure 34 Source Definition dialog

Table 17 Source Definition Settings

Source radiant emittance profile	Two source radiant emittance profiles are available: Gaussian and top-hat. The Gaussian profile provides a radiant emittance pattern that decays according to a Gaussian in the transverse plane normal to the ray propagation direction. The Gaussian profile is cut off at the source width. The top-hat profile provides a uniform radiant emittance across the transverse plane within the source width.
Distance from sample	Sets the distance of source from skin model surface, and is measured in millimeters. The source must be created external to the sample (that is, this value cannot be less than or equal to zero), but there is no maximum value for this distance.
Angle of incidence (for an oblique source angle)	Defines incident angle of source rays with respect to skin surface normal. This angle is measured from the surface normal, and may vary from -90 to +90 degrees (see Figure 35).
Auto-adjust source location	When you choose any incident angle other than normal incidence, we recommend activating this option to ensure that rays intersect the sample. This is especially true for a large incident angle. When this option is activated, RSM rotates the source according to the specified angle of incidence along an arc that is centered at the sample surface center, and with a radius defined by the source distance (see Figure 35). By doing so, rays emitting from the source are always pointing towards the sample center and cannot miss.

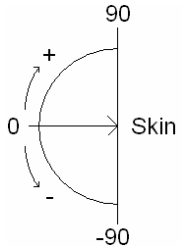


Figure 35 Angle of incidence—varies from -90 to +90 degrees

CREATING SOURCES WITH GAUSSIAN RADIATION PROFILE

If the Gaussian radiant emittance profile option was selected in the Source Definition dialog, (see Figure 34 on page 42), the Gaussian Radiation Profile dialog (Figure 36) is displayed for entering parameters. See Table 18 for descriptions of the settings.

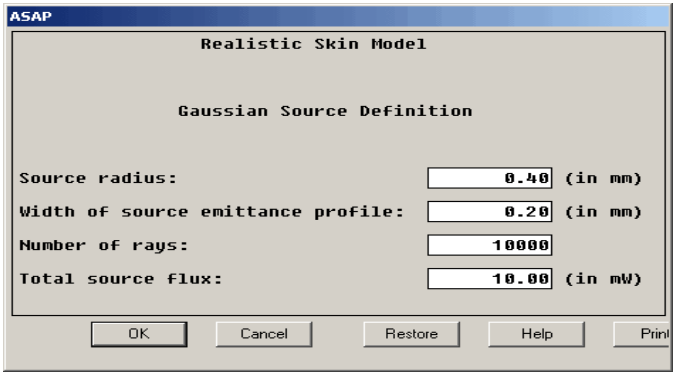


Figure 36 Set Gaussian Radiation Profile dialog—enter parameters

Table 18 Gaussian Radiation Profile Settings

Source radius	Defines the geometrical width of the source (in millimeters)
Width of Gaussian radiant emittance profile	Defines the width (W_0) of the Gaussian radiant emittance profile (in millimeters). It is usually smaller than the source radius. The width is defined as the point at which the radiant emittance (flux per unit area, M) of the source decays to exp(-2) of its peak value (M_0) as described by: $M(R) = M_0 \exp\left(\frac{-2R^2}{W_0^2}\right)$ See Figure 37.
Number of rays	Specifies the number of rays to be created. The actual number of rays created is different from this number (see “Default source creation” on page 40).
Total source flux	Specifies the total flux of the source in milliwatts.

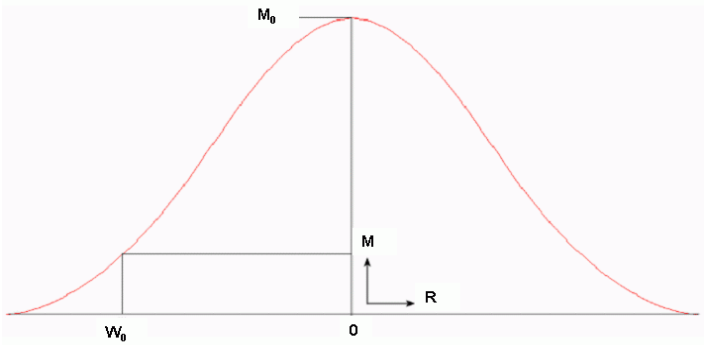


Figure 37 Gaussian radiant emittance profile

CREATING TOP-HAT SOURCES

If a top-hat profile was selected in the Source Definition dialog (see Figure 34 on page 42), the dialogs shown in Figure 38, Figure 39, and Figure 41 allow you to set the parameters for the top-hat source creation.

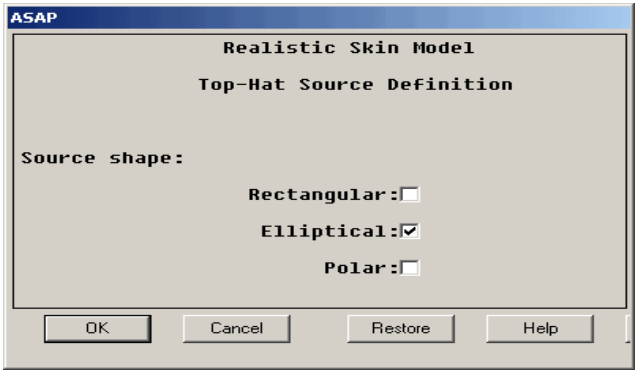


Figure 38 First Top-Hat Source Definition dialog—select a source shape

The Top-Hat Source Definition dialog provides three types of source geometry: rectangular, elliptical, and polar. If either a rectangular or elliptical source shape is selected, the dialog in Figure 39 is displayed to define related parameters. See Table 19 for descriptions of the settings. If the polar source is selected, the dialog in Figure 41 is displayed. See Table 20 for descriptions of the settings for polar sources.

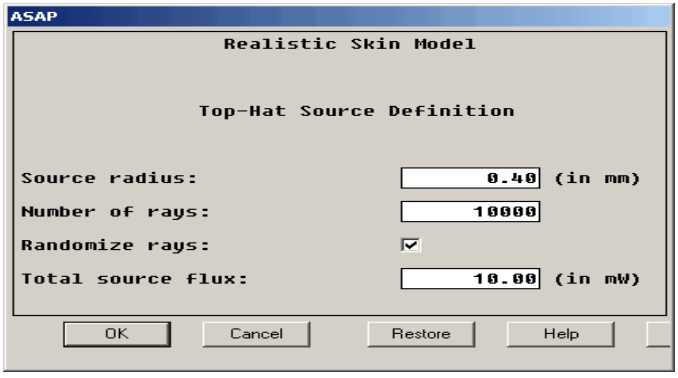


Figure 39 Second Top-Hat Source Definition dialog—select parameters for rectangular and elliptical sources

Table 19 Top-Hat Source Definition Settings for Rectangular or Elliptical Sources

Source radius	Defines the radius of the source if the selected source is elliptical. If the source is rectangular, this corresponds to the semi-width of the source.
Number of rays	For a rectangular source, the number of rays created is exactly equal to the number of rays entered in this field. For an elliptical source, the number of created rays is smaller than the number of rays entered in this field. (See Table 16 on page 41 for description.) The number of ideal rays for simulations may vary widely, depending upon the application, computer speed, and required accuracy.
Randomized rays	When selected, the locations of individual rays are randomly perturbed within 1 unit of the local grid spacing to produce a more realistic distribution of the source.
Total source flux	Input total power for the source in milliwatts. Total flux is then divided among the total number of created rays.

The third option for the top-hat source is a polar source, which has a ray pattern that is different from rectangular or elliptical sources. A polar source contains rays arrayed in concentric rings (Figure 40).

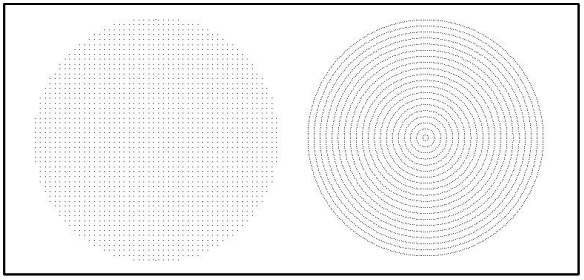


Figure 40 The ray pattern is different in a polar source (right) from that in an elliptical source (left), although both sources have an elliptical aperture

The parameters needed to define the polar source can be entered in the Polar Source dialog (Figure 41). See Table 20 for descriptions of the settings.

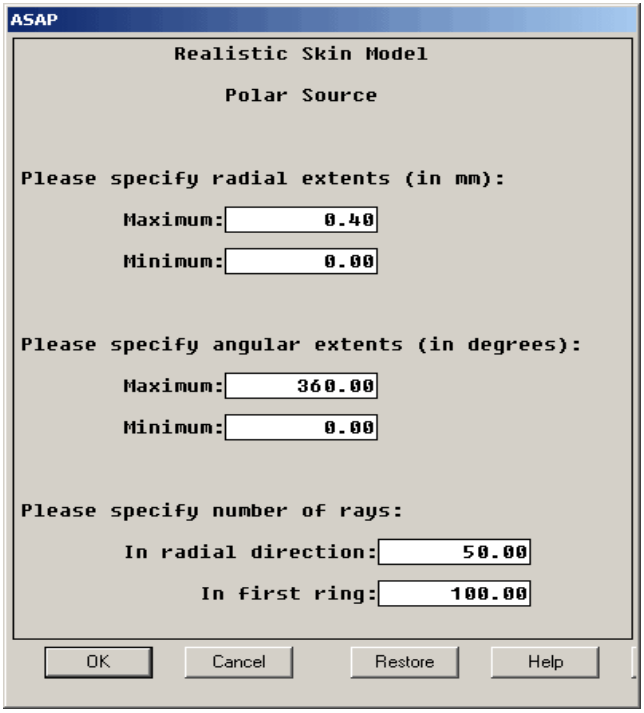


Figure 41 Polar Source dialog—set the parameters

Table 20 Polar Source Settings

Radial extents	Maximum radial extent of a polar source can be considered as the source radius. If a non-zero value is assigned to the minimum radial extent (the next field), a ring source is created. If the minimum is set to 0, a single ray is placed in the center of the source. If no central ray is intended, set the minimum to a number close to zero; for example, 1E-15.
Angular extents	Specifies starting and ending angles of the polar source around a circle (in degrees).
Number of rays: In radial direction	Specifies the number of concentric “rings” for the ray pattern.
Number of rays: In first ring	Specifies number of rays to be placed in the innermost ring, The number of rays in the outer rings is scaled accordingly.

Tracing rays

After source creation is complete, the RSM displays the Trace Options dialog (Figure 42). See Table 21 for descriptions of the settings.

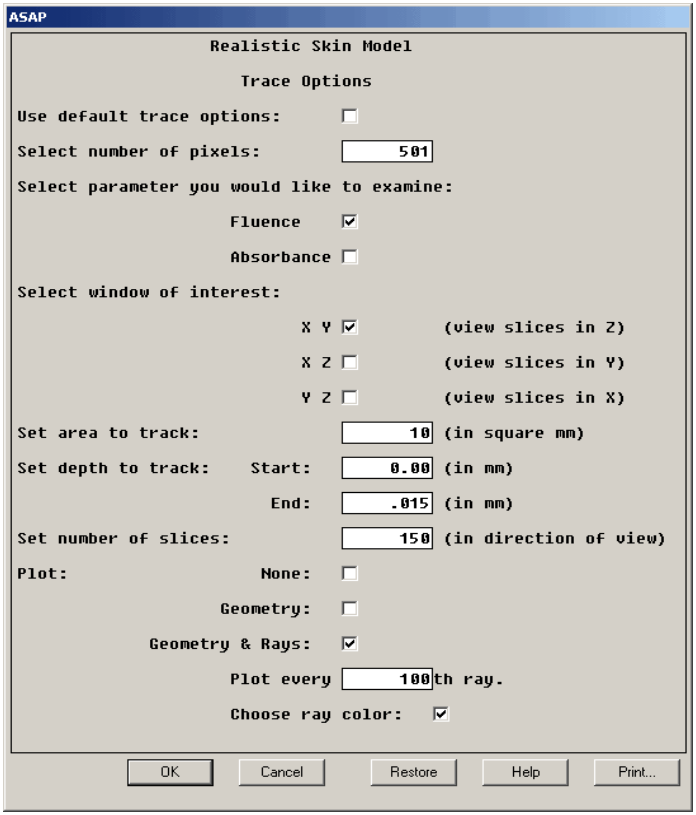


Figure 42 Set trace options

Table 21 Trace Option Settings

Use default trace options	If this option is selected, these default settings are applied: Pixels: 101 Voxel type: fluence Voxel area: total skin area Voxel starting depth: 0mm Voxel ending depth: Dermis-hypodermis interface Slices: 50 slices are generated for the x and y directions; 200 slices are generated along the z axis, which corresponds to the depth of the sample. Plot: The RSM plots the geometry and rays (every 100th ray), with the rays colored in blue. Select Help for more information on default options. Settings can be specified for ray tracing by selecting other parameters in Figure 42.
Select number of pixels	Controls resolution of display output. A higher number of pixels correlates to a display output of higher resolution.
Select analysis mode: Fluence or Absorbance	Fluence examines the amount of flux passing through the layer of interest. Absorbance allows exploration of flux absorbed in the slices or voxels. See NOTE after this table.
Select window of interest (view slices)	Sets the plane of slices to the XY, YZ, or XZ plane. It determines which cross-sectional images are available to you in the analysis procedure. See NOTE after this table.
Set area to track	Determines total surface area over which voxels extend. This value can be as small as necessary, but cannot be larger than the skin sample area.
Set depth to track	Enter starting and ending locations for the slices.
Set number of slices	Set number of slices in the 3rd dimension, which is perpendicular to the plane of slices.
Plot	Select parameters to plot the geometry of the sample or rays, or deselect if plot is not needed. These values have no impact on the Trace setting. If **Choose ray color** is selected, the Ray Color Preference) dialog (Figure 43) is displayed.

***NOTE** The RSM uses the VOXELS command in ASAP to track the amount of energy deposited in your sample, either fluence or absorption in flux per unit area. This command makes it possible to examine absorption or fluence within a volume in three dimension. See the Knowledge Base for the technical guide, "Using VOXELS in ASAP for Modeling Fluorescence and Volume Scatter", http://www.breault.com/k-base.php?kbaseID=25*

Choosing a ray color: When you select "Choose ray color" on the Trace Options dialog (see Figure 42 on page 48), the Ray Color Preference dialog (Figure 43) is displayed.

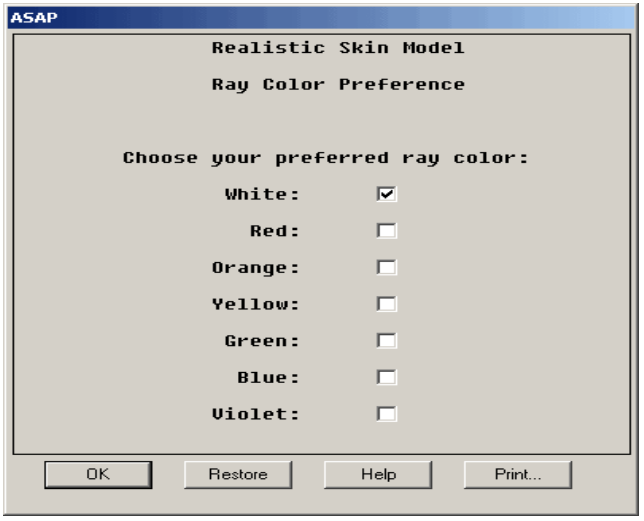


Figure 43 Select ray color

The color you select is applied to ray paths rendered during the trace. It does not affect the wavelength of the source in any way, and has no impact on the result of the trace.

Performing analysis

The Analysis Preferences dialog (Figure 44) is displayed when the following conditions are met:

- You selected the "Perform Dialog Driven Analysis" option on the Model Initiation dialog (Figure 4 on page 8).
- You used the RSM dialogs to create your source and trace your rays.
- Your ray trace is complete.

See Table 22 for descriptions of the settings.

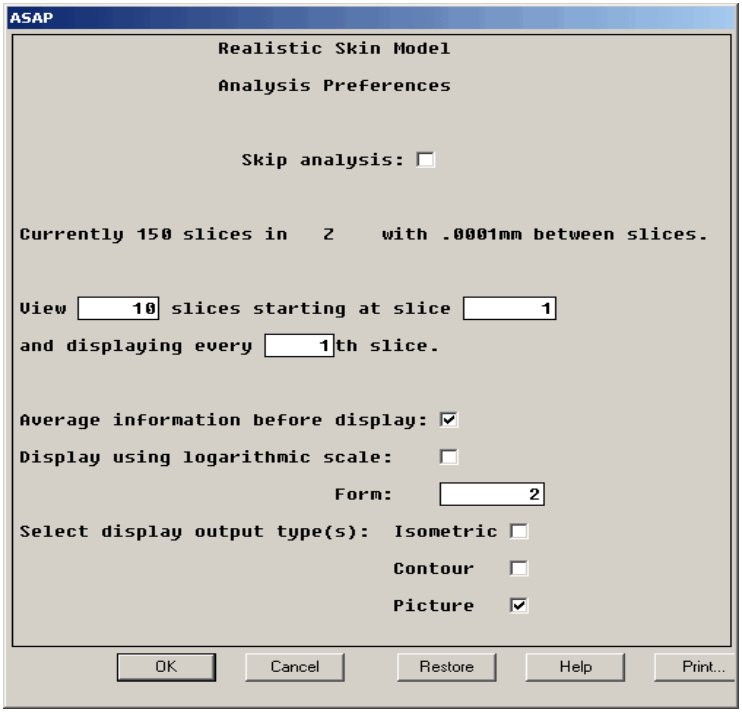


Figure 44 Analysis preferences dialog

Table 22 Analysis Preferences Settings

Skip analysis	If selected, no analysis is performed by the RSM. Leave deselected if analysis is desired.
View __ slices	The RSM provides information on the number of slices available for viewing, orientation of the slices, and distance between adjacent slices of the analysis. The number and orientation of the slices are defined in the Trace Options dialog (see Figure 42). Using information on the locations of the first and last slices and the total number of slices, the distance between adjacent slices is determined. You can enter the number of slices to view, starting slice number, and interval between slices to be displayed in accordance with the information provided.
Average information before display	If selected, the RSM performs two consecutive averages on the raw data. Each average is performed using a 3x3 pixel box around the individual pixels.

Table 22 Analysis Preferences Settings

Display using logarithmic scale	If selected, the RSM displays data on a log scale rather than linear.
Form	Specifies the "form" values (f) that determine how the raw data can be modified. See the topic, "FORM (ASAP Command)" in ASAP Help, for a better understanding on the command's functionalities and syntax. If the form value (f) is positive, it specifies the power to which the raw data is raised before being displayed. For example, **`FORM 0.5`** takes the square root of the data. If the form value (f) is negative, ASAP transforms raw data into a logarithmic (base 10) space with the form value (f) setting a lower cutoff.
Select display output type(s)	If desired, select one or more display options among the available display types: Isometric, Contour, or Picture. For more information on each of these types, see the corresponding ASAP command topics (**`ISOMETRIC`**, **`CONTOUR`**, **`PICTURE`**) in ASAP Help.

Outputting sample to a file

The Model Code Output feature in the RSM (see Figure 45) is used to save a copy of the skin model, which can be used in ASAP for any future analysis. If **Analysis Options** or the **Use no source** option was selected in the Model Initiation dialog (see Figure 4 on page 8), this dialog is displayed immediately after skin sample properties have been defined.

Figure 45 Model Code Output dialog—select whether to output your model

NOTE ***The RSM output is accurate for only the wavelength you designated in the options dialog. When using the output model in ASAP for further analysis, make sure that the wavelength is set accordingly in the ASAP file. If the analysis involves multiple wavelengths, BRO recommends you run the RSM for each desired wavelength.***

If the option to output your model was selected from the Model Code Output dialog (Figure 45), the Model Positioning Preferences dialog (Figure 46) is displayed.

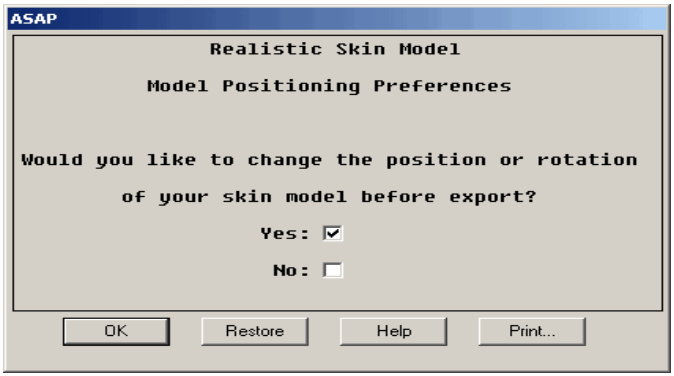


Figure 46 Model Positioning Preferences dialog—select whether to change the position or rotation of your model

If the option, **Yes**, was selected to change the position or orientation of the model in the Model Positioning Preferences dialog (Figure 46), the dialog for position/rotation is displayed (Figure 47). It is used to specify the shifting amount for sample position, and/or the angle of rotation for the sample orientation modification. All shifts and rotations of the sample are performed using the center of the top surface of the skin sample as the point of reference. The specific shift and rotation are applied to the skin sample and saved with the model. See Table 23 for descriptions of the settings.

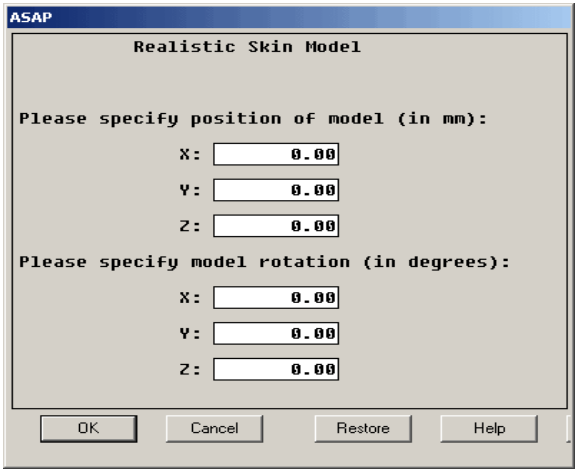


Figure 47 Specify the position and rotation of the sample

Table 23 Position and Rotation Settings

Model position	Specifies the shift of the skin sample in the X, Y, and Z directions.
Model rotation	Specifies the rotation angles around the X, Y, and Z axes.

The Model Code Output dialog (Figure 48) is used to specify the output to be saved and the file name (without the file extension). See Table 24 for descriptions of the settings.

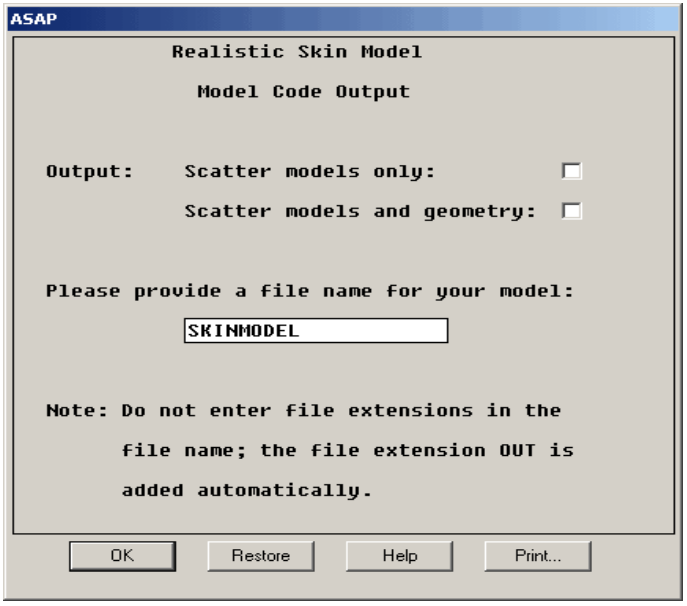


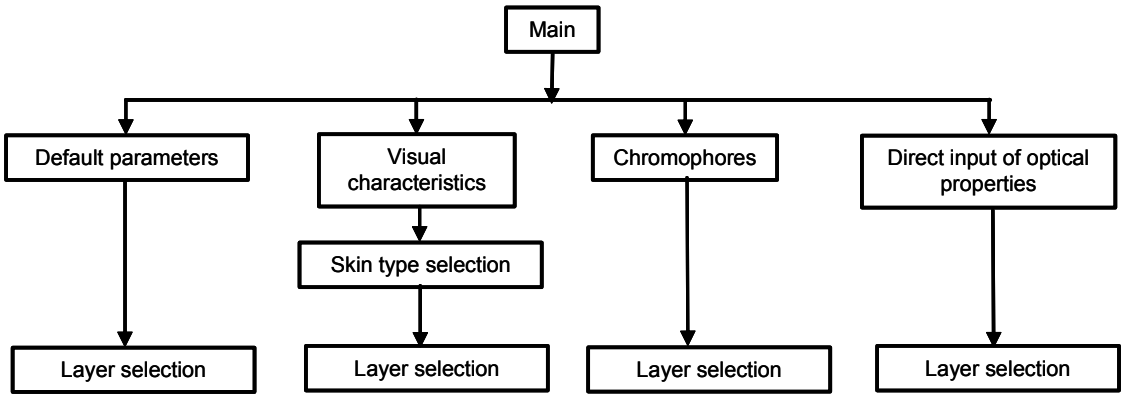
Figure 48 Model Code Output dialog—specify information to save and the file name

Table 24 Model Code Output Settings

Output	Select **Scatter models only** if you want access to only the scatter and absorption properties of the skin sample in a future analysis. Select **Scatter models and geometry i**f you plan to use both the geometry and the scattering/absorption properties of the skin model.
File name	Specify the file name of the modeled skin sample for future access. The file name can be alphanumeric, but cannot contain any of the special characters: \ /**:*?"**<>| The file is saved to your Working Directory with an *.out extension. The file contains all code necessary to recreate the skin model as you defined it. Copy the text in the *.out file to an ASAP *.inr file to use it.

APPENDIX

The RSM provides the optional features of modeling hair, blood vessel, and two-layer dermis with skin layers. However, these features are exclusive to each other, which means that for each model, only one feature can be selected. Availability of a particular feature also depends on the selection of the skin layers being modeled. In this appendix, block diagram illustrations explain allowed combinations for these features and skin layers modeling.



Appendix Figure 1 Illustration of available input methods for skin sample parameters

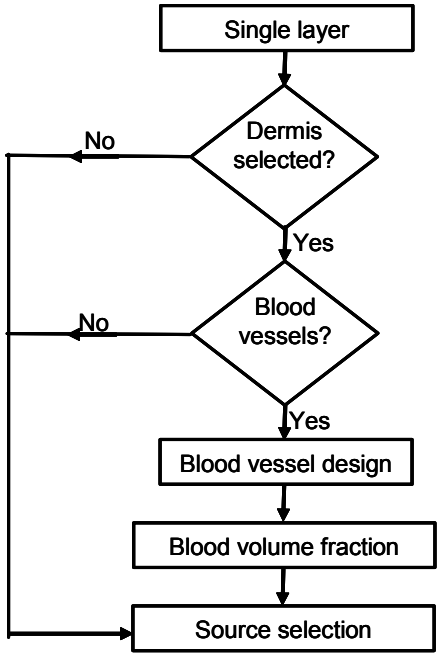


Figure 2 The RSM single-layer skin sample work flow

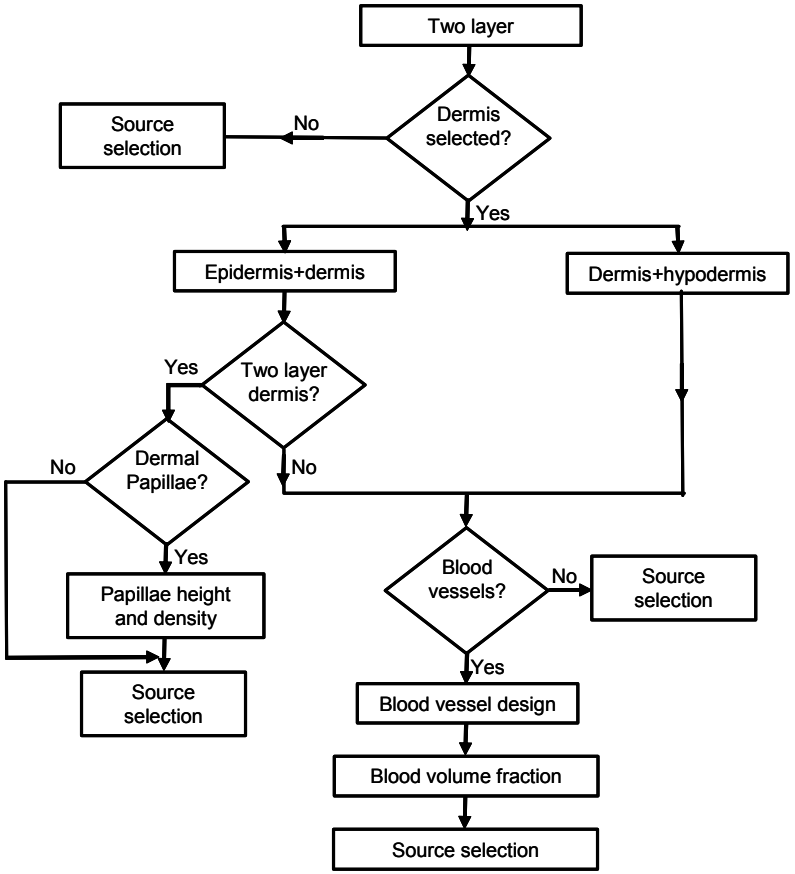


Figure 3 The RSM two-layer skin sample work flow

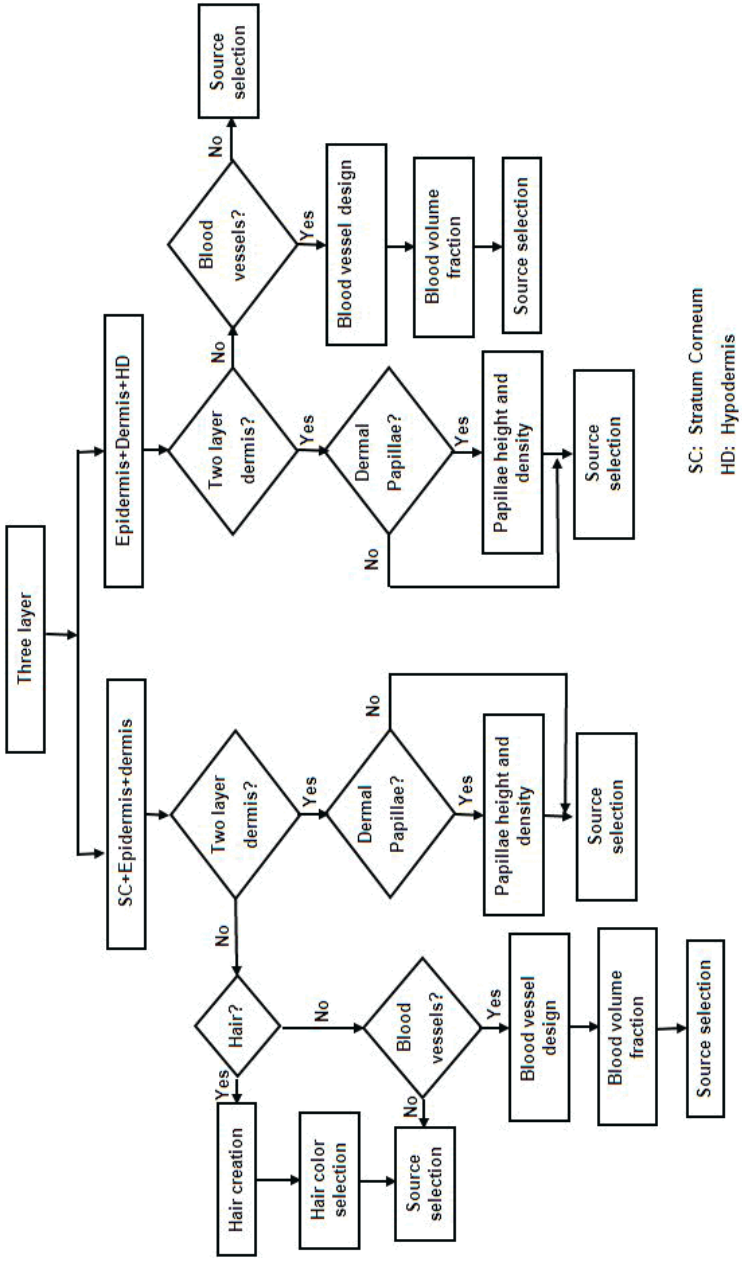


Figure 4 The RSM three-layer skin sample work flow

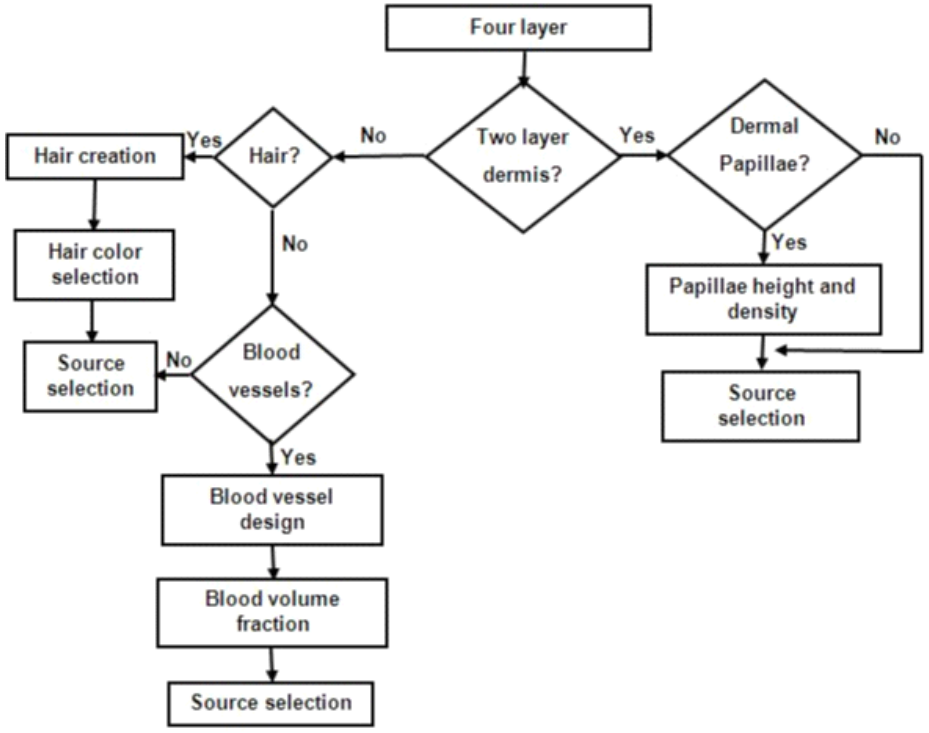


Figure 5 The RSM four-layer skin sample work flow