Received: 31 October 2023 | Accepted: 20 December 2023

DOI: 10.1111/srt.13602

ORIGINAL ARTICLE

WILEY

Predicting the evolution of clinical skin aging in a multi-ethnic population: Developing causal Bayesian networks using dermatological expertise

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Abstract

Introduction: Software to predict the impact of aging on physical appearance is increasingly popular. But it does not consider the complex interplay of factors that contribute to skin aging.

Objectives: To predict the +15-year progression of clinical signs of skin aging by developing Causal Bayesian Belief Networks (CBBNs) using expert knowledge from dermatologists.

Material and methods: Structures and conditional probability distributions were elicited worldwide from dermatologists with experience of at least 15 years in aesthetics. CBBN models were built for all phototypes and for ages ranging from 18 to 65 years, focusing on wrinkles, pigmentary heterogeneity and facial ptosis. Models were also evaluated by a group of independent dermatologists ensuring the quality of prediction of the cumulative effects of extrinsic and intrinsic skin aging factors, especially the distribution of scores for clinical signs 15 years after the initial assessment.

Results: For easiness, only models on African skins are presented in this paper. The forehead wrinkle evolution model has been detailed. Specific atlas and extrinsic factors of facial aging were used for this skin type. But the prediction method has been validated for all phototypes, and for all clinical signs of facial aging.

Conclusion: This method proposes a skin aging model that predicts the aging process for each clinical sign, considering endogenous and exogenous factors. It simulates aging

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curves according to lifestyle. It can be used as a preventive tool and could be coupled with a generative AI algorithm to visualize aging and, potentially, other skin conditions, using appropriate images.

KEYWORDS
causal Bayesian networks, elicitation, multi-ethnic, phototypes, skin aging, skin aging model, skin of color

1 | INTRODUCTION

Skin is the most visible and aesthetic indicator of human aging, and has an important social and psychological impact.[1–3] In addition, skin aging may also decrease the skin's immune defense and slow down skin repair, while increasing the risk of developing skin cancers following sun exposure.[4–7]

Facial skin aging is affected by intrinsic (chronologic) aging, triggered mainly by genetic and extrinsic aging caused by environmental factors.[8–10] Dermatologists know that these factors influence facial aging, depending on the age range, the type of clinical signs of aging and the intensity of the extrinsic factor involved. Considering data from medical investigations, such as medical history, lifestyle (including tobacco and alcohol consumption), UV exposure habits, sensitivity to UV, and from clinical examination including constitutive pigmentation, apparent versus real age, and the shape of the face, the first signs of exposure to the sun may allow experienced dermatologists to predict, to a certain extent, the skin aging evolution in a given individual.[11] However, this evaluation remains subjective and may not be transposable from one individual to another.

Currently, software that predicts and modifies digital photographs to visualize facial aging can be easily accessed. However, these programs do not consider the complex interplay of the various factors that contribute to facial skin aging. Thus, in a reliable and objective matter for a given individual, it is impossible to obtain compiled information about specific facial skin ageing. Developing a method, using expert knowledge elicitation that allows to creation of a predictive model validated by dermatologists in a multiethnic population and to build a facial skin aging model usable in all individuals, is of great interest.

Causal Bayesian Belief Networks (CBBNs) may be useful to develop this type of model. CBBNs are graphical models, representing the causal relationships between risk factors and their influence on skin aging progression. They provide a framework for assessing the impact of various lifestyle habits. Their intuitive representation, made of nodes and arcs, makes them both user-friendly and easy to interpret.

The aim of this project was to develop CBBNs to objectively predict the evolution of facial skin aging in all phototypes 15 years after their initial assessment, by considering the knowledge and experience of an international group of experienced dermatologists, through a causal modelling method with expert knowledge elicitation.

2 | MATERIAL AND METHODS

The development of CBBN models was performed in four consecutive steps.

- Step 1: Selecting skin aging risk factors

During step 1, in 2022, an international group of 22 dermatologists from Brazil (1; assessing phototypes V to VI; African skin), China (6; assessing phototypes I to IV; Asian skin), France (10; 7 assessing phototypes I to IV; European-origin skin and 4 assessing phototypes V and VI; African skin), South Africa (2; assessing phototypes V and VI; African skin) and the United States (3; assessing phototypes V and VI; African skin) with at least 15 years' experience in dermatology, discussed facial skin aging, and selected the visible clinical signs which are typical markers of skin aging. These markers were grouped into 3 families: wrinkles, pigmentary heterogeneity, and ptosis. The different facial skin atlas for Asian, European-origin, and Afro-American skin, covering all 6 phototypes, served as metrics for scoring facial skin aging signs.[12–15]

Extrinsic and intrinsic parameters constitute the causes of skin aging evolution. For each skin aging marker, risk factors (extrinsic) were listed independently of the intrinsic aspect of aging.

While extrinsic factors are easy to define, it is more difficult to define intrinsic factors. Therefore, a node with all potential *chrono-aging* intrinsic information—named *Chronos*—was defined by the experts.

For each risk factor, a set of states was defined, corresponding to the possible values of this risk factor. For example, a "Tobacco consumption" factor can be associated with a "no," "mild" or "high" risk. Among these states, one is considered as neutral (not impacting evolution, for example, "none" is the neutral state for tobacco consumption). For the sake of simplicity, all risk factors that refer to skin pathologies and medication intake were not considered (all models were conditioned on healthy people). Moreover, menopaused women under hormone replacement therapy and who had undergone aesthetic invasive practices such as facial lifting or injections were not considered.

CBBNs were constructed based on expert knowledge elicitation. This elicitation process was segmented into two distinct phases: the development of a graphical structure, which involved defining nodes and establishing causal relationships (step 2); and determining the corresponding conditional probabilities (step 3). A distinct model was constructed for each marker, designed for the specific skin types of European origins, Asians, and Africans.

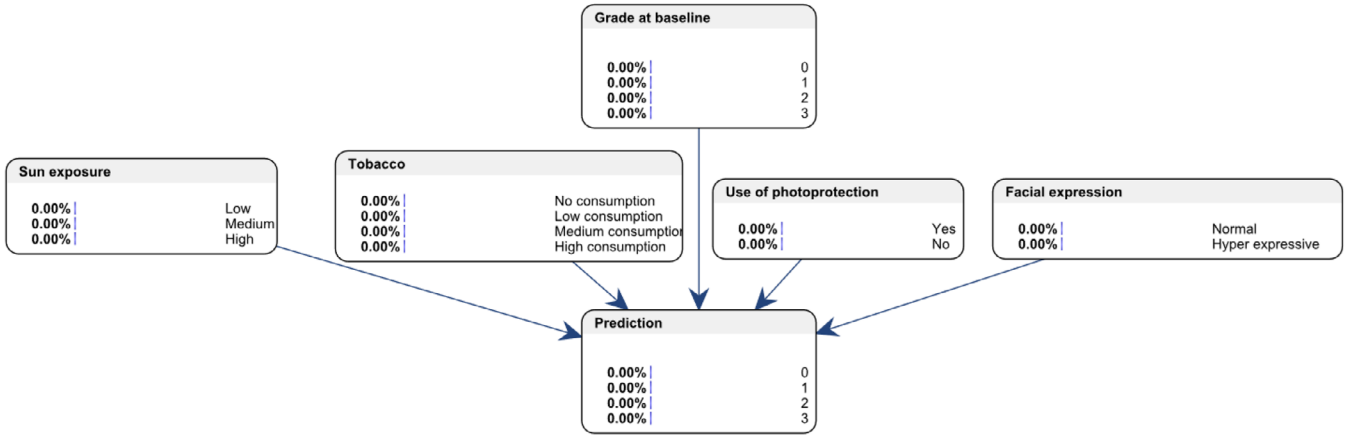


FIGURE 1 Example of structure with all causes connected to the prediction. In this structure, five nodes were considered, each with state counts of 3, 4, 2, 2 and 4, respectively. Multiplying these numbers of states, the total number of states for prediction is: $n = 3\times4\times2\times2\times4 = 192$.

The BayesiaLab® software and its BEKEE® web module (Bayesia S.A.S., Changé, France) were used for the elicitation of the structure and parameters of the CCBNs. This software provides a comprehensive "lab" environment for machine learning, knowledge modelling, analytics, simulation, and optimization.

- Step 2: Elicitation of the graphical model structure

The approach to constructing structures was based on agreed facial skin aging signs. Models were built for all phototypes (I to VI) and for all ethnic origins, as well as for age groups ranging from 18 to 65 years.

The models had to represent how individual risk factors influence the baseline grade (score) to determine the resulting grade 15 years later. In a CBBN, each node represents a specific dimension or aspect of the domain, for example, "Sun Exposure." An arc linking two nodes means that there is a cause-to-effect relationship. For example, if a node representing "Sun Exposure" with states (Low, Medium, High) is connected by an arc to another node called "Photoprotection" with states (Occasionally, Daily), the probabilities related to "Photoprotection" are conditioned by the states of "Sun Exposure." More precisely, probability values must be defined for "Photoprotection" to be "Occasionally" or "Daily" for each state of "Sun Exposure": Low, Medium, and High (6 in total)

A straightforward approach may link all causal nodes directly to the effect node (Figure 1). However, such an approach would entail an overwhelming number of probabilities to assess, thereby making it impractical.

The Independence of Causal Influence (ICI) approach offers a solution to the complexity of establishing a direct link between all causal nodes and the effect node.[16–19] In the ICI structure, an independent "impact" node is associated with each risk factor. This node captures the local effect of the risk factor on the prediction, specifically the influence when all other causes are in their neutral state. Although these impacts are presumed to operate independently, they are combined using functions such as OR, AND, MAX, MIN, SUM, etc., as depicted in Figure 2.

- Step 3: Elicitation of probabilities—Quantification of the CBBNs

During step 3, dermatologists were asked to determine the probabilities associated with the different grades, according to a given scenario for all skin aging markers. As a result, the models did not provide a single grade, but all possible grades, each associated with its corresponding probability.

For each extrinsic factor related to a specific marker, experts were asked to determine, on the baseline grade, the likelihood of observing either a worsening (i.e., an increase of +1 to +3 grades) or an attenuating effect (−3 to −1). Each expert carried out an elicitation for each extrinsic factor concerning its impact on facial skin aging signs over a span of 15 years, in addition to the intrinsic effect, referred to as "*Chronos*."

For the quantification of the skin aging models, the Bayesia Expert Knowledge Elicitation Environment BEKEE® was used. BEKEE® was designed to mitigate the adverse group biases that may emerge during knowledge elicitation brainstorming sessions via a DELPHI approach. To guarantee the independent elicitation of probabilities, experts were provided with web-based interactive questionnaires, which were integrated with the session facilitator's BayesiaLab® application.

- Step 4: Independent evaluation

During this step, the quality of the models was evaluated by a cohort of independent dermatologists. These dermatologists did not take part in the initial model design process and relied on established skin aging references for their assessments.[10–13,16] Upon different simulating various scenarios, they assigned scores to the different outputs based on the following scale: 0 for a random model, 1 for not realistic, 2 when some predictions seemed realistic, 3 when predictions were realistic but some impacts were under- or over-estimated, 4 when they were

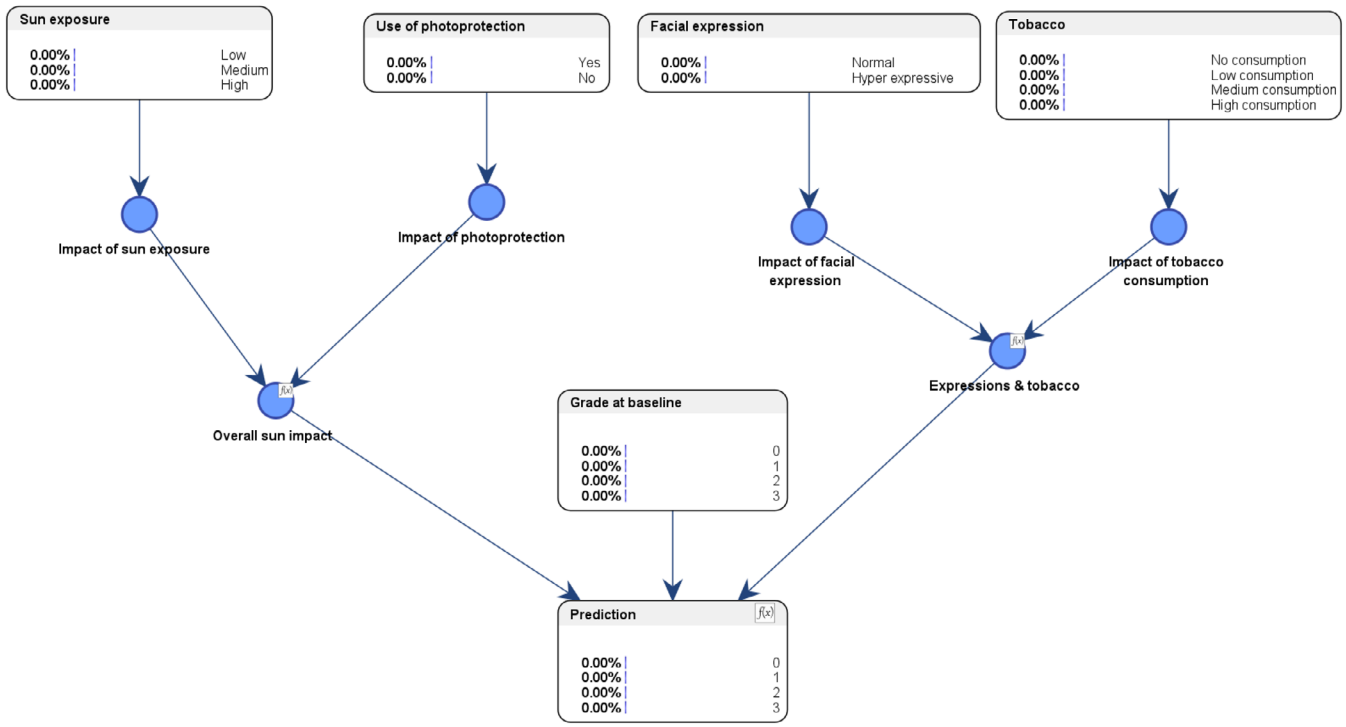


FIGURE 2 ICI with local effects, dimension of prediction node, using the ICI structure, the number of states for prediction were significantly reduced to a total of $n = 32$.

realistic, and 5 to denote state-of-the-art models. This methodology allowed us to gauge the realism of predictions regarding the combined impacts of extrinsic and intrinsic factors on skin aging, especially focusing on the distribution of grades for clinical signs over a 15-year span.

3 | RESULTS

For the sake of simplicity, this paper only describes models related to skin phototypes V or VI. Based on expert recommendations, ITA values (a colorimetric measure of skin tone) were used as they were considered to be more pertinent than phototype assessments for assessing the significance of extrinsic factors related to photo-aging and pigmentary heterogeneity.[20] Furthermore, for this demographic, experts highlighted the influence of certain specific risk factors, such as the use of skin-lightening products or an aggressive scrubbing regimen. These factors might not be relevant or may be of lesser significance, for other phototypes.

Facial skin aging signs selected by the experts, and which were considered for the models, are given in Table 1.

- Step 1: Selecting skin aging risk factors.

As examples, the models focus on forehead wrinkles and nasolabial folds. Table 2 lists risk factors identified by experts and that influence the development of both clinical signs.

- Step 2: Elicitation of graphical model structure

TABLE 1 Facial skin aging signs considered for models.

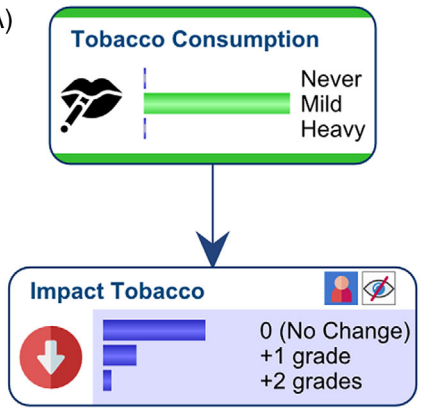
Wrinkles—Upper Part of the face	Forehead, glabella, inter-ocular, crow's feet, under-eye, eye bags
Wrinkles—Lower Part of the face	nasolabial, upper lip, marionettes lines
Pigmentation & skin texture	Pigmentary heterogeneity, lower face ptosis, cheek pores

TABLE 2 Risk factors that may impact forehead wrinkles or nasolabial folds.

Clinical sign	Risk factors
Forehead wrinkles	Sun exposure, ITA, geographic location, frequency of photoprotection, sun protection factor, tobacco consumption Sleep quality, skin thickness, facial expression, uncorrected vision problem, use of moisturizers, use of anti-aging products, baseline wrinkle severity
Nasolabial folds	Sun exposure, ITA, geographic location, frequency of photoprotection, sun protection factor, tobacco consumption Stress, facial expression, body mass index, baseline wrinkle severity, genetic predisposition

For each risk factor, an "impact node" was created, representing the local causal effect of the given risk factor on the progression of skin aging. The different states of this impact node denote potential shifts,

(A)



(B)

	0	x+1	x+2	Mean
Never (non-smoker)	100.000	0.000	0.000	0
Mild (social smoker)	70.60	23.25	6.15	+0.36
High (heavy smoker)	36.341	37.154	26.504	+0.90

FIGURE 3 Example of the impact of tobacco consumption on the evolution of forehead wrinkles starting at the age of 35 years in individuals with a phototype V or VI, In the example presented, dermatologists estimated that, on average, individuals who are social smokers experience a worsening of +0.36 grade over a span of 15 years. It became +0.9 grade if individuals are heavy smokers. Note that the "non-smoker" state served as the neutral state in these assessments.

whether worsening or attenuating. For instance, an impact node with states (+0;+1; +2) signifies that the associated risk factor can either have no influence (no change), amplify the baseline grade by +1, or intensify it by +2, over a span of 15 years.

Figure 3A provides a visual representation of a risk factor linked to its respective impact node.

- Step 3: Knowledge elicitation
  - *Knowledge elicitation of impact nodes*

Independent dermatologists defined a probability distribution over the states of the impact nodes via the BEKEE® interface (under the assumption that all other risk factors remain in their neutral states). Along with this distribution, they also specified a confidence level, which ranged from 0% (indicating complete uncertainty) to 100% (indicating absolute certainty).

Following this, a consensus probability distribution was derived by combining all individual distributions and their associated confidence levels. This consensus distribution served as the foundation for group discussions within the BayesiaLab® interface. After these deliberations, experts added their answers. This cycle of providing input, discussing, and revising, was repeated until no further revision was required, mirroring the DELPHI method. The output of this process corresponds to the consensual conditional probability table, which encapsulates the collective insights of the expert group.

Figure 3 shows the impact of tobacco consumption on the development of forehead wrinkles.

  - *Combination of impacts*

Once probability distributions for the impact of extrinsic factors were determined, they were combined using deterministic mathematical functions, selected by experts based on associated risk factors.

Figure 4 illustrates the combination of impacts from facial expression (F) and uncorrected vision problems (S) to derive an overall wrinkling impact (W). Based on expert insights and referencing various skin atlases, only the most significant contributor was considered for determining W. This approach was mathematically represented by considering the maximum impact between F and S, to establish the conditional probability table for W. In this example, both F and S are fully observed, yielding a deterministic value for W. However, in practical applications of the model where the impacts are not directly observed with only risk factors being observed), the output for W is presented as a probability distribution.

Figure 5 illustrates an example of an additive combination approach. The impact of tobacco consumption (T) is combined with the effect of sleep quality (SQ). Consequently, a social smoker with poor sleep quality may experience a more pronounced effect than a social smoker with better sleep habits. Specifically, the probability of no change decreases while the probabilities of a +1 and +2-grade increase rise. This combined probability is derived from summing the effects of T and SQ, with the final value capped at the highest point on the severity scale.

Specific factors may exacerbate facial aging signs over time, and within the models. The latter are defined by impacts that are exclusively associated with positive or neutral values. Examples include tobacco consumption, facial expression, and sun exposure.[4] On the other hand, several other factors may have a protective or improving effect on facial aging over a 15-year period, such as photoprotection using clothes or tinted sunscreens. While improving impacts are associated with negative values, protective impacts are represented with a "protective" coefficient.

Combination nodes were combined to obtain the overall exogeneous impact node, as illustrated in Figure 6.

Once all factors were in their neutral state, the overall exogenous impact equaled a +0 grade, indicating no change over a 15-year period.

The intrinsic impact, labeled as *"Chronos,"* served as a corrective mechanism to prevent predictions that might have neglected a fundamental or "minimal" level of aging. It encompasses all internal factors, from genetic predispositions to tissue degeneration. When combined with the exogenous factors it, defines the "Beauty Trajectory" (BT) which cannot take a negative value as the aging is not reversible: *Grade (t+15) ≥ Grade (t)*

  - *Adding age information and prediction*

The prediction labeled "+15 years" is determined by combining the baseline grade and the "Beauty Trajectory" with the Sum function (Figure 7).

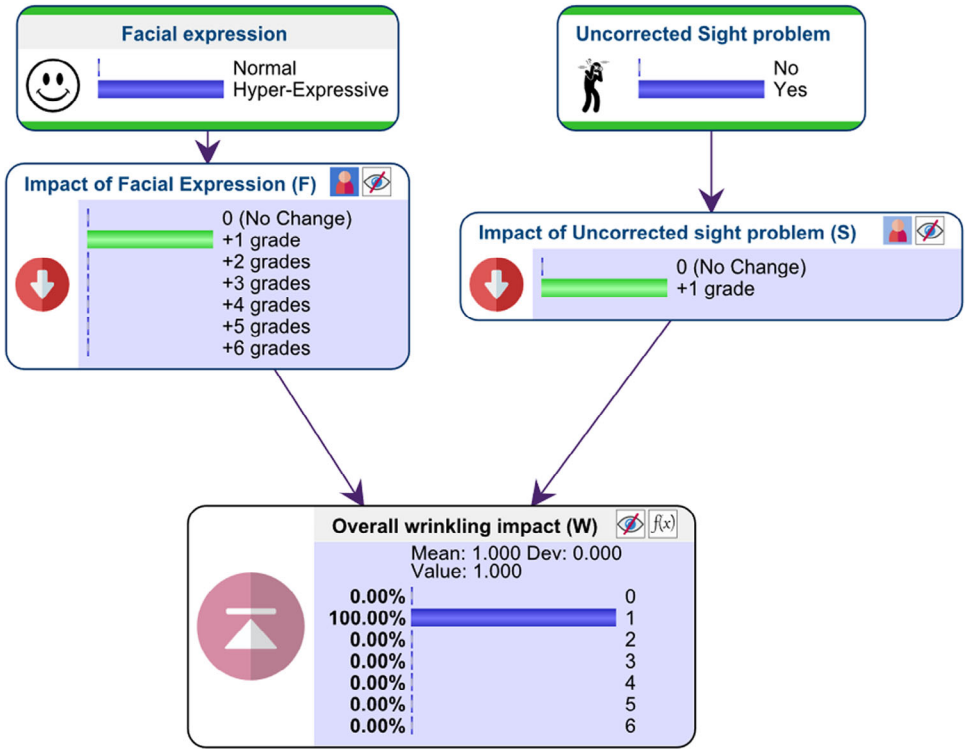


FIGURE 4 Examples of grouped impacts based on the evolution model of forehead wrinkles starting at the age of 35 years in individuals with a phototype V or VI.

Initially, experts evaluated all impact nodes to forecast the evolution from the age of 35 to 50 years. To streamline the process and to avoid repetitive evaluations for age brackets between 18–35 and 50–65, an "age factor" was introduced. This factor adjusts the overall exogenous impact as the age category changes. Concurrently, a specific *Chronos* is specified for each age group.

By incorporating an "Age" node, the model gained the ability to make predictions at 15 years, across a continuum of ages. This was achieved by appropriately weighing the ages of 18, 35, or 50 years. As an example, to calculate the skin aging grade of a 28-year-old individual at 43 years, the model combines the predictions for the age of 18 years (41.2%) and of 35 yea rs (58.8%).

o *Verification*

The experts validated the probability estimates for each impact node by running a series of test scenarios on hypothetical individuals. If the results from these test scenarios did not align with expectations or were not consistent, the experts checked and revised the previous steps.

To further evaluate the model's quality, a sensitivity analysis was conducted using a tornado plot. This plot showcases the relative influence of each factor on the outcome, indicating which variables have the most significant impact on the predictions. An illustrative tornado plot is presented in Figure 8.

o *Modeling of genetic predispositions for nasolabial folds*

The evolution of a certain number of facial skin aging signs is mainly driven by genetic predisposition and extrinsic factors, while chrono-aging should not be considered the same according to this predisposition (genetically predisposed individuals may present with a faster evolution compared to non-predisposed individuals).[21] These clinical signs include the evolution of cheek pores, eye sagging or nasolabial folds.[22–25] For the latter sign, some individuals may present with a specific face shape that predisposes them to an unfavorable evolution. For this reason, the face shape is nested within the information of the genetic dimension.

For example, genetic predisposition is the common cause of increased severity of nasolabial folds at baseline and for chrono-aging acceleration. The causal structure that considers this rational is given in Figure 9.

o *Grade at baseline and past worsening behavior*

The cumulative impact of a past exposition to extrinsic factors on facial skin aging signs is given by a defined severity grade at baseline.[12–15,26]

As an example, individuals over the age of 50 years with a phototype III who frequently exposed themselves to sunlight without protection display a higher baseline severity for crow's feet wrinkles compared to those who consistently used an effective photoprotection. Thus, the baseline grading serves as a marker of previous detrimental influences.

- Step 4: Independent verification

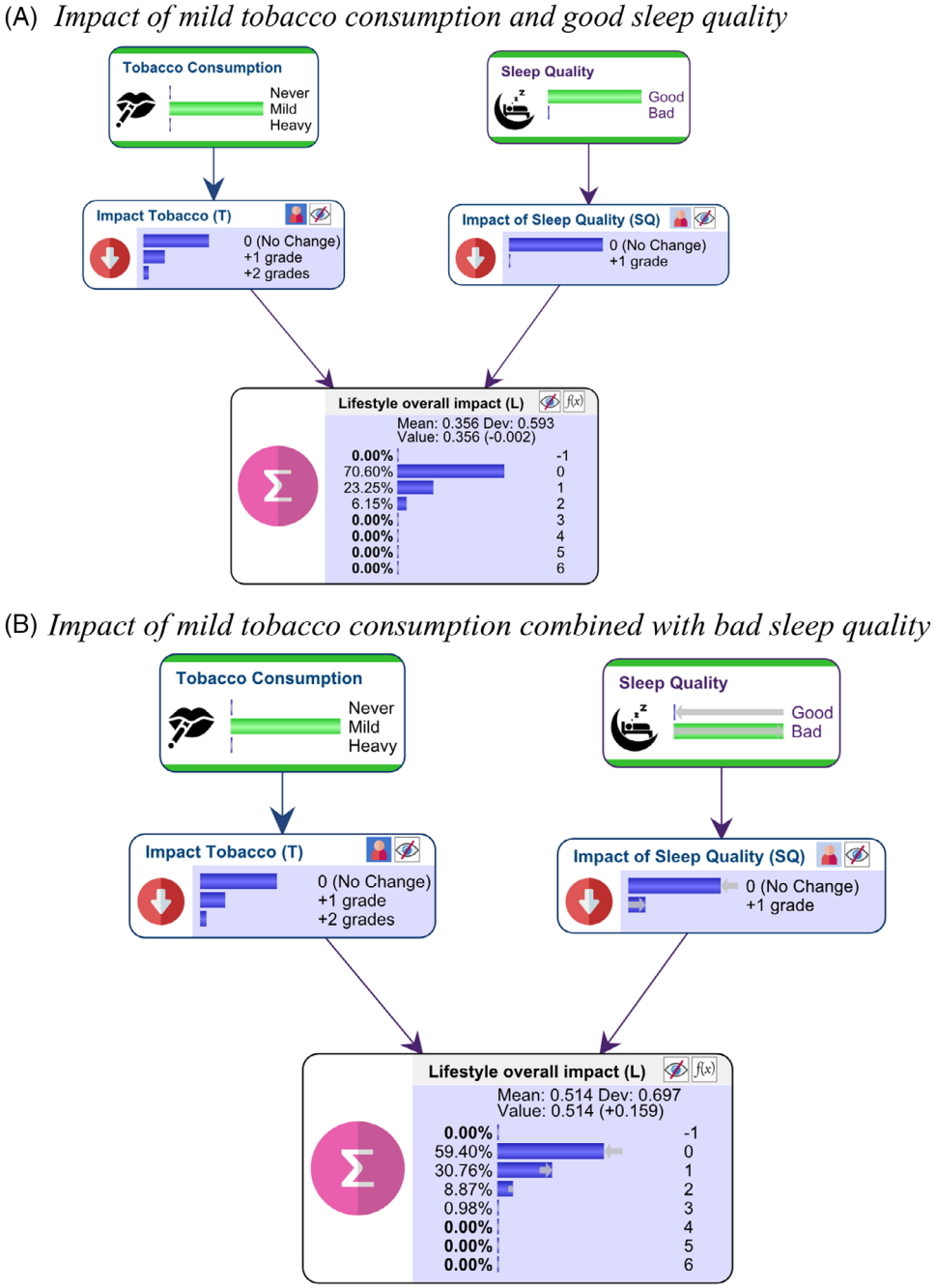


FIGURE 5 Example of impact grouping with an additive impact L = min(6,T+SQ) based on the evolution model of forehead wrinkles at the age of 35 years in individuals with a phototype V or VI. (A) Impact of mild tobacco consumption and good sleep quality. (B) Impact of mild tobacco consumption combined with bad sleep quality.

Models were validated by independent dermatologists who were not involved in the initial model elicitation. All of these dermatologists provided scores of 3 or higher for every model.

o *Simulations*

The completion of the models enabled simulations that provided insights into aging trajectories based on lifestyle choices.

In Figure 10, various simulation scenarios, as detailed in Table 3, are depicted. For example, smoking increases the probability of prominent forehead wrinkles. Adding a daily sun protection routine reduces this risk. Stopping tobacco consumption may mitigate the progression of forehead wrinkles, but not to the degree achieved by complete abstinence. Thus, not smoking offers a more favorable aging trajectory compared to a progressive cessation. This outcome underscores the lasting influence of past behaviors on skin aging.

Figure 11 illustrates the varying progression of nasolabial folds between individuals who are genetically predisposed, compared to those with no genetic predisposition, given that both groups maintain

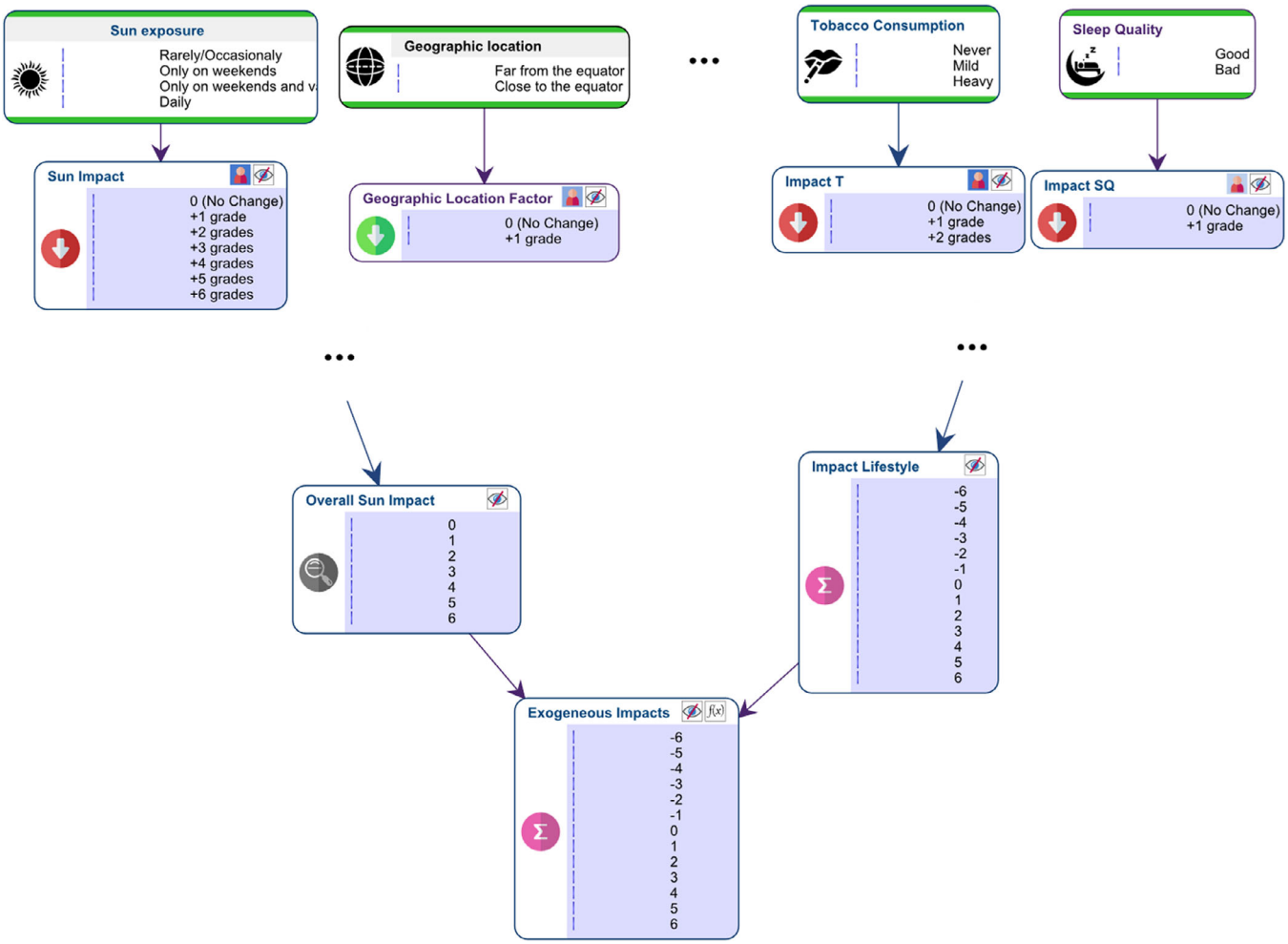


FIGURE 6 Example of exogeneous impact from the evolution model of forehead wrinkles in individuals with a phototype V or VI.

TABLE 3 Scenarios of impact factors on forehead wrinkles.

Scenario	Profile (all scenarios)	Sunscreen routine and tobacco consumption
S0	Recreational exposure Far from the equator ITA between 10 and −30 normal expression without view problems medium skin thickness good sleep quality frequent use of moisturizers only	Never smoke and protect daily
S1		Net stop of smoking at 35 years with daily protection
S2		Progressive stop of smoking with daily protection
S3		Net stop of smoking at 35 years without sun protection
S4		Progressive stop of smoking without sun protection
S5		Heavy smoker without sun protection

a consistent lifestyle. This highlights the influence of genetic factors on skin aging, independent of lifestyle choices.

4 | DISCUSSION

This innovative project uses knowledge elicitation from experienced dermatologists from different countries worldwide and CBBNs to predict facial aging in all phototypes, especially for each clinical sign, considering different endogenous and exogenous factors.

Twenty-two dermatologists created the models, which were subsequently verified by an independent group of six other dermatologists. These models represent the first multi-ethnic inclusive framework for all phototypes.

One of the challenges faced during this process was to determine the optimal model structure allowing to minimize the number

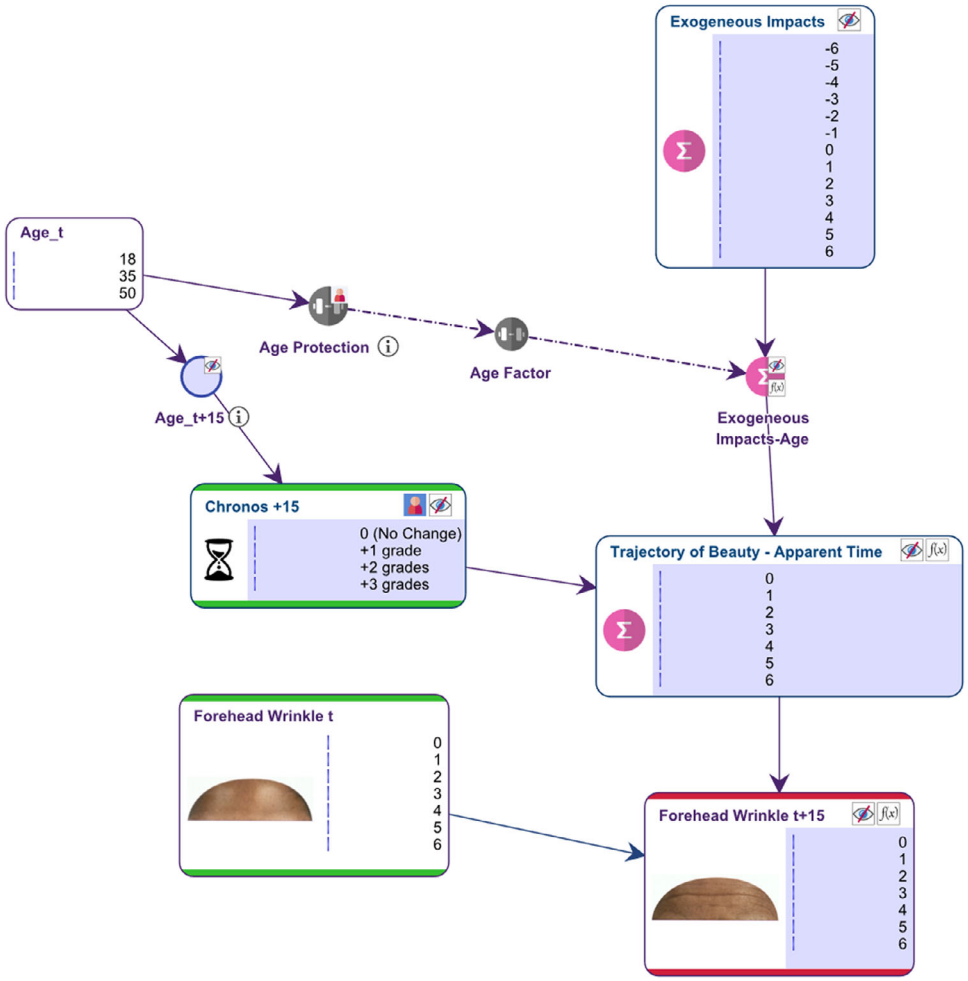


FIGURE 7 Prediction structure: Example of the evolution model of forehead wrinkle evolution in individuals with a phototype V or VI, The "Beauty Trajectory" is derived from the sum of the overall exogenous impact and Chronos. The severity grades for wrinkles 15 years into the future are determined by adding the baseline wrinkle severity grade to the Beauty Trajectory. It is important to note that the Beauty Trajectory is locked at 0, ensuring that the model does not project any form of rejuvenation.

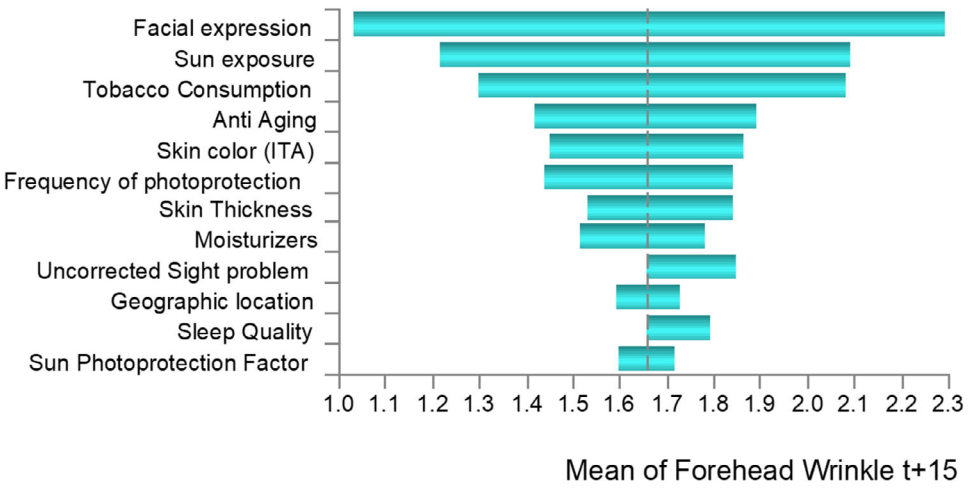
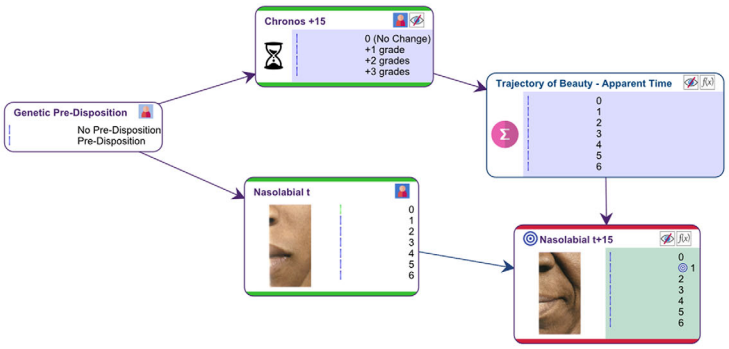
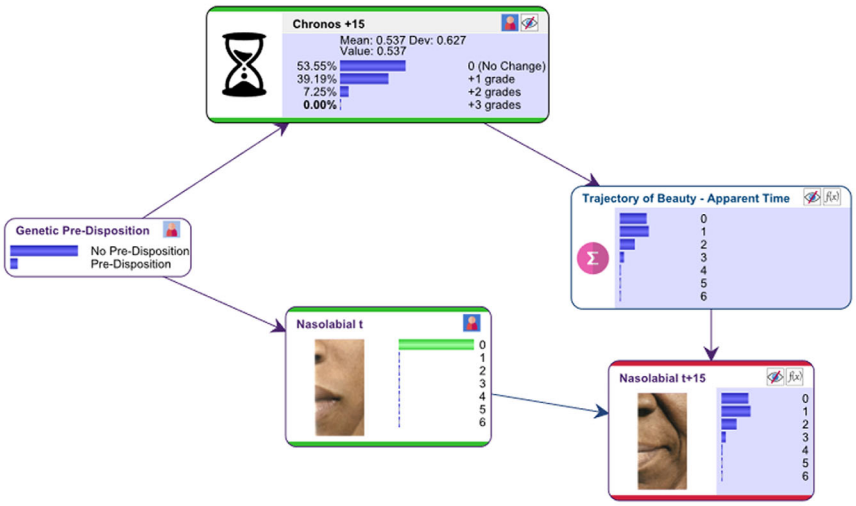


FIGURE 8 Example of a tornado plot for forehead wrinkles. Each bar in the tornado plot illustrates the sensitivity of the prediction to a particular risk factor. This visualization facilitates the ranking of all identified risk factors in terms of their influence on the outcome. In the given example, facial expression, sun exposure, and tobacco consumption emerge as the most influential factors when evaluating the progression of forehead wrinkles. In contrast, the quality of sleep has a minimal effect, whereas a change in routine facial expression can significantly influence the development of forehead wrinkles.



(A) *If Grade 0 is observed at the age of 35 years, the probability of no predisposition is high, while the intrinsic chrono-aging is relatively low. Thus, the evolution is mainly impacted by extrinsic factors.*



(B) *If Grade 3 is observed at the age of 35 years, then the chance of a genetic predisposition is higher and the probability of a faster Chronos evolution is increased (gray arrows representing the change vs the previous case)*

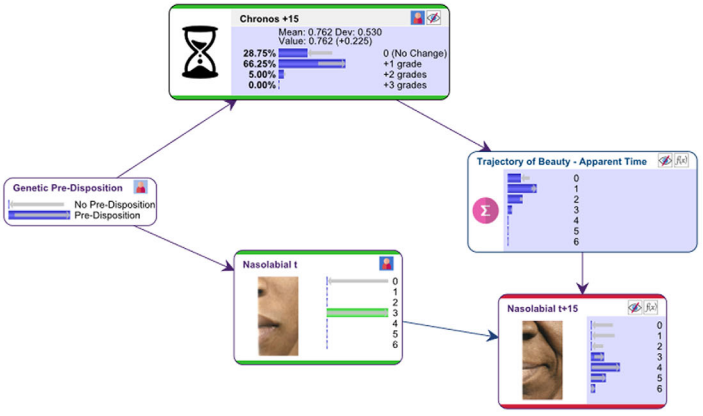


FIGURE 9 Modeling of genetic predispositions: Example of the evolution model of nasolabial folds evolution starting at the age of 35 years in individuals with a phototype V or VI Causal structure for genetic predisposition. If Grade 0 is observed at the age of 35 years, the probability of no predisposition is high, while the intrinsic chrono-aging is relatively low. Thus, the evolution is mainly impacted by extrinsic factors. If Grade 3 is observed at the age of 35 years, then the chance of a genetic predisposition is higher and the probability of a faster Chronos evolution is increased (gray arrows representing the change vs. the previous case).

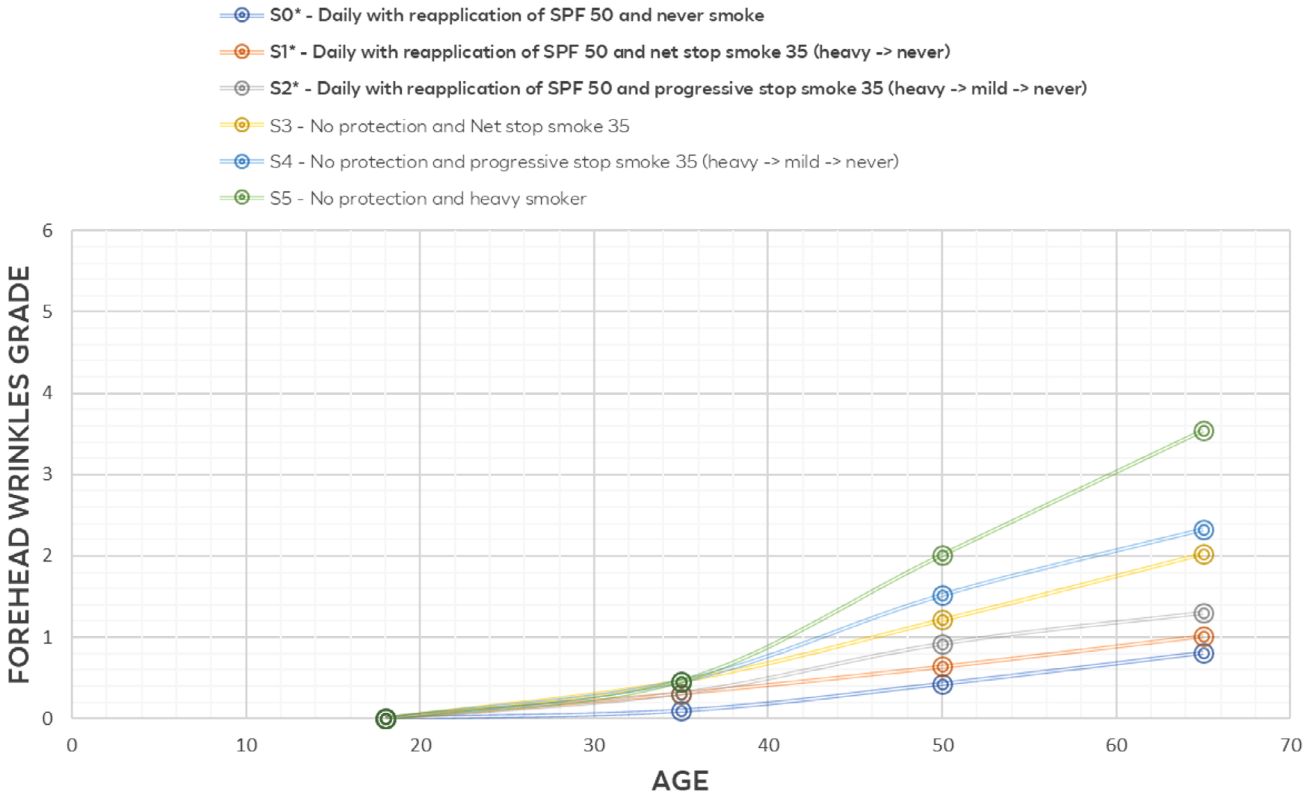


FIGURE 10 Aging curve of forehead wrinkles comparing different sunscreen and tobacco consumption routines. *: Scenarios with Sun protection.

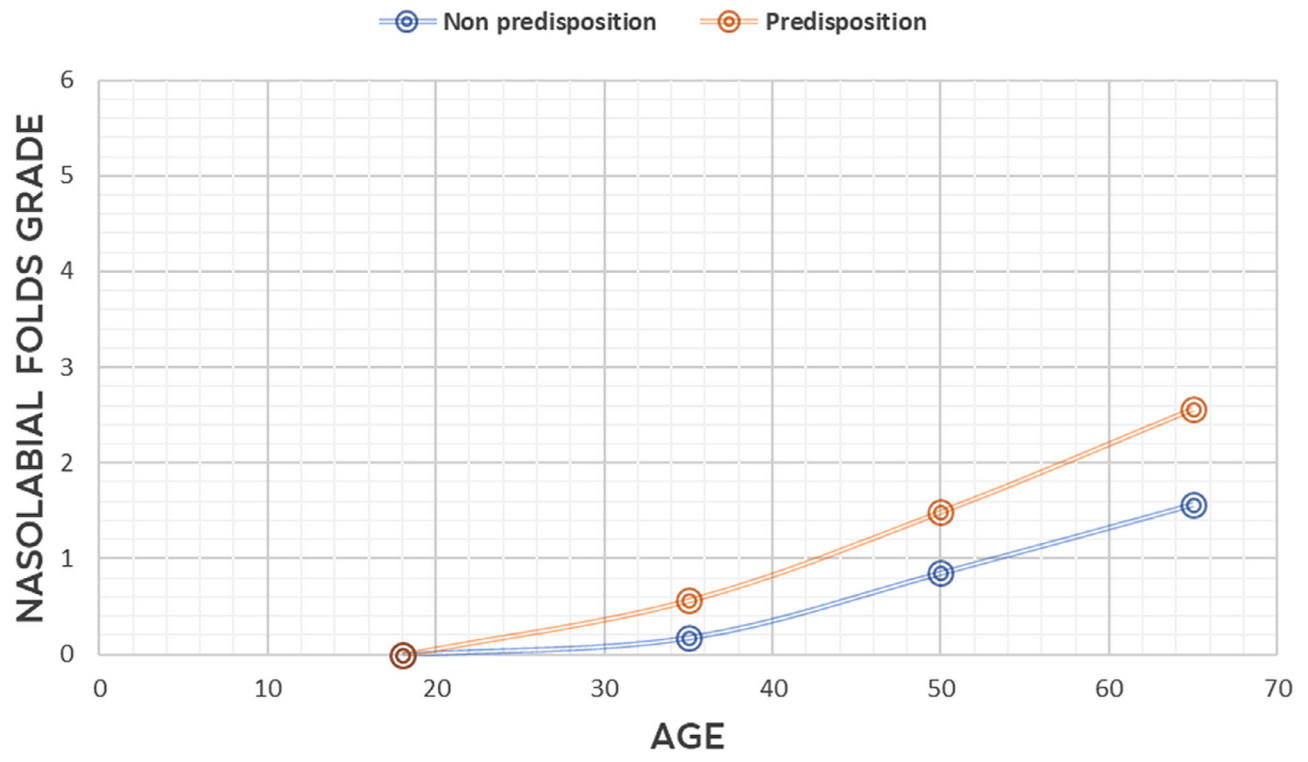


FIGURE 11 Aging curve comparing the evolution of nasolabial folds evolution between a predisposed population and a non-predisposed population.

of elicitation probabilities of ICI models bound by stringent assumptions underscoring the importance of leveraging the iterative DELPHI methodology in order to ensure that the resultant models align with real-world phenomena.

Within this framework, only extrinsic risk factors are clearly delineated, mainly because they can be conveniently gauged using questionnaires. The intrinsic aspect of aging is also included, albeit not in an exhaustive manner. The "*Chronos*" node symbolizes all potential unobserved factors that influence skin aging, rather than detailing each factor.

The method was used for all photo- or skin types (European-origin, African, Asian skin). The specificities defined by the experts were considered, constituting one of the strengths of this approach. For example, using depigmenting products in African skin or skin color measured by the ITA were included in the models to assess the impact of the sun, especially regarding the onset of signs of aging and spots.

However, harnessing expert-reviewed empirical data remains essential in order to enhance these models further. The use of this data supports the update of probabilities, resulting in predictions of even greater accuracy. A significant advantage of employing CBBNs is their ease of use and their transparent nature, where all computational steps are explicitly known.

In conclusion, this paper introduces a pioneering methodology designed for creating multi- ethnic skin aging progression models for all individuals aged between 18 and 65 years, of all phototypes and including European-origin, Asian, and African skin.

The presented models project the 15-year progression of initial skin aging markers. In contrast to existing tools, this innovative method takes both extrinsic and intrinsic risks into account, shaping them to reflect individual lifestyles and their involvement as facial aging markers. The robust Causal Bayesian Belief Networks formed the mathematical backbone of this expert- driven modeling, facilitating the simulation of aging trajectories. The models do not only facilitate the simulation of aging pathways but, when paired with a generative AI algorithm, are also able to visualize potential appearances 15 years into the future, and thus may allow to simulate progression models for other skin conditions that are influenced by exposome factors.

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ACKNOWLEDGMENTS

The authors acknowledge the collaboration with Dr. Jenna Lester, Stephanie Nouveau, Anissa Azouaoui, Virginie Hourblin, and the support of Karl Patrick Göritz, SMWS, France. This work was funded by L'Oréal Research and Innovation.

CONFLICT OF INTEREST STATEMENT

Hussein Jouni, Emmanuelle Tancrede-Bohin, Charles Gomes and Jun Wu are employees of L'Oréal Research and Innovation. Lionel Jouffe and Edouard Raynaud are consultants for L'Oréal Research and Innovation. The other authors have no conflict of interest to disclose.

DATA AVAILABILITY STATEMENT

The data that support the findings of this work are available from the corresponding author upon reasonable request.

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How to cite this article: Jouni H, Jouffe L, Tancrede-Bohin E, et al. Predicting the evolution of clinical skin aging in a multi-ethnic population: Developing causal Bayesian networks using dermatological expertise. *Skin Res Technol*. 2024;30:e13602. https://doi.org/10.1111/srt.13602