Contribution of multi and hyperspectral imaging to skin pigmentation evaluation

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Publications available on https://team.inria.fr/ayin/publications-hal/
Problematic introduced by Galderma R&D for early clinic evaluation

**General context:**
- Use measuring techniques such as spectrocolorimetry or imaging, to evaluate skin diseases severity during clinical studies to avoid the *variability of a human diagnosis* based evaluation and to shorten the trial duration.

**Specific context:**
- Use *multi-spectral imaging* to get both spectral and spatial description of the disease.
- Focus on hyperpigmentation and especially on *melasma*
Introduction
   Melasma: hyper-pigmentation
   Data: clinical study description
   State of the art methods
   Goals

Proposed method using spectral imaging

Technologies comparison

Conclusion & Perspectives
Disease showing **darker and irregular spots on the face**. This disease is caused by an abnormal melanocytes activity in response to a hormonal reaction.
**MASI: Melasma Area and Severity Index** is a clinical index to measure melasma severity. It is based on three measurements:

### 3 criteria

- **Area (A): 0 - 6**
  - 0%: normal
  - >90%: severe

- **Darkness (D): 0 - 4**
  - normal
  - severe

- **Homogeneity (H): 0 - 4**
  - normal
  - uniform

### MASI definition

\[
\text{MASI} = 0.3A (D+H) + 0.3A (D+H) + 0.3A (D+H) + 0.3A (D+H)
\]

Source: Journal of the American Academy of Dermatology 2011; 64:78-83.e2
We use 2 clinical studies of melasma. One is used to tune the algorithm, and the other to validate the algorithm:

**Tuning clinical study**

- 384 multi-spectral images (960*1280 pixels and 18 spectral bands)
- 48 patients in 3 groups of 16 (1 treatment per group)
- 3 months study: 1 measure at baseline, then 1 measure per month
- Compare 3 treatments:
  - $S_t$ Standard product for melasma
  - $A_{d2}$ Studied product with dose $d2$
  - $A_{d3}$ Studied product with dose $d3$
- Comparator: $A_{d1}$ such as $d1 < d2 < d3$

**Testing clinical study**
We use 2 clinical studies of melasma. One is used to tune the algorithm, and the other to validate the algorithm:

**Tuning clinical study**

**Testing clinical study**

- 352 multi-spectral images (960*1280 pixels and 18 spectral bands)
- 44 patients in 2 groups of 22 (1 treatment per group)
- 3 months study: 1 measure at baseline, then 1 measure per month
- Compare 2 treatments:
  - A Standard product
  - T Studied product
- Comparator: Vehicle without any active product.
Selected patients have a **symmetrical disease**, one cheek receive the active treatment, and one cheek the comparator.
<table>
<thead>
<tr>
<th>CIE $L^*a^*b$</th>
<th>CIE $L^*a^*b$</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Mixed hemoglobin and melanin</em></td>
<td><em>Mixed hemoglobin and melanin</em></td>
</tr>
</tbody>
</table>

**Pigmentation analysis**

$L^*$ or “Individual Topology Angle: ITA”:

$$ITA = \arctg \left( \frac{L^* - 50}{b^*} \right) \frac{180}{\pi} \leadsto \text{melanin}$$

[Stamatas et al., Pigment cell res, 2004]
Figure: X-axis: wavelength in \textit{nm}. Y-axis: relative absorption (\%) 

\textbf{Stamatas et al. algorithm}

\[ A_{\text{melanine}}(\lambda) = a\lambda + b, \quad \forall \lambda \in [600\,\text{nm}, 700\,\text{nm}], \]
\[ A_c(\lambda) = A(\lambda) - A_{\text{melanine}}(\lambda). \]
\[ A_c \rightarrow \text{corrected absorption.} \]
Clinical study analysis

- Being able to evaluate a treatment efficacy with multi-spectral imaging:
  - With a statistical test on a population of patients
  - By creating a "differential MASI" related to the clinical MASI

Technologies comparison

- Compare spectral imaging with other technologies:
  - Spectrocolorimeter
  - Color imaging
  - Hyper-spectral imaging
Introduction

Proposed method using spectral imaging
  Spectral criterion
  Registration
  Classification
  Change detection
differential MASI

Technologies comparison

Conclusion & Perspectives
We choose to consider **sequentially** the extraction of the **spectral**, the **spatial**, and the **temporal** information

- For an easier understanding of the results
- For computation complexity

We prefer to use a **differential** disease measurement

- It allows to fully use the image information
- It gives intermediate results (changes maps) in addition to MASI values
Proposed method

- **Classification**
  - Classification masks \( t_0 \)
  - Classification

- **Spectral integration**
  - MS images \( t_0 \)
  - MS images \( t_k \)
  - MS images \( t_n \)
  - Registration
  - Monochrome images \( t_0 \)
  - Monochrome images \( t_k \)
  - Monochrome images \( t_n \)
  - Change detection

- **Cartography**
  - Cartography \( t_0/t_k \)
  - Cartography \( t_0/t_n \)
  - Differential MASI

- **MASI**
  - MASI \( t_0/t_k \)
  - MASI \( t_0/t_n \)
Proposed method

- Classification
  - Classification masks $t_0$
- MS images $t_0$
- MS images $t_k$
- MS images $t_n$
- Spectral integration
  - Registration
    - Monochrome images $t_0$
    - Monochrome images $t_k$
    - Monochrome images $t_n$
  - Change detection
    - Cartography $t_0/t_k$
    - Cartography $t_0/t_n$
- Differential MASI
  - MASI $t_0/t_k$
  - MASI $t_0/t_n$

*patents 1 and 2
ICIP’11*
Find the spectral criterion $M$ that allows to highlight the evolution of the pathology in a group of patients receiving a treatment.

We define the criterion $M$ as the vector of the weights assigned to each spectral bands: $M = [\alpha_1, \ldots, \alpha_{N_b}]$

Then the spectral integration is:

$$I_M = \sum_{b=1}^{N_b} \alpha_i l(b),$$

where $l$ is the original spectral image, $N_b$ the number of bands in the initial image, and $I_M$ the integrated image.
Need of a normalisation:

- Normalisation by the comparator treatment
  \[ D_t^e = d_{t,A}^e - d_{t,C}^e \]

- Normalisation by the healthy area
  \[ d_t^e = \mu_{M_h} - \mu_{M_p} \]
  or
  \[ d_t^e = \mu_{M_p} \]
Need of a normalisation:

- Normalisation by the comparator treatment
  \[ D_t^e = d_{t,A}^e - d_{t,C}^e \]

- Normalisation by the healthy area
  \[ d_t^e = \mu_{M_h} - \mu_{M_p} \]
  or
  \[ d_t^e = \mu_{M_p} \]

Finally, we get:

\[ D_t^e = (\mu_{M_{h,A}} - \mu_{M_{p,A}}) - (\mu_{M_{h,C}} - \mu_{M_{p,C}}) \]

or

\[ D_t^e = \mu_{M_{p,A}} - \mu_{M_{p,C}} \]
We focuses on methods that allow to get a **linear combination of spectral bands**

- For feature interpretation.
- For repeatability of the obtained feature.
We look forward the spectral band that maximizes both the distance between healthy and pathological area and between the measurement at time $t_0$ the measurement at $t$:

$$ f = \max_M f(M) $$

with

$$ f(M) = [f_1(M_1), ..., f_{Nb}(M_{Nb})] $$

such as

$$ M_i = [0, ..., 0, 1, 0, ..., 0] $$

and

$$ f_i = \sum_{t=t_1}^{t_{N_t}} \sum_{e=1}^{N_e} [D_t^e(M_i) - D_{t_0}^e(M_i)] $$
Spectral integration: by ICA

When we perform an ICA on multi-spectral image of melasma, we get a component which visually represents the disease:

![Image of spectral integration by ICA]

To get a single spectral combination for all the images, we take the average combination for the whole images of a clinical study.

![Graph showing spectral band index vs. weights]

**Figure:** X-axis: spectral band index, Y-axis: weights
Criteria $L^*$ and $ICA$

- Few correlation between $M_{L^*}$ and the interest spectral areas
- $M_{ICA}$ and interest areas correspond only in the area 600-700 nm

Criterion $f$

- Highest weights of $M$ (in absolute value) correspond to spectral areas where melanin curve dominates the hemoglobin one.
### Spectral integration: Results

Results obtained in the “test study” with the **Wilcoxon test** and the normalisation: 

\[
D^e_t = (\mu_{M_h,A} - \mu_{M_p,A}) - (\mu_{M_h,C} - \mu_{M_p,C})
\]

**Significant disease evolution:**

\[ p \text{ value } < 0.05 = 5.10^{-2} \]

<table>
<thead>
<tr>
<th>Test</th>
<th>Treatment</th>
<th>( t_1 - t_0 )</th>
<th>( t_2 - t_0 )</th>
<th>( t_3 - t_0 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>( L^* )</td>
<td>( S_t )</td>
<td>7.959 ( 10^{-1} )</td>
<td>5.014 ( 10^{-1} )</td>
<td>7.173 ( 10^{-1} )</td>
</tr>
<tr>
<td></td>
<td>( A_{d2} )</td>
<td>3.793 ( 10^{-1} )</td>
<td>1.128 ( 10^{-2} )</td>
<td>8.793 ( 10^{-2} )</td>
</tr>
<tr>
<td></td>
<td>( A_{d3} )</td>
<td>9.798 ( 10^{-2} )</td>
<td>3.204 ( 10^{-3} )</td>
<td>5.312 ( 10^{-4} )</td>
</tr>
<tr>
<td>( b_{590} - b_{405} )</td>
<td>( S_t )</td>
<td>1.476 ( 10^{-1} )</td>
<td>1.089 ( 10^{-1} )</td>
<td>7.563 ( 10^{-1} )</td>
</tr>
<tr>
<td></td>
<td>( A_{d2} )</td>
<td>5.571 ( 10^{-2} )</td>
<td>3.400 ( 10^{-2} )</td>
<td>4.373 ( 10^{-2} )</td>
</tr>
<tr>
<td></td>
<td>( A_{d3} )</td>
<td>8.360 ( 10^{-3} )</td>
<td>3.204 ( 10^{-3} )</td>
<td>9.350 ( 10^{-4} )</td>
</tr>
<tr>
<td>ICA no IR</td>
<td>( S_t )</td>
<td>5.694 ( 10^{-1} )</td>
<td>8.767 ( 10^{-1} )</td>
<td>9.587 ( 10^{-1} )</td>
</tr>
<tr>
<td></td>
<td>( A_{d2} )</td>
<td>4.080 ( 10^{-1} )</td>
<td>2.289 ( 10^{-2} )</td>
<td>8.793 ( 10^{-2} )</td>
</tr>
<tr>
<td></td>
<td>( A_{d3} )</td>
<td>7.873 ( 10^{-2} )</td>
<td>5.233 ( 10^{-3} )</td>
<td>9.350 ( 10^{-4} )</td>
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</table>
Results obtained in the “test study” with the Wilcoxon test and the normalisation: \( D_t^e = (\mu_{M_p,A} - \mu_{M_p,C}) \)

Significant disease evolution: \( p \text{ value} < 0.05 = 5.10^{-2} \)

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<td>( L^* )</td>
<td>( S_t )</td>
<td>7.959 ( 10^{-1} )</td>
<td>6.791 ( 10^{-1} )</td>
<td>6.416 ( 10^{-1} )</td>
</tr>
<tr>
<td></td>
<td>( A_{d2} )</td>
<td>1.306 ( 10^{-2} )</td>
<td>2.289 ( 10^{-2} )</td>
<td>9.798 ( 10^{-2} )</td>
</tr>
<tr>
<td></td>
<td>( A_{d3} )</td>
<td>1.788 ( 10^{-1} )</td>
<td>7.169 ( 10^{-3} )</td>
<td>1.918 ( 10^{-3} )</td>
</tr>
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<td>( b_{590} - b_{405} )</td>
<td>( S_t )</td>
<td>7.173 ( 10^{-1} )</td>
<td>5.349 ( 10^{-1} )</td>
<td>5.014 ( 10^{-1} )</td>
</tr>
<tr>
<td></td>
<td>( A_{d2} )</td>
<td>2.289 ( 10^{-2} )</td>
<td>1.737 ( 10^{-2} )</td>
<td>3.400 ( 10^{-2} )</td>
</tr>
<tr>
<td></td>
<td>( A_{d3} )</td>
<td>1.997 ( 10^{-2} )</td>
<td>1.609 ( 10^{-3} )</td>
<td>9.725 ( 10^{-3} )</td>
</tr>
<tr>
<td>ICA no IR</td>
<td>( S_t )</td>
<td>6.416 ( 10^{-1} )</td>
<td>5.694 ( 10^{-1} )</td>
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<td>1.123 ( 10^{-3} )</td>
</tr>
</tbody>
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Proposed method

Classification

Classification masks $t_0$

MS images $t_0$

Spectral integration

Registration

Monochrome images $t_0$

Monochrome images $t_k$

Monochrome images $t_n$

Change detection

Cartography $t_0/t_k$

Cartography $t_0/t_n$

Differential MASI

MASI $t_0/t_k$

MASI $t_0/t_n$
Proposed method

- Classification
  - Monochrome images $t_0$
  - Monochrome images $t_k$
  - Monochrome images $t_n$

- Spectral integration
  - Registration
    - Change detection
      - Cartography $t_0/t_k$
      - Cartography $t_0/t_n$

- Differential MASI
  - MASI $t_0/t_k$
  - MASI $t_0/t_n$

- Classification masks $t_0$

- WHISPERS'10
- ICIP'10

- Patents 3 and 4
Classification: state of the art

Spectral image

Spectral
- Non-supervised:
  - k-means
  - ISODATA
  - Fuzzy-c-means
  - Mixing (EM)
  - Mean Shift
- Supervised:
  - Knn
  - Max Likelihood
  - SVM

Spectral / Spatial

Spectral extended
- Post treatments
  - MRF
- Constraints
  - [Noordam 2002]
  - [Bandyopadhyay 2005]
  - [Chuang 2006]
  - [Wang 2008]
- Kernel
  - [Mercier 2003]
  - [Camps-Valls 2006]
  - [Fauvel 2007]
  - [Moser 2010]

Joint
- Methods
  - [Gorgetta 2009]
  - [Tarabalka 2010]
  - [Pony 2000]
  - [Jackson 2002]
  - [Tsai 2006]
  - [Collet 2009]
  - [Aksoy 2006]
  - [Farag 2005]
  - [Huang 2009]
  - [Fauvel 2007]
  - [Linden 2007]
  - [Dell’Acqua 2004]
  - [Benediktsson 2005]
  - ...

Spatial (extended)
- Split/Merge
  - ECHO
  - HSEG
  - BTP
- MRF
  - [Pony 2000]
  - [Rellier 2002]
  - [Hazel 2002]
  - [Plaza 2002]
  - [Velasco-Forero 2010]
  - [Pesaresi 2001]
  - [Dell’Acqua 2004]
  - [Della Murra 2011]
  - [Li 2007]
  - [Noyel 2008]
Classification into two classes with a linear separator

1- Training

Determine the separator on a training set by maximizing the margin.

2- Classification

Assign a class to each pixel according to its relative position to the separator.

[V. Vapnik, John Wiley and Sons, Inc., 1998]
Non-linear case

Kernel:

\[ K(\vec{x}_i, \vec{x}_j) = \Phi(\vec{x}_i) . \Phi(\vec{x}_j) = \exp \left( -\frac{||\vec{x}_i - \vec{x}_j||^2}{2\sigma^2} \right) \]
Accurate classification in the flat area.
No detection in area affected by the face volume.
Need a training for each image.

⇒ Need volume compensation
⇒ Need global training
Accurate classification in the flat area.
No detection in area affected by the face volume.
Need a training for each image.

⇒ Need volume compensation
⇒ Need global training
Classification: Global scheme

- Training pixels
  - Data reduction
  - Fourier filtering
  - Volume Compensation
  - Histogram specification
  - SVM training

- MS images
  - Data reduction
  - Fourier filtering
  - Volume Compensation
  - Histogram specification
  - SVM classification
  - Connected components analysis
  - SVM classification map
  - Gaussian mixture analysis
  - Connected components analysis
  - Segmentation map

- Operator
- Final classification
Classification: Interactive classification

(a) Selection on the SVM classification

- I - Segmentation map with a 80% high pass Fourier filter
- II - Segmentation map with a 60% high pass Fourier filter
- III - Original interest band
- IV - Final classification

(b) Selection on the segmentation map
Classification: results

(a) image 1  (b) image 2  (c) image 3

(d) classification  (e) classification  (f) classification
Correlation of the pathological area between the dermatologist and the proposed method

- Test study: 0.76 correlation (0.58 for SVM alone)
- Validation study: 0.71 correlation (0.45 for SVM alone)

Figure: X-axis: area measured by the algorithm, Y-axis: area measured by the dermatologist
Proposed method

Classification

Classification masks $t_0$

MS images $t_0$

Spectral integration

Registration

Monochrome images $t_0$

Monochrome images $t_k$

Monochrome images $t_n$

Change detection

Cartography $t_0/t_k$

Cartography $t_0/t_n$

Differential MASI

MASI $t_0/t_k$

MASI $t_0/t_n$

patents 5 (part 1)

ISBI’13 (submitted)

IEEE TMI (submitted)
Change detection: state of the art

- Change detection based on image difference and thresholding
  - + Preserve the image structures
  - - Need to set a threshold (often arbitrary)
- Change detection based on a statistical test and a local analysis
  - + Good theoretical background to make the significance decision
  - - Loss of resolution
  - - Can alter the image structures
- Change detection based on transformations (PCA...)
  - Techniques for multi-variate data (video, multi-channel...)
Examples of change maps

(a) $l^1_c$ equalised

(b) Binary map $t_1$

(c) Level map $t_1$

(d) $l^2_c$ equalised

(e) Binary map $t_2$

(f) Level map $t_2$

(g) $l^3_c$ equalised

(h) Binary map $t_3$

(i) Level map $t_3$
Proposed method

- Classification
  - Classification masks $t_0$
  - MS images $t_0$
  - MS images $t_k$
  - MS images $t_n$

- Spectral integration
  - Monochrome images $t_0$
  - Monochrome images $t_k$
  - Monochrome images $t_n$

- Registration

- Change detection
  - Cartography $t_0/t_k$
  - Cartography $t_0/t_n$

- Differential MASI
  - MASI $t_0/t_k$
  - MASI $t_0/t_n$

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Contribution of multi and hyperspectral imaging to skin pigmentation evaluation
differential MASI: Examples

(a) $I_c^1$ equalised
(b) $I_c^2$ equalised
(c) $I_c^3$ equalised

(d) MASI $t_1$
(e) MASI $t_2$
(f) MASI $t_3$
differential MASI: Examples

(a) $I_c^1$ equalised
(b) $I_c^2$ equalised
(c) $I_c^3$ equalised
(d) MASI $t_1$
(e) MASI $t_2$
(f) MASI $t_3$
Reminder: clinical analysis of the validation study:

<table>
<thead>
<tr>
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<th>$t_1 - t_0$</th>
<th>$t_2 - t_0$</th>
<th>$t_3 - t_0$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$L^*$ spectro-colorimeter</td>
<td>$A$</td>
<td>$9.482 \times 10^{-1}$</td>
<td>$4.169 \times 10^{-1}$</td>
<td>$8.582 \times 10^{-1}$</td>
</tr>
<tr>
<td></td>
<td>$T$</td>
<td>$1.831 \times 10^{-1}$</td>
<td>$2.508 \times 10^{-2}$</td>
<td>$8.755 \times 10^{-4}$</td>
</tr>
</tbody>
</table>

Differential MASI results on the validation study:

- **Darkness:**

<table>
<thead>
<tr>
<th>Test</th>
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<th>$t_1 - t_0$</th>
<th>$t_2 - t_0$</th>
<th>$t_3 - t_0$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Darkness</td>
<td>$A$</td>
<td>$6.494 \times 10^{-1}$</td>
<td>$5.589 \times 10^{-1}$</td>
<td>$1.045 \times 10^{-1}$</td>
</tr>
<tr>
<td></td>
<td>$T$</td>
<td>$6.729 \times 10^{-1}$</td>
<td>$3.743 \times 10^{-4}$</td>
<td>$3.553 \times 10^{-4}$</td>
</tr>
</tbody>
</table>

- **Area:**

<table>
<thead>
<tr>
<th>Test</th>
<th>Treatment</th>
<th>$t_1 - t_0$</th>
<th>$t_2 - t_0$</th>
<th>$t_3 - t_0$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Area</td>
<td>$A$</td>
<td>$2.840 \times 10^{-1}$</td>
<td>$3.986 \times 10^{-1}$</td>
<td>$1.045 \times 10^{-1}$</td>
</tr>
<tr>
<td></td>
<td>$T$</td>
<td>$4.552 \times 10^{-1}$</td>
<td>$3.478 \times 10^{-3}$</td>
<td>$2.438 \times 10^{-4}$</td>
</tr>
</tbody>
</table>
**Homogeneity:** The homogeneity criterion makes sense only for patient whose pathological area changes. We then focus on the treatment $T$ of the validation study:

![Graph](image)

**Figure:** X-axis: time in weeks, Y-axis: Homogeneity for each patients receiving $T$

- 11 patients evolve after 4 weeks
- 4 patient evolve after 8 weeks
- 7 patients did not evolve for area criterion $\rightarrow$ no homogeneity measurement
The differential MASI allows to measure the time evolution of melasma with the three criteria defined from the clinical MASI (Area, Darkness, Homogeneity).

The Area and Darkness criteria allow to retrieve the clinical analysis conclusions.

The Homogeneity criterion allows to get a supplementary information for patients whose Area and Darkness evolve.
Introduction

Proposed method using spectral imaging

Technologies comparison
- Spectrocolorimetry vs multi-spectral imaging
- Color imaging vs multi-spectral imaging
- Hyper-spectral vs multi-spectral imaging

Conclusion & Perspectives
Wilcoxon test between $t_0$ and $t$:

<table>
<thead>
<tr>
<th>$M$</th>
<th>Treatment</th>
<th>$t_1 - t_0$</th>
<th>$t_2 - t_0$</th>
<th>$t_3 - t_0$</th>
</tr>
</thead>
<tbody>
<tr>
<td>L* spectro-colorimeter</td>
<td>$S_t$</td>
<td>$2.552 \times 10^{-1}$</td>
<td>$6.416 \times 10^{-1}$</td>
<td>$9.176 \times 10^{-1}$</td>
</tr>
<tr>
<td></td>
<td>$A_{d2}$</td>
<td>$6.416 \times 10^{-1}$</td>
<td>$1.337 \times 10^{-1}$</td>
<td>$4.942 \times 10^{-2}$</td>
</tr>
<tr>
<td></td>
<td>$A_{d3}$</td>
<td>$6.267 \times 10^{-2}$</td>
<td>$1.609 \times 10^{-3}$</td>
<td>$9.725 \times 10^{-3}$</td>
</tr>
<tr>
<td>$b_{590} - b_{405}$ spectro-colorimeter</td>
<td>$S_t$</td>
<td>$1.476 \times 10^{-1}$</td>
<td>$4.691 \times 10^{-1}$</td>
<td>$4.379 \times 10^{-1}$</td>
</tr>
<tr>
<td></td>
<td>$A_{d2}$</td>
<td>$5.694 \times 10^{-1}$</td>
<td>$1.961 \times 10^{-1}$</td>
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The spectral imaging is equivalent to a “2D” spectrocolorimeter
Wilcoxon test between $t_0$ and $t$:

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<th>$M$</th>
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<th>$t_2 - t_0$</th>
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<td></td>
</tr>
</tbody>
</table>

The spectral imaging is more discriminative than a RGB image.
The spectral resolution of the hyper-spectral imaging is larger than multi-spectral imaging. We can think that it allows to quantify more precisely skin characteristics.

Nevertheless:

The hyper-spectral camera requires fine adjustments and a precise calibration.

Duality between acquisition time and spatial resolution ⇒ long acquisition time for a face.

Multi-spectral imaging seems to be more adapted for a practical use on in-vivo skin analysis.
Outlines

Introduction

Proposed method using spectral imaging

Technologies comparison

Conclusion & Perspectives
We design a strategy to analyse a clinical study involving about 4*90 multi-spectral images:
We design a strategy to analyse a clinical study involving about 4*90 multi-spectral images:

- **Automatic analysis:**
  - A registration algorithm (~ 12-24 hours on a 2.2Ghz core)
  - A feature extraction algorithm (~ 1 min on a 2.2Ghz core)
  - A classification algorithm (~ 2 hours on a 2.2Ghz core)

- **Operator interactions:**

- **Automatic statistic calculation:**
  - A change detection algorithm (~ 1.5 hours on a 2.2Ghz)
  - Integration of the extracted informations in a severity criterion ("diagnostic MASI")
We design a strategy to analyse a clinical study involving about 4*90 multi-spectral images:

- **Automatic analysis:**
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- **Operator interactions:**
  - Interactive classification (about 1 hour on about 90 images)
  - Registration control

**Conclusion**

S. Prigent  
Contribution of multi and hyperspectral imaging to skin pigmentation evaluation 48/51
We design a strategy to analyse a clinical study involving about 4*90 multi-spectral images:

- **Automatic analysis:**
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  - A feature extraction algorithm (∼ 1 min on a 2.2Ghz core)
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  - Registration control

- **Automatic statistic calculation:**
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  - Integration of the extracted informations in a severity criterion (“differential MASI”)

Contribution of multi and hyperspectral imaging to skin pigmentation evaluation
We validate the methodologies on a complete clinical study.

We implement the process on a software.

We compare the multi-spectral technology with spectrocolorimetry, color imaging and hyper-spectral imaging.

- Multi-spectral imaging fits the best the problem, in terms of both provided information and practical use.
The proposed algorithms are quite general. The methodology can then be extended to other pathologies such as vitiligo, rosacea or scars.

- The classification step should be adapted
- The clinical criterion should match the disease clinical analysis

- Perform change detection in the spectral space and not only in the 1D feature space?
- Analyse the pathology evolution both in positive and negative senses.
Contribution summary

- **Answer to the question** "Contribution of multi-spectral imaging":
  - multi-spectral ↔ 2D spectrocolorimeter
  - multi-spectral is more adapted than RGB or hyper-spectral
- **Design** a severity score on multi-spectral images
- **Implement** the proposed methods on a software

- **Publications**:
  - 5 patents
  - 3 international conference articles ([WHISPERS’10](#), [ICIP’10](#), [ICIP’11](#))
  - 1 international conference article submitted (ISBI’13)
  - 1 international journal paper submitted (IEEE TMI)
  - 2 Inria research reports ([RR-8105](#) and [RR-8136](#))