

ProForM: A simulation model for the management of mountain protection forests

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ABSTRACT

Protection from gravitational natural hazards such as snow avalanches and rockfall is among the most important ecosystem services provided by forests in steep mountain terrain such as the European Alps. These so-called “protection forests” often have to be actively managed to ensure a sustainable ecosystem service provision in time and space. For studying these slowly developing ecosystems, dynamic forest models are important tools to assess the effect of management on the protective function. However, existing models focus on the current protective effect and in many cases neglect aspects of stand resistance and resilience to large disturbances, which are important factors for maintaining the long-term protective function. Therefore, we developed ProForM, a new dynamic forest model aimed at (1) reproducing stand dynamics of managed temperate mountain forests and (2) assessing their protective function in detail. ProForM is a structurally simple model that contains mechanistic formulations of basic demographic processes but was developed mainly with empirical data. It is spatially explicit and was developed with a focus on regeneration dynamics. The model is parameterized for four tree species (*Picea abies*, *Abies alba*, *Fagus sylvatica*, and *Acer pseudoplatanus*) and four elevational zones, ranging from mixed species submontane to spruce-dominated subalpine forests. ProForM was calibrated with and validated against independent data from long-term forest inventories from Switzerland. It exhibited a satisfactory performance in reproducing measured basal area, stem number, diameter distribution and mean crown ratio at the stand level, comparable to the performance of other, typically more complex models. Illustrative example simulations demonstrate the assessment of the protective function of a stand against gravitational hazards according to multiple criteria used in forestry practice in Alpine countries. ProForM is a valuable new tool to study the impacts of management on the protective effect of mountain forests, and to inform forest managers.

1. Introduction

Mountain forests provide important ecosystem services (ES) such as timber, carbon storage, water regulation, scenic beauty, and protection of human infrastructure from gravitational natural hazards (so-called “protection forests”; cf. EEA, 2010). In the Alpine countries of Switzerland and Austria, 49% and 42%, respectively, of the forested area provides a protective function against mass movements such as snow avalanches, rockfall, and landslides (Bundesministerium für Land- und Forstwirtschaft, 2022; Losey and Wehrli, 2013). In general terms, the protective quality of a forest depends on stand structure and composition (Brang et al., 2006), which are arising from site conditions

and climate as well as the local disturbance and management history. In many mountain forests, protective ES should be provided continuously and on a relatively small spatial scale (single stands to hillslopes), e.g., above villages or other human infrastructure such as roads. To ensure protection in the long-term, these stands should not only reduce the risk of natural hazards, but also be resistant and resilient to disturbances and therefore feature a species composition in accordance with site conditions, a sustainable diameter distribution, and continuous regeneration (Brang, 2001). To meet these requirements, most protection forests have to be managed regularly, as natural forest dynamics at small spatial scales may, e.g., lead to low resistance and high risks of bark beetle outbreaks with increasing stand density, low resilience due to

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suppressed regeneration, and insufficient protection after large disturbances (Brang et al., 2006; Dorren et al., 2004; O'Hara, 2006).

Mountain forests develop slowly, and hence observation or even experimentation alone are unlikely to be able to unravel appropriate approaches to sustainable protection forest management. Dynamic vegetation models (DVMs) are valuable tools to study the impacts of natural and anthropogenic drivers such as climate change and management on forest dynamics and ES provision (Maréchaux et al., 2021). To assess the protection effect of simulated forest stands against natural hazards, two approaches have been used.

First, dynamic forest models have been coupled with models that explicitly simulate natural hazards, mainly rockfall. Examples include Wehrli et al. (2006), who fed outputs of the forest gap model ForClim into the rockfall model Rockfor^{NET} (Berger and Dorren, 2007) and estimated the residual hazard of a stand, calculated as the percentage of rocks that are not stopped within the forest. Further examples were provided with the growth simulator PROGNAUS (Brauner et al., 2005) and the hybrid patch model PICUS (Rammer et al., 2010; Woltjer et al., 2008).

Second, a more common approach is to derive indices of ES provision from metrics describing forest structure and composition, the main output of DVMs, via so-called linker functions (Blatter et al., 2017). The linker function's output can be classified in two groups: a) categorical assessment in two or three categories using threshold values for stand characteristics such as stem density, gap size, basal area, or projected canopy area (e.g., Brang and Hallenbarter, 2007; Cordonnier et al., 2008; Wehrli et al., 2007), and b) numerical indices quantifying the degree of protection a forest provides (e.g., Briner et al., 2013; Cordonnier et al., 2014; Elkin et al., 2013). The widely used numerical indices for snow avalanches and rockfall by Cordonnier et al. (2014) are examples for complex linker functions: The index for avalanche protection incorporated basal area, average diameter at breast height (DBH) and slope, whereas the one for rockfall protection used stem density, average DBH, the percentage of evergreen and deciduous species, slope, rock diameter and density, and initial rock fall height.

Many of the linker functions for quantifying the ES "protection from natural hazards" that are used with DVMs in Europe are based directly or indirectly on NaiS (Frehner et al., 2005), the system for assessing protection forest quality in Swiss forestry practice. It specifies the minimal and ideal attributes of a forest stand for each combination of site type, i.e., phytosociological association, and natural hazard, by describing forest states that are expected to provide sufficient and sustainable protection. These attributes, called "minimal" and "ideal" profiles, consist of threshold values for a series of forest attributes including species mixture, vertical and horizontal stand structure, stand stability, and various aspects of tree regeneration.

Most linker functions used in DVMs focus on natural-hazard-specific prerequisites regarding stem density, canopy cover, and gap size (for the spatially explicit models). However, aspects related to resistance, such as species composition or stand stability, and to resilience, such as abundance and composition of regeneration, have hardly ever been included. Exceptions are the indices used with LandClim (Briner et al., 2013; Elkin et al., 2013) that include the number of species or distinguish between coniferous and broadleaved species, and the assessment of regeneration density as a measure of resilience (Cordonnier et al., 2008; Irauschek et al., 2017a). In simulation studies so far, the protective function has never been estimated based on the full breadth of NaiS indicators (Frehner et al., 2005), which are used in multiple Alpine countries. One of the main reasons is that very few of the models actually provide the outputs to do so, particularly regarding tree regeneration dynamics.

For these reasons, we developed and evaluated ProForM (PROtection FORest Management), a new forest simulation model specifically aimed at studying the impacts of management on forest dynamics and the detailed assessment of the protective function. The focus on regeneration and spatial stand structure in model development allows for the

assessment of the protective quality with a broad set of indices adapted from NaiS. ProForM is a process-based model operating at the stand scale that was developed mostly with empirical data. It is parameterized for four of the most important stand-dominating tree species in Switzerland, i.e., Norway spruce (*Picea abies* (L.) H. Karst), silver fir (*Abies alba* Mill.), European beech (*Fagus sylvatica* L.), and sycamore maple (*Acer pseudoplatanus* L.) (Brändli et al., 2020), and four distinct elevational zones in the Swiss Alps. The current version of the model does not represent large disturbances and assumes a constant climate. In this paper, we present the model structure, its parameterization and validation as well as examples for the assessment of the protective quality of simulated stands.

2. Materials and methods

2.1. System NaiS

The indices used in ProForM to assess the protection forest quality are based on NaiS, the Swiss guidelines for protection forest management (Frehner et al., 2005). In the neighboring countries France (Gauquelin and Courbaud, 2006), Italy (Berretti et al., 2006; Vacik et al., 2010a, 2010b), Austria and Germany (Amt der Tiroler Landesregierung, 2019; BASCH and Interreg, 2021), similar frameworks that are based on NaiS are used. In NaiS, minimal and ideal profiles are formulated for each combination of site type and prevailing natural hazard. The minimal profile describes the stand's state that is required to provide an effective and sustainable protective function, while the ideal profile describes the long-term ideal state, i.e., a forest state well above the minimum requirements. The profiles comprise threshold values and ranges in seven categories: (1) species mixture in terms of their share of canopy cover, (2) vertical structure, i.e., the stand's diameter distribution, stem number, and basal area, (3) horizontal arrangement, i.e., the spatial clustering of trees (texture), maximum gap size, and total canopy cover, (4) stability of "support trees", i.e., those trees that contribute most to the stand's stability, in terms of crown length and shape, stem slenderness, and rooting stability, (5) seedbed quality in terms of the abundance of competing ground vegetation and suitable microsites for germination, (6) seedlings (trees 10 to 40 cm in height) and (7) saplings and thicket (trees 40 cm in height to 12 cm DBH), both latter categories in terms of species composition and abundance. Thus, the NaiS system allows for the assessment of a stand's current protective quality, its resistance against severe disturbances and its resilience after a disturbance based on an assessment of the stand structure (species composition, vertical and horizontal arrangement, regeneration, structural stability, etc.).

The minimal and ideal profile for each category is compared to the current forest state as well as the state expected for 50 years in the future, assuming that no interventions were to take place. To this end, a semi-quantitative index value is awarded for each category, ranging from "very bad" across "minimal" to "ideal". If the minimal profile is not met presently or in the coming 50 years in at least one category, management interventions are defined to ameliorate the protective function, provided that they are cost-efficient (for more details, cf. Brang et al., 2006).

2.2. Description of ProForM

Here, we present an abbreviated and simplified description of the ProForM model, version 1.0. The complete description following the ODD (Overview, Design concepts, Details) protocol (Grimm et al., 2006) as updated by Grimm et al. (2020) is available in the Supplementary material S1. There, all model equations, algorithms, parameters including their values as well as the parameterization and calibration procedures are described. ProForM is implemented in R (R Core Team, 2021) and the source code is freely available (Schmid et al., 2023).

2.2.1. Overview

The purpose of ProForM is to predict the dynamics of managed forest stands and to assess the resulting protective function against gravitational natural hazards. ProForM is a dynamic, spatially explicit, process-based model. The main premise in its development was to keep the processes and functions simple and interpretable, and to develop and parameterize them with empirical data as much as possible. ProForM is parameterized for the four most important tree species in Swiss protection forests, Norway spruce (*Picea abies*; subsequently abbreviated as pabi), silver fir (*Abies alba*; abbr. aalb), European beech (*Fagus sylvatica*; abbr. fsyl), and sycamore maple (*Acer pseudoplatanus*; abbr. apse) (Brändli et al., 2020). The model is parameterized for four elevational zones (henceforth called “strata”), i.e., submontane (SM), upper montane (UM), high montane (HM), and subalpine (SA) according to NaiS (Frehner et al., 2005). For the time being, we have assumed the climate to be constant and do not simulate disturbances (other than management). Simulated stand development emerges from the growth of trees on spatially explicit cells. In turn, stand development is determined by the basic demographic processes, spatial interactions, and management.

The model is based on two main entities: grid cells and cohorts. The grid cells form the spatial basis, and each cell is characterized by its size, its location within the grid, its capacity for regeneration (*cell quality*) and its *local topography* (Table 1). These qualities are static state variables *sensu* Grimm et al. (2006). Each cell contains either one or two cohorts, depending on the simulation settings (for details see further below). Cohorts are the basic unit to describe trees in the model and consist of aggregations of identical trees. They are characterized by the true state variables (i.e., changing over time) species (*Spc*), stem number (*N*), diameter at breast height (*D*), height (*H*), and height to crown base (*HCB*). The number of cohorts per cell is constant, and they can therefore

Table 1
State variables used in the ProForM model.

Entity	Variable name	Variable type; dynamic/static; unit; range	Meaning
Grid cell	<i>Cell ID</i>	integer; static; -; non-negative	Unique cell identification
	<i>Cell location</i>	set of coordinates (doubled and cartesian); static; no unit and m; any value	X and Y coordinates of the cell's center
	<i>Local topography</i>	categorical; static; -; {even, mound, pit}	Local topography of cell
	<i>Cell quality</i>	double; static; -; {0..1}	Proxy for abiotic factors of a cell, affecting maximal stem number per cohort
Cohort	<i>Cohort No.</i>	integer; static; - non-negative	Unique cohort identification within one cell
	<i>Cohort ID</i>	integer; static; -; non-negative	Unique cohort identification including the cell it lays on
	<i>Spc</i>	categorical; dynamic; -; {none, pabi, aalb, fsyl, apse}	Tree species of cohort
	<i>N</i>	integer; dynamic; -; non-negative	Stem number of cohort
	<i>D[†]</i>	double; dynamic; cm; non-negative	Diameter at breast height of all trees in cohort
	<i>H</i>	double; dynamic; cm; non-negative	Tree height of all trees in cohort
	<i>HCB</i>	double; dynamic; cm; non-negative	Height to crown base of all trees in cohort
Environment	<i>Time step</i>	integer; dynamic; year; non-negative	Time step of simulation

[†] In the text, we use *D* (in italics) to refer to the state variable and DBH (in regular font) to diameter at breast height in more general terms.

also be empty (bare ground) and hence have the species “none” assigned (Table 1). The positions of individual trees within a cohort are unknown. The environment is represented by the current time step of the simulation.

One time step equals one year, and for each time step two distinct states of the state variables are calculated: state 1 in spring, before the growth period, and state 2 in fall, after the growth period but before management. Total simulation time can be chosen by the user; typically, it is ca. 100 years. ProForM is a three-dimensional model, containing x- and y-coordinates of each cell and the height of each cohort as the z-coordinate. Grid cells cover the entire simulation area and are hexagonal in shape (Fig. 1) in order to facilitate the calculation of neighbor interactions, as in this setting all neighbors are equidistant. Depending on the simulation settings, their size ranges between 40 and 100 m², chosen so that the canopy of a dominant tree can fill the entire cell. The size and dimensions of the simulation grid can be chosen freely, with a typical size of around 1 ha. Spatial interactions occur between cohorts on neighboring cells, and depending on the process, the state variables of the cohorts on one or two “rings” of equidistant neighbors of the target cell are considered (Fig. 1). The model uses a toroidal representation of space to avoid edge effects.

At initialization, ProForM assembles the stand based on a table containing the state variables for each cohort on each cell and the grid specifications (cell size and grid dimensions) provided in the simulation settings and establishes the neighbor relationships. Using a stochastic process, values of *local topography* and *cell quality* are assigned to each cell according to parameterized ranges. Management instructions can be passed as input data to the model. In the simulation settings, a series of parameters have to be defined: the *stratum*, i.e., the elevational zone, determining the potential species composition of the stand and the sets of parameter values to be applied in the functions describing the demographic processes; the total *simulation time* in years; *site aspect* and *slope* in degrees, used for calculating certain competition indices and the characterization of gaps; and the species composition of the surrounding forest, which is used to determine the probabilities of species assignment at germination (and thus, potential species change after the death of the last tree of a cohort).

Furthermore, the stand's *site* and *regeneration quality* have to be defined on an ordinal scale of 1 (low) to 5 (high). These parameters are

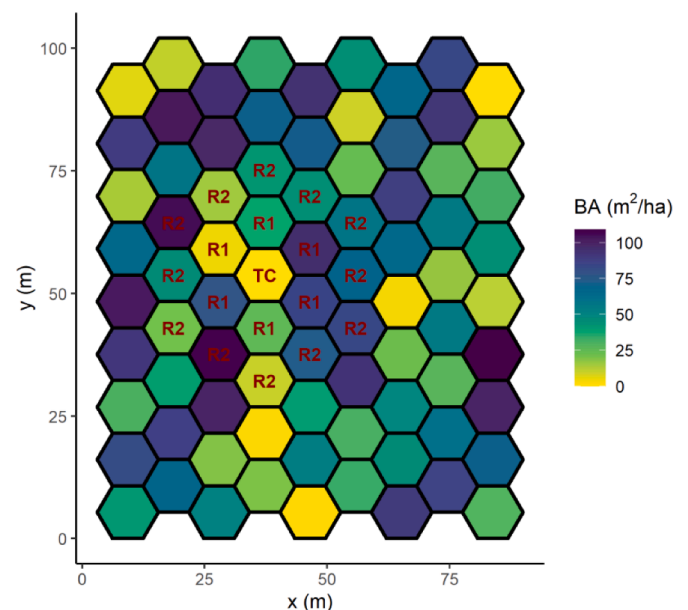


Fig. 1. Spatial distribution of basal area (BA) on a simulation grid made up of 81 cells with a cell area of 100 m² and the two rings of neighbor cells (R1 and R2) around a target cell (TC).

aggregated proxies for a series of abiotic and biotic factors such as nutrient availability, soil water content or browsing pressure that influence tree growth (*site quality*) and regeneration growth and abundance (*regeneration quality*) and are used for calculating stratum-specific reduction factors (called “pre-factors”) for growth and regeneration, respectively (linear interpolation between a minimal value and 1, cf. Eq. (S1.2) in Supplementary material S1).

There are two main processes in ProForM that are executed consecutively (Fig. 2). First, stand development is calculated based on natural forest dynamics and the scheduled management interventions. Second, the protective function of the stand over time is assessed. Forest dynamics and management are calculated in a loop of eight steps over each time step after the variable values from the initialization data have been assigned to state 2 (fall) of the first time step: (1) calculation of auxiliary variables for state 2; (2) calculation of the change in stem numbers through management, if scheduled for the current time step; (3) saving of a copy of the current state; (4) increasing the time step by one; (5) updating the state variables of state 1 (spring); (6) calculation of the auxiliary variables for state 1; (7) calculation of changes in state variables through natural forest dynamics (growth, mortality, and regeneration); and (8) updating the state variables of state 2. The calculation of changes in state variables and the updating processes are applied to all cohorts simultaneously.

In the second process, using the complete simulation results, the protective quality is assessed retrospectively for each time step in turn, in three steps. (1) Gaps, i.e., areas without trees ≥ 12 cm in DBH are identified and characterized in terms of area, length along the slope, and width perpendicular to the slope. (2) Relevant stand characteristics are derived; and (3) these characteristics are compared to the minimal and ideal profiles of the respective stratum and natural hazard, and the indices of protection quality are calculated.

2.2.2. Forest dynamics and management

Growth is calculated differently for cohorts below and above a threshold D of 12 cm. For cohorts between the minimal H of 10 cm and $D < 12$ cm, referred to as “regeneration”, height growth (dH) is modeled

(Eq. (1)). Potential height growth (dH_{pot}) is a linear function of height H , the competition index CI_H , local topography, site slope and aspect, as well as stratum-specific constants of the degree-day sum and the standard evapotranspiration index SPEI, including an intercept (abbreviated in matrix notation $X\beta$ in Eq. (1), written out in Eqs. (S1.28) - (S1.32)). The auxiliary variable CI_H is a proxy of competition for multiple resources such as light, nutrients, and rooting space. It is calculated as the weighted sum of the auxiliary variable basal area (BA) of the neighboring cells (Schmid et al., 2021 and Eq. (S1.12)). Potential height growth is reduced by site conditions (pre-factor PF_{dH}) based on the *regeneration quality* of the stand (Eq. (1)).

$$dH = PF_{dH} \cdot dH_{pot} = PF_{dH} \cdot \exp(X\beta) \quad (1)$$

Diameter growth (dD) of this regeneration is derived from height using a linear allometric function (Eq. (S1.35)).

For cohorts with $D \geq 12$ cm, referred to as “adult trees”, diameter growth is modeled (Eq. (2)). We assume that trees have a potential growth rate (dD_{pot}) that is constant between a D of 12 cm and a species-specific threshold D^* (Fig. 3a; based on data of the Swiss National Forest Inventory, cf. Fig. S1.9 in Supplementary material S1), above which it declines linearly to zero at a species-specific maximum D_{max} (Eq. (S1.37)). This potential growth rate is reduced by a reduction factor RF_{dD} , calculated as a function of the local competition index CI_D and an exponent exp_{dD} (Fig. 3b and Eq. (S1.38)), and by site conditions (pre-factor PF_{dD}), based on the *site quality* of the simulated stand (Eq. (2)). The auxiliary variable CI_D (Eq. (S1.18)) is closely related to CI_H . Height growth of adult trees is derived from diameter using a logistic allometric function of D (Eq. (S1.33)). All growth functions are species-specific, and the functions for adult trees are also stratum-specific.

$$dD = PF_{dD} \cdot RF_{dD}(CI_D) \cdot dD_{pot}(D) \quad (2)$$

Mortality is modeled explicitly in cohorts with $H > 130$ cm only, as stem numbers are not tracked below this threshold. Single-tree mortality, i.e., the reduction of N per cohort (dN_{mort}), is determined in a stochastic process using a species-specific mortality probability. The

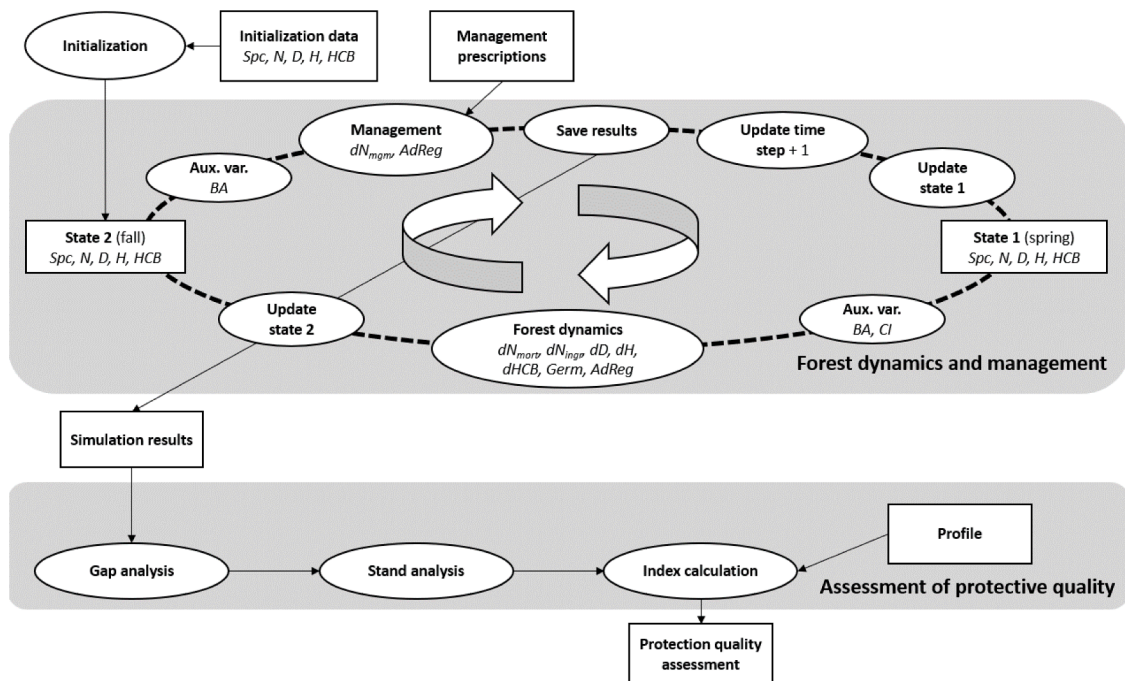


Fig. 2. Conceptual diagram of the ProForM model with the two main processes highlighted in gray. In italics, the state variables (cf. Table 1) and their respective changes, marked with a d as a prefix, are listed. In some cases, such changes are further attributed to specific processes by subscript-suffixes: *mgm* refers to management, *mort* to mortality, and *ingr* to ingrowth. Further abbreviations: Aux. var. = auxiliary variables; *BA* = basal area; *CI* = competition indices; *AdReg* = advance regeneration; *Germ* = germination.

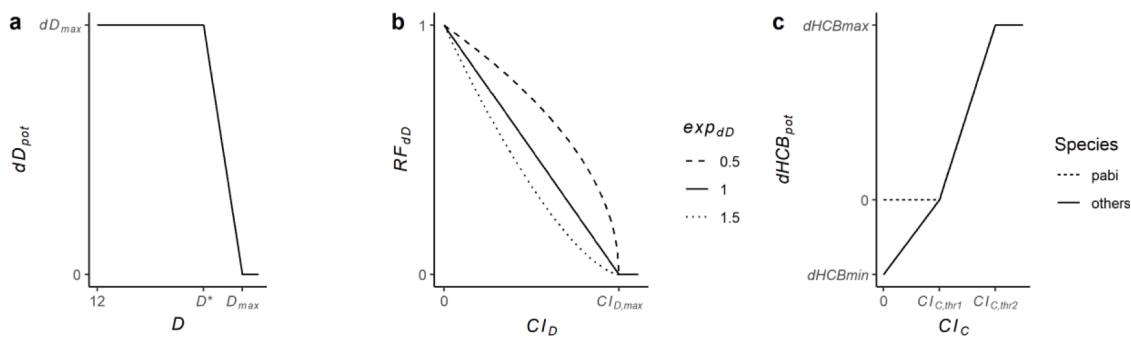


Fig. 3. Graphical representation of three model functions: a) potential diameter growth of adult trees (dD_{pot}) as a function of D (Eq. (S1.37)); b) diameter growth reduction factor RF_{dD} as a function of the competition index Cl_D and the exponent exp_{dD} (Eq. (S1.38)); c) simplified representation of the potential change in HCB ($dHCB_{pot}$) as a function of the competition index Cl_C , with the function values below the first Cl_C -threshold ($Cl_{C,thr1}$) being different for *Picea abies* (pabi) than the other three species (others) (cf. Eq. (S1.57)).

mortality probability of trees with $D \geq 4$ cm is determined using empirically derived logistic probability functions that have previously been used in the model ForClim (Hülsmann et al., 2018). They depend on relative basal area increment ($relBAI$, calculated from D and dD) and, in the case of spruce, the competition index Cl_M (Eqs. (S1.46) - (S1.49)). The auxiliary variable Cl_M is a proxy for stand age and is calculated as the mean diameter of all cohorts with $D \geq 7$ cm in the entire stand. To avoid extrapolation beyond the data range underlying these functions, the mortality probability of trees with $D < 4$ cm is assumed to be constant.

Regeneration, i.e., the appearance of new trees, is represented by two processes: either through (a) germination from bare ground or (b) the presence of advance regeneration directly after the last tree of a cohort has died or has been harvested. Both processes contain a stochastic element and are modified by site conditions (pre-factor PF_{GI}) based on the *regeneration quality* of the simulated stand. The potential annual germination probability of seedlings in an empty cohort is calculated based on a Bernoulli trial defined by a cumulative success probability of 95% over a stratum-specific time (T_{germ}). This potential germination probability is multiplied by PF_{GI} and further reduced if there is another non-empty cohort on the same cell (Eqs. (S1.60) - (S1.63)) to determine the actual germination probability. The process of advance regeneration is only modeled in strata with one cohort per cell, where regeneration below the canopy is not kept track of explicitly (HM and SA, see further below). If advance regeneration occurs, the cohort is immediately populated with saplings instead of being changed to bare ground, assuming that the germination has happened previously. The probability for advance regeneration being present depends on the cohort's D before death or harvest, and on PF_{GI} (Eq. (S1.66)).

Cohorts with $H < 130$ cm (seedlings and saplings) have no stem numbers assigned, as the development of the stem number of the early phase of regeneration is poorly understood due to its high stochasticity and because in a management context, usually merely the presence of and area covered by seedlings and saplings are of relevance, but not their exact stem number. Therefore, only when a cohort grows beyond that threshold, dN_{ingr} and thereby future N is determined in the process referred to as “ingrowth”. dN_{ingr} is calculated from a species-specific maximal stem number that is modified by *cell quality* (a proxy for the suitability of a microsite for regeneration), and by PF_{GI} (the pre-factor based on the *regeneration quality* of the simulated stand) and further reduced if there is already a cohort with $H > 130$ cm on the same cell (Eqs. (S1.41) - (S1.43)).

The change in height to crown base ($dHCB$), is modeled with a function developed from theoretical considerations. The main driver of $dHCB$ is the competition index Cl_C , an auxiliary variable that is a proxy for the shading that a cohort experiences from its neighbor cells. It is calculated as a variant of the BAL (basal area of larger trees) in the neighboring cohorts, including all cohorts with D larger than a certain

fraction of the target cohort's D (Antos et al., 2010), as not only larger neighbors influence crown growth or recession, but considerably smaller neighbors do not (Eq. (S1.22)). In a first step, the potential change in HCB ($dHCB_{pot}$) is calculated. Below a first threshold value of Cl_C , i.e., in situations with only few or small neighboring cohorts, the crown base is lowered through secondary crown development (stagnation in case of spruce). Above this value, $dHCB_{pot}$ is positive and the crown base is elevated. Above a second threshold value of Cl_C , $dHCB_{pot}$ increases at its maximal rate (Fig. 3c and Eq. (S1.57)). This maximum value of $dHCB_{pot}$ is determined by (1) an absolute maximum, and (2) a maximum fraction of tree height (Eq. (S1.53)). The minimum value at a Cl_C of zero is calculated as a negative share of the maximal value (Eq. (S1.55)). To obtain the definitive $dHCB$, $dHCB_{pot}$ is, if necessary, capped to ensure that (1) a minimal crown ratio (fraction of tree height occupied by the crown) is retained and (2) HCB does not drop below zero (Eqs. (S1.54), (S1.56), and (S1.58)).

Currently, there are two management types in ProForM. Both are based on the concept of relative diameter classes (RDC; Mina et al., 2017). The instructions for each management intervention state the time step of the intervention and the share of basal area to be removed by species from a fixed number of relative diameter classes of equal width, spanning the respective current range of diameters. This formulation allows for a reliable translation of empirical single-tree harvest records, as usually found in inventories, into model instructions (Mina et al., 2017). The management type “RDC tree” randomly removes single trees from cohorts according to the instructions and thereby mimics a single-tree selection type of Continuous-Cover Forestry (CCF; Brang et al., 2014; Pommerening and Murphy, 2004). The management type “RDC cohort”, which is not used in this study, randomly removes entire cohorts and corresponds to a fine-grained version of group selection in CCF. Both algorithms determine dN_{mgm} , the number of trees to be harvested within each cohort.

The functions updating the state variables of state 1 and 2 depend on their previous values and the changes since then, either through management or forest dynamics. Hence, there are no time lag effects. A cohort's species can change at germination and after the complete harvesting or natural death of the entire cohort with or without advance regeneration. The new species is randomly selected according to probabilities for each species that are determined by the currently simulated species share and the species shares of the surrounding forests, defined in the simulation settings. Ecological differences between species, e.g., shade tolerance, are not included in this simplified approach (cf. S1 for the rationale). The updated stem number results from the previous stem number, dN_{ingr} , dN_{morts} and dN_{mgm} . In case only growth occurred, the updated diameter, height, and height to crown base are calculated from the respective previous value and the corresponding change (dD , dH , and $dHCB$, respectively). If all trees in a cohort died naturally or were harvested and no advance regeneration is present, these state variables

are set to zero. If advance regeneration is present, D is set to zero, H to the corresponding parameterized minimum height, and HCB is randomly selected from within the possible values restricted by the minimal crown ratios, according to the updated species. If germination occurs, D and HCB remain at zero, and H is set to the minimal cohort height of 10 cm.

2.2.3. Assessment of protection quality

To assess the protective quality of the simulated stand, the minimal and ideal profiles (Frehner et al., 2005) according to the simulation's stratum and the selected natural hazard (snow avalanche, landslide/erosion/debris flow, rockfall, or torrents/floods) are defined in terms of the modeled variables. The profiles used in ProForM reflect the combination of site types in the stratification (see Section 2.3) and the natural hazards. Threshold values and ranges of the different stand characteristics for all but one category (seedbed quality) are derived.

The assessment for each time step is based on the state variables of state 1 and starts by the analysis of gap size. In NaiS, gaps are defined as areas without trees that have a diameter larger or equal to 12 cm. In ProForM, assuming that a cohort's canopy covers the entire cell, gaps are defined as continuous areas of adjacent cells with no cohorts with $D \geq 12$ cm, irrespective of their size or shape. For each gap, the area in m^2 , the maximal length along the slope, and the maximal width perpendicular to the slope, both in m, are determined using the cell borders as limits and taking the stand's slope into account. In NaiS, gap borders in rockfall protection forests are delimited by stem positions rather than canopy borders. Therefore, an extended gap length is calculated, assuming a mean position of the outermost tree within a cell, as the exact tree positions are unknown.

A numerical index for each NaiS category is calculated by comparing the respective stand characteristics to the profiles. The indices per category are calculated as the mean of multiple subindices, each relating to one stand characteristic within that category. An index value of -1 indicates that the minimal profile is not met in any subindex, 0 that the minimal but not the ideal profile is met, and 1 that the ideal profile is achieved. To avoid compensation of below-minimal subindex values, a maximum combined index value of -0.1 is enforced if a single subindex is valued below zero.

The index for species mixture checks the species composition in terms of basal area of trees with $D \geq 12$ cm. The index for vertical structure checks the canopy cover shares of four diameter classes (< 12 cm, $12 - 30$ cm, $30 - 50$ cm, and ≥ 50 cm), and in rockfall protection forests also the stem numbers in four diameter classes ($8 - 12$ cm, $12 - 24$ cm, $24 - 36$ cm, and ≥ 36 cm) as well as the total basal area of trees with $D \geq 8$ cm. Three rockfall scenarios are implemented, one with small rocks ($0.02 m^3$) and two with larger rocks of $1 m^3$ vol, the latter differentiating hillslope lengths of 250 and 500 m, with the prerequisites determined using Rockfor^{NET} (Berger and Dorren, 2007). The index for the horizontal arrangement (texture) checks gap area, maximal length and width, as well as total canopy cover, with the minimal thresholds depending on the natural hazard. The stability of "support trees" is assessed with an index based on mean crown ratios. Support trees are defined as the trees with the largest diameter within the four diameter classes used for the species mixture index. A total of 100 trees per hectare are selected for the assessment, with the number of trees per diameter class corresponding to the total share of cohorts within these classes. The index for seedlings ($10 \leq H < 40$ cm) checks seedling abundance and their species composition in gaps. The index for saplings and thicket ($H = 40$ cm to $D = 12$ cm) checks the total area covered by this regeneration class and its composition.

2.3. Model parameterization

Most of the parameter values used in ProForM were determined at the submodel level based on the analysis of empirical data or on expert knowledge (parameterization, described here). Additionally, some

parameter values were calibrated by comparing simulated emergent patterns to independent stand measurements (see section "Model calibration").

The four strata that ProForM is currently parameterized for encompass the most abundant site types of the corresponding elevational zone in Swiss protection forests (ARGE, 2020; Frehner et al., 2021, 2005). Currently, 56% of the protection forest area lie in the upper montane (UM; mixed-species forests naturally dominated by beech and silver fir, occurring between 800 and 1400 m a.s.l.), high montane (HM; naturally homogenous spruce-silver fir forests, 1200 – 1700 m a.s.l.), and subalpine zones (SA; spruce-dominated forests with cluster texture, 1500 – 2000 m a.s.l.). Under climate change, elevational zones are expected to shift upwards, and an increasing share of the protection forest area will come to lie in the submontane zone (SM; multi layered beech-dominated mixed-species forests, currently located between 350 and 700 m a.s.l.). Projections based on two variants of the A1B climate scenario ($4.2^\circ C$ and $2.9^\circ C$ increase in annual mean temperature and -13.7% and $+4.6\%$ annual precipitation, respectively) place roughly 40% of today's protection forest area in this elevational zone (Losey and Wehrli, 2013; Frehner and Huber, 2019). The detailed method for and results of the selection of the corresponding site types are described in Schmid et al. (2021) and in S1, respectively.

The strata and their corresponding site types were used on the one hand to guide the collection of field data of regeneration growth (Schmid et al., 2021) and to determine the subset of inventory data for the parameterization of the model, and on the other hand to set basic model characteristics depending on the stratum, including potential species composition, the number of cohorts per cell, and cell size. In SM, silver fir, beech, and maple can occur, in UM all four species, in HM spruce and silver fir, and in SA only spruce. In SM and UM, each cell contains two cohorts, as regeneration below the canopy is an important trait of forests at lower elevations. In HM and SA, there is only one cohort per cell, as regeneration at higher elevations occurs primarily in gaps, although we acknowledge that in HM, fir regeneration can be found under a spruce canopy.

Two data sets were used to parameterize multiple model functions. First, the Swiss National Forest Inventory (Brändli et al., 2020; WSL, 2020), from which a subset of all four inventories corresponding to the site types of each stratum was used (ARGE, 2020; Frehner et al., 2021). This data set is simply referred to as "NFI data". The second dataset, henceforth called "regeneration growth data", comprises height growth data of regeneration in forest gaps (Brüllhardt et al., 2020; Schmid et al., 2021). The data of Schmid et al. (2021) contains measurements of spruce in HM and SA and was extended for this study to silver fir, beech, and maple as well as the strata SM and UM. Brüllhardt et al. (2020) gathered data on beech and maple regeneration growth in low elevation forests, of which only the explicitly measured height growth data was used. Both studies followed very similar field protocols in terms of site selection and data collection and could therefore be readily combined. The regeneration growth data (Table 2) consists of 5'004 measurements of tree height and tree height growth of 928 dominant and co-dominant trees within regeneration clusters located in small gaps and under the canopy, collected across large parts of Switzerland (Fig. 4). Competition from the surrounding stand was assessed by indices derived from an inventory of all trees in a 9 to 15 m radius around each plot center, including tree positions (Schmid et al., 2021). Field sites are characterized by slope, aspect, local topography, and data on the degree-day sum and drought index (SPEI) (Remund et al., 2016).

Three basic stratum-specific cell parameters are assigned during the initialization: cell size, local topography, and cell quality. Cell size was parameterized using crown projection areas (Pretzsch, 2014) of the four target species so that a large tree would fill an entire cell with its canopy. The probabilities for each class of local topography to be assigned at initialization were derived from the observations within the regeneration growth data. The possible range of cell quality was estimated based on expert knowledge.

Table 2

Summary of the regeneration growth data by species. Mean annual temperature and mean precipitation sums (Remund et al., 2016) refer to the years 2012–2018, the period of the height growth observations. P stands for plot, T for tree.

	<i>Picea abies</i>	<i>Abies alba</i>	<i>Fagus sylvatica</i>	<i>Acer pseudoplatanus</i>
Strata	UM, HM, SA	SM, UM, HM	SM, UM	SM, UM
# Plots	136	43	45	25
# Trees	353	117	263	195
# Observations	2'529	856	986	633
P Elevation (m a.s.l.)	880 – 2018	349 – 1555	387 – 1228	387 – 1475
P Mean. temp. (°C)	1.4 – 9.0	4.3 – 11.6	5.5 – 11.7	4.5 – 11.7
P Prec. Sum (mm/y)	670 – 2853	712 – 2689	690 – 2038	690 – 1797
T Height (cm)	5/198/887	5/231/1027	25/526/1871	8/655/1880
T Growth (cm/y)	1/13.1/83	1/19.7/77	0.2/27.8/101	1/33.2/121

The growth functions were parameterized using both the regeneration growth data and the NFI data. The detailed methodology for deriving the potential height growth functions from the regeneration growth data are described in Schmid et al. (2021). The diameter-height allometries for the regeneration were parameterized using the same data set, using the final height and DBH measurements of all target trees. For the diameter growth of adult trees, maximal growth rates (dD_{max}), the threshold diameter above which growth declines (D^*), and the maximal diameter (D_{max} ; Fig. 3a) were derived directly from NFI data. The exponent determining the shape of the helper function (exp_{dD} ; Fig. 3b) that is used to calculate the reduction factor based on local competition was estimated based on expert knowledge. The maximum value of the competition index above which no growth occurs ($CI_{D,max}$; Fig. 3b) was determined from the largest measured values in the regeneration growth data. The allometries for calculating the height of adult trees from their diameter were parameterized using NFI data to determine the asymptote and shape of the functions, and the output of the diameter allometries for regeneration to ensure a smooth transition between the two growth functions at $D = 12$ cm.

The parameters of the species-specific functions for the mortality probability of trees with $D \geq 4$ cm were adopted as is from Hülsmann et al. (2018). The species- and stratum-specific annual mortality probabilities for smaller trees were determined based on the mean passing times for the regeneration to grow from 130 cm height to 4 cm in diameter resulting from the height growth function and the expected reduction in stem numbers in an average cohort during that time. The stem number reduction was estimated from (1) average stem numbers at 130 cm height resulting from modeled ingrowth and (2) plausible stem numbers at 4 cm diameter based on measured crown projection areas (Pretzsch, 2014) and density assumptions.

The stratum-specific annual germination probability of bare-ground cohorts and the probability for the occurrence of advance regeneration in the strata HM and SA were parameterized using NFI data. The expected time until germination has occurred with a 95% probability in a bare ground cohort (T_{germ}) was estimated based on an analysis of the temporal development of regeneration cover in the different strata. The probabilities for the occurrence of advance regeneration were determined using the share of NFI plots stratified by their developmental stage that exceeded a certain regeneration cover. The initial height of newly germinated trees was set to 10 cm, the height of advance regeneration to 40 cm. The species-specific maximum number of ingrowing trees per cell was determined based on expert knowledge estimates on crown projection areas of trees at 130 cm height and mean regeneration densities.

To calculate the change in HCB, the maximal absolute and relative rates of crown height change, the species-specific minimal crown ratios as well as the relative diameter threshold for trees in the corresponding competition index were estimated based on expert knowledge.

2.4. Model calibration

A total of five parameter values in ProForM were calibrated using long-term empirical time series of inventory data. Three of these parameters relate to the pre-factors PF_{dH} , PF_{dD} , and PF_{GI} , which are used to reduce regeneration height growth, diameter growth of adult trees, and germination and ingrowth, respectively. The calibrated stratum-specific parameters describe the values of these the pre-factors when *site quality* (in case of PF_{dD}) or *regeneration quality* (in case of PF_{dH} and PF_{GI}) are set to their minimal value of 1. The other two parameters are used for calculating the species- and stratum-specific change in HCB and represent the threshold values for the competition index CI_C marking the limits between secondary crown development, crown base recession, and maximal crown base recession ($CI_{C,thr1}$ and $CI_{C,thr2}$ in Fig. 3c).

As calibration data, inventories of Experimental Forest Management (EFM) plots (Forrester et al., 2021b, 2019) were used. The main criteria for plot selection were that they were managed, the elevational zone had to match the ones included in the model, and the stands could not contain more than a few individual trees of species not included in ProForM. Furthermore, the time series length should be > 50 years and the plot size > 0.5 ha, if possible. 16 plots fit these criteria, of which seven were selected for calibration and the remaining nine for later validation (Table 3 and Fig. 4). Two calibration plots belonged to stratum SM, three to UM, and one each to HM and SA, ranging in elevation from 550 to 1640 m a.s.l. and in slope from 5 to 28°. Four plots were monospecific and three were mixed-species stands. Only very few

Table 3

EFM plots used for model calibration and validation. Further information can be found in Table S2.1.

Stratum	Name	Elevation (m)	Inventories (Period, Nr.)	Species	Used for
SM	Biel West	670	1921–2008 (15)	fsyl, aalb	Calibration
SM	Zollikon	550	1919–1976 (9)	fsyl	Calibration
SM	Biel East	670	1921–2008 (15)	fsyl, aalb	Validation
UM	Buttes BDP	983	1913–2016 (17)	aalb, fsyl, pabi	Calibration
UM	Rougemont LA	1294	1928–2013 (14)	pabi, aalb	Calibration
UM	Sigriswil lower	1370	1925–1997 (10)	pabi	Calibration
UM	Buttes LCR	970	1913–2014 (13)	aalb, fsyl, pabi	Validation
UM	Le Chenit	1340	1925–2014 (11)	pabi, aalb	Validation
UM	Rougemont G	1185	1928–2013 (14)	aalb, pabi	Validation
UM	Sigriswil upper	1405	1925–1997 (10)	pabi	Validation
HM	Morissen	1640	1905–1952 (9)	pabi	Calibration
HM	Siat	1570	1998–2018 (3)	pabi	Validation
HM	Triesenberg 1	1460	1996–2019 (3)	pabi	Validation
HM	Triesenberg 2	1460	1998–2020 (3)	pabi	Validation
SA	Hospental	1515	1898–1985 (13)	pabi	Calibration
SA	Realp	1680	1898–1969 (11)	pabi	Validation

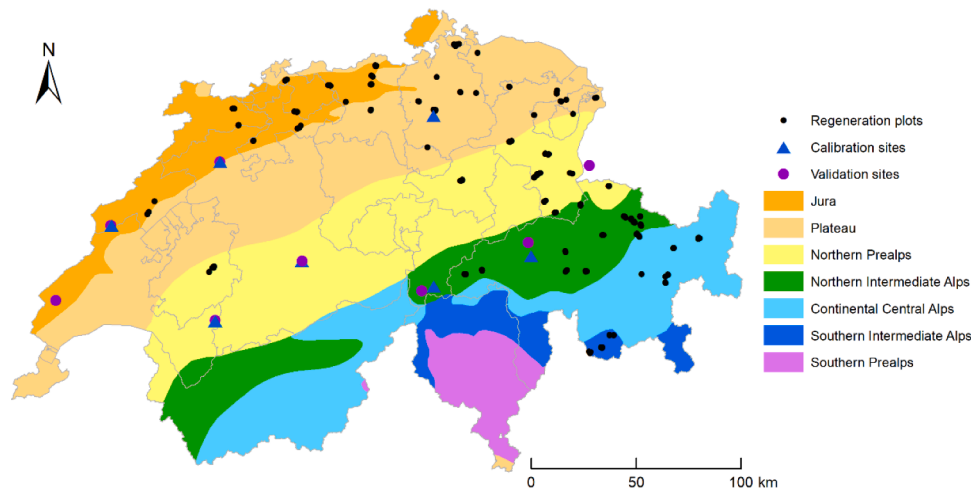


Fig. 4. Distribution of the 249 plots included in the regeneration growth data (small black dots) and the Experimental Forest Management (EFM) plots (Forrester et al., 2021b, 2019) used for model calibration (blue triangles) and validation (large purple dots) across Switzerland and the ecoregions according to NaiS (Frehner et al., 2005). As the regeneration plots are locally clustered, they overlay at this scale. Base map of Switzerland: [swisstopo \(2020\)](#).

sycamore maples were present in one UM plot, and the HM plot was a pure spruce stand. Plot sizes ranged from 0.2 to 2 ha, time series lengths from 47 to 103 years with 9 to 17 inventories. At the time of the first inventory, three stands were uniform thickets, one a uniform stand in timber stage, and three uneven-aged forests. Detailed information on the selected plots can be found in Table S2.1 in Supplementary material S2. The single-tree inventories contain measured and derived information on tree species, DBH, height, crown projection area, status (alive, to be harvested, dead, or missing). Inventories were carried out in autumn and usually followed by an intervention in the subsequent winter.

The first inventories were used to create initialization data for ProForM. The data of small plots was replicated to create virtual plots of ca. 1 ha. Same-species trees with similar DBH were aggregated into cohorts, with the reported crown projection areas in conjunction with the model's cell size dictating the maximum number of trees per cohort. Based on stand descriptions and ingrowth patterns in subsequent inventories, additional cohorts containing regeneration below the caliper threshold had to be added. All cohorts were distributed randomly in space, as no spatial information was available for the first inventories. Management instructions (times of interventions and species-specific removal intensities) for the management type "RDC tree", i.e., single tree removal, were derived from the inventory data using five relative diameter classes. Both initialization data and management instructions only depict the four parameterized species. Based on the stand descriptions, the raw inventory data, and preliminary simulations using the uncalibrated model, each plot was assigned a *site* and *regeneration quality* as well as species' shares of the surrounding forest, which then remained unchanged throughout the calibration process. Calibration simulations with the length of the respective measured time series were run, and the outputs of those time steps corresponding to years with inventories, before and after the management interventions, were compared to the measured data. Additionally, simulations initialized with bare ground conditions and without management were run for 1'000 years ("equilibrium simulations") to assess the long-term effects of the parameter settings.

Model calibration was done for each stratum in a two-step iterative process. First, the parameters relating to the pre-factors were jointly calibrated. Starting with multiple sets of parameter values covering a plausible range, simulations were run and the following metrics of the entire stand and per species were compared visually: basal area, stem number, and diameter distributions. Parameter values were then iteratively adjusted by hand for further simulations until the simulation outputs matched the entire empirical time series to a satisfactory extent,

aiming for an overall deviation of less than 30%. To ensure realistic parameter values, pre-factor-values were not set below 0.3, i.e., a 70% reduction of growth and germination on the worst site conditions compared to the best. Second, the CI_C thresholds for crown base change were calibrated analogously, comparing simulated and measured mean crown lengths. The initial set of tested parameter values was informed by the distribution of CI_C in previous simulation runs. Equilibrium simulations were used to guide parameter value estimates when the empirical records were uninformative.

2.5. Model validation

Model validation was carried out using the other nine out of the 16 EFM plots (Table 3 and Fig. 4). One plot belonged to stratum SM, four to UM, three to HM, and one to SA, and they were situated between 670 and 1680 m a.s.l. at slopes between 9 and 36°. All but one of the SM and UM plots were mixed species stands, again without a marked share of sycamore maple. HM and SA plots were pure spruce stands. While the validation plots in HM only contained three inventories recorded over 20–23 years and were therefore of limited use, the remaining plots spanned 71–101 years with 10–16 inventories. Plot sizes ranged from 0.2 to 2 ha. At the time of the first inventories, two plots were uniform thickets, four uniform stands in timber stage, one a two-layered stand, and two uneven-aged forests. Detailed information on the calibration plots can be found in Table S2.1. The creation of model initialization data, management prescriptions, and simulation settings followed the same procedure as for the calibration plots.

Using a caliper threshold of 8 cm, the simulated time series of total basal area (BA) and stem number (SN), as well as of the crown ratio of the 100 thickest trees per ha (CR) were validated using three metrics: bias, precision, and accuracy (Pretzsch et al., 2002). Bias is expressed as the percentage bias pBias (Eq. (4)) and precision as the standard deviation of the errors (SD; Eq. (5)), with both metrics being based on relative errors (Eq. (3)). Accuracy is quantified by the normalized root mean square error NRMSE (Eq. (6) and (7)). These metrics were calculated for each time step, before and after the intervention, for which an inventory was available for comparison, and they were averaged over the entire simulation period. Furthermore, simulated and measured diameter distributions (DD) were compared using a two-sample Kolmogorov-Smirnov test. In Eqs. (3)–(7), $Ypred_i$ and $Yobs_i$ are the predicted and observed stand metric of time step i , and $Ypred_{min}$ and $Yobs_{max}$ the respective minimal and maximal values.

$$\Delta Yrel_i = \frac{Ypred_i - Yobs_i}{Yobs_i} \cdot 100$$

$$pBias = \frac{1}{n} \sum_{i=1}^n \Delta Yrel_i$$

$$SD = \sqrt{\frac{1}{n-1} \sum_{i=1}^n (\Delta Yrel_i - \overline{\Delta Yrel_i})^2}$$

$$RMSE = \sqrt{\frac{1}{n} \sum_{i=1}^n (Ypred_i - Yobs_i)^2}$$

$$NRMSE = \frac{RMSE}{Yobs_{max} - Yobs_{min}} \cdot 100$$

3. Results

3.1. Model calibration

Most parameter values could be calibrated directly using the data from the respective strata and the equilibrium simulations as a further guide. However, some parameter values had to be estimated using calibrated values from other strata or species. In HM and SA, only one plot was available for calibration (Morissen and Hospental, respectively). Therefore, the minimal values of PF_{GI} and PF_{dH} for HM and the minimal value of PF_{dB} for SA had to be derived from other strata because in Morissen no ingrowth occurred and there were relatively few trees below 12 cm DBH. In Hospental, *site quality* is ideal (i.e., 5) and therefore the minimal value of PF_{dB} has no effect. Furthermore, as very few records of sycamore maple were available in SM and UM and none for silver fir in HM, the respective CI_C thresholds for modeling crown length change were assumed to be identical to those of beech and spruce,

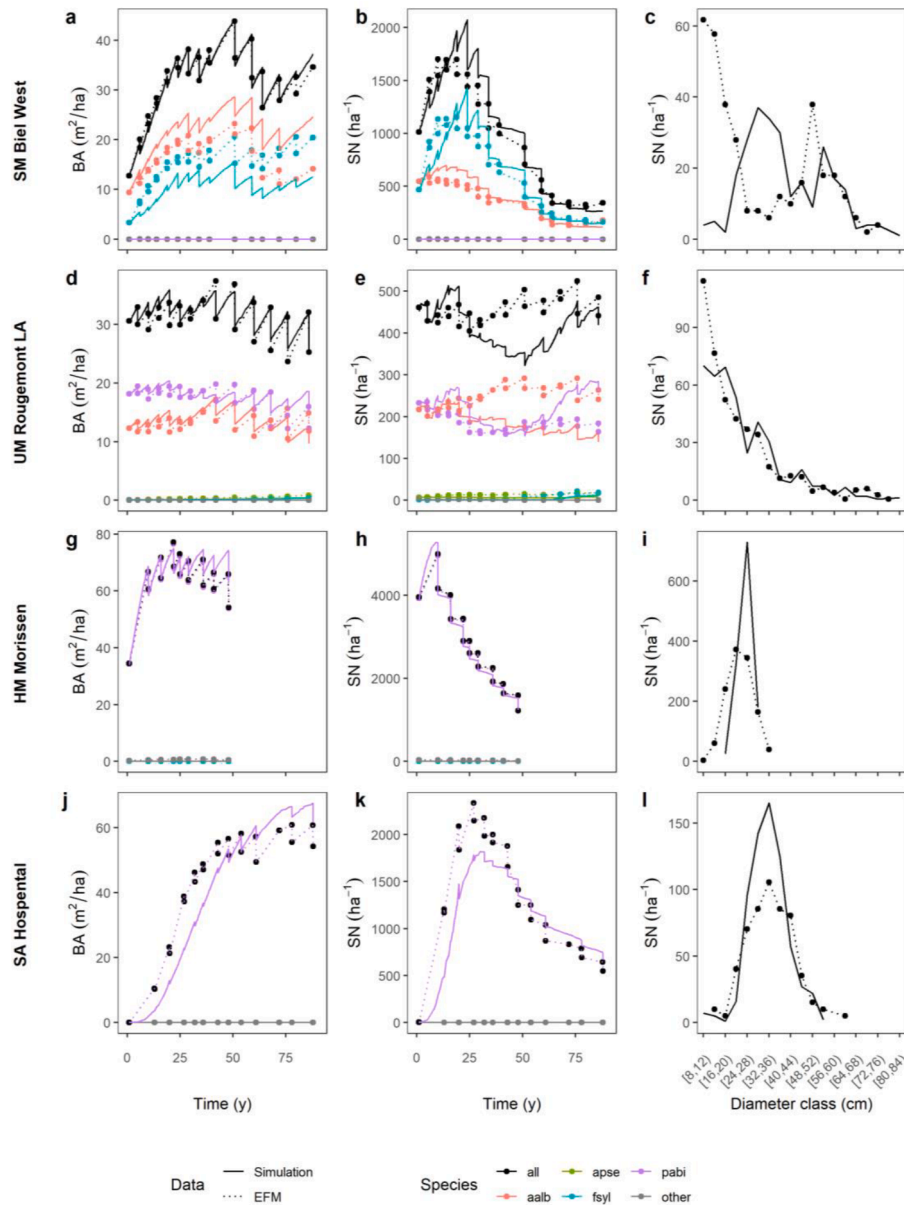


Fig. 5. Simulated and measured stand characteristics of one calibration plot per stratum. First column: basal area (BA); second column: stem numbers (SN); third column: diameter distribution (DD) at the time of the last inventory. Simulated values (solid lines) are shown for each time step, while inventory data (dots) are connected with straight dotted lines for better legibility only. A caliper threshold of 8 cm was used for all graphs.

respectively.

The calibrated model yielded satisfactory results. Most simulated total BA, SN, and CR matched the empirical data closely (Fig. 5; full results in S3). When applying the validation metrics to the calibration simulations, model performance was high: mean pBias over all calibration plots for BA, SN and CR ranged between -2.2 and 8.5% , the mean standard deviation of the error between 7.3 and 10.8% , and the mean NRMSE between 11.6 and 35.6% (Table S3.1).

At the time of the last inventory, the results of BA, SN, and CR of all species combined never deviated more than 30% from the empirical data except for two cases, but only temporarily over several consecutive inventories: In Biel West (SM), the mean CR of the 100 thickest trees per ha was overestimated strongly during about half of the simulation period (Fig. S3.1); and in Hospental (SA), BA and SN were underestimated strongly during the first 30 simulated years (Fig. 5j/k) due to an overestimation of mortality. Even though the simulated and measured DD of all species combined at the time of the last inventory were significantly different on a 5% level according to the Kolmogorov-

Smirnov test in all plots except Sigriswil lower (UM) and Hospental (SA) (Table S3.1), they were quite similar in shape in most cases (Figs. 5 and S3). Obvious differences could be observed in Biel West, where the initially unimodal stand structure developed into a bimodal (two-layered) structure, which was not reproduced correctly by the model (Fig. 5c). Furthermore, the initially quite narrow range of tree diameters in Morissen (HM) did not broaden sufficiently over time in the simulation (Fig. 5i).

The species-specific results in mixed stands deviated more from the measured data than the total stand data. In Biel West, the SN per species matched the records rather well (Fig. 5b), but the final stand was simulated to consist of a dominant silver fir layer and a large group of intermediately sized beech, instead of an upper layer and suppressed regeneration with both species mixed (Fig. S3.1). In the two mixed-species UM stands (Buttes BDP and Rougemont LA), the species-specific BA was reproduced accurately, but the SN of silver fir was underestimated while that of spruce was overestimated (Fig. S3.3 and Fig. 5d/e).

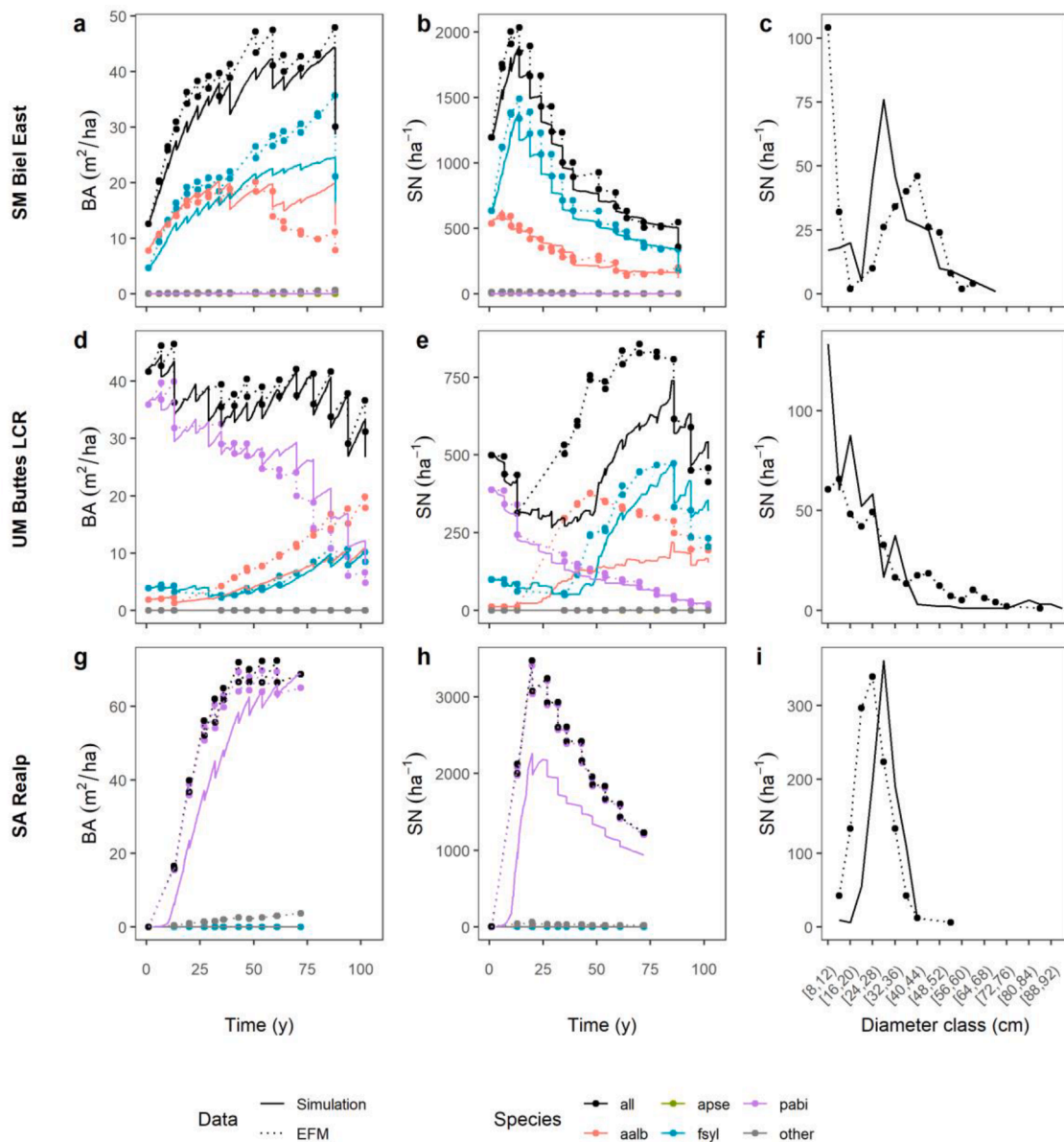


Fig. 6. Simulated and measured stand characteristics of one validation plot per stratum, except for HM. First column: basal area (BA); second column: stem numbers (SN); third column: diameter distribution (DD) at the time of the last inventory. Simulated values (solid lines) are shown for each time step, while inventory data (dots) are connected with straight dotted lines for better legibility only. A caliper threshold of 8 cm was used for all graphs.

The accuracy of the simulated growth of initialized regeneration and the appearance of new regeneration throughout the simulations was assessed qualitatively. In half of the simulations, the growth of the initialized regeneration conformed to measurements, in the other half it tended to be overestimated. The amount and species composition of newly appearing regeneration matched the empirical data well. Furthermore, in some simulations, regeneration waves were simulated to appear too late.

3.2. Model validation

The model validation yielded very good results for most plots (Fig. 6; full results in S4). Due to the short time series and incomplete records of the three HM validation plots, the results of this stratum are of limited value and are reported only in S4. Furthermore, as very few records of sycamore maple were available, the performance of this species cannot be evaluated thoroughly. Model performance was high, with overall absolute mean pBias values of -3.2% , -10.4% and 7.6% for BA, SN, and CR, respectively, a maximum mean SD value of 15.9% , and mean NRMSE values of 18.4% , 31.2% , and 48.8% for BA, SN, and CR, respectively (Table S4.1). The simulated DD at the time of the last inventory differed significantly from the measured data on a 5% level according to the Kolmogorov-Smirnov test (Table S4.1) but were similar in shape in most cases (Figs. 6 and S4).

The simulation results for Biel East (SM) matched measured total BA and total as well as species-specific SN well over time, but the BA of silver fir was over- and that of beech underestimated in the second half of the simulation (Fig. 6a/b). This can be attributed to the initially dominant silver fir, which remained very dominant throughout the simulation, leading to the excessive suppression of beech. Mean CR were overestimated for both species during the entire simulated period (Fig. S4.1). The DD at the last inventory revealed that the resulting stand did not correspond well to the expected two-layered stand, as the number of small trees was considerably underestimated (Fig. 6c). The appearance of a new group of regeneration was simulated to arrive 15 years too early, and its growth was not sufficiently suppressed (not shown).

In three of the four UM validation plots (Buttes LCR, Rougemont G, and Sigriswil upper), simulated total BA agreed well with the empirical data (Figs. 6d, S4.2, S4.4, and S4.5), but it was systematically overestimated by roughly 20% in Le Chenit (Fig. S4.3). In the two mixed-species plots Buttes LCR and Rougemont G, the BA of spruce was overestimated while it was underestimated for silver fir. The temporal trend in SN was reproduced well in Buttes LCR, but the observed increase in SN was simulated with a delay of ca. 25 years (Fig. 6e). In Rougemont G, simulated total SN deviated negatively from the measured data over the course of the simulation but matched them again well at the end (Fig. S4.4). However, the species shares of spruce and silver fir were inverted at this point, as the newly appearing regeneration consisted mostly of spruce instead of silver fir. In the spruce-dominated plots Le Chenit and Sigriswil upper, measured total SN were reproduced well (Figs. S4.3 and S4.5). In all UM plots, simulated overall and species-specific CR and the DD of the larger trees matched the empirical data well over time. Growth rates of the initialized regeneration were slightly too high in two simulations (Le Chenit and Rougemont G), and the amount of new regeneration was overestimated in two simulations (Buttes LCR and Sigriswil upper) and underestimated in one (Rougemont G), while the timing of its appearance was accurate except for the delay in Buttes LCR mentioned above (not shown).

In the SA validation plot Realp, mortality was overestimated in the first 30 years of the simulation, and hence BA and SN were underestimated in this period (Fig. 6g/h). Simulated BA matched the records well towards the end of the simulation, but SN continued to be underestimated. CR of spruce agreed with the empirical data over the entire period (Fig. S4.9). The analysis of the DD revealed that the growth rate of regeneration was overestimated (not shown), causing an increasing

shift towards higher diameters while the shape of the curve was tracked well (Fig. 6i).

3.3. Assessment of protection quality

As an example for the assessment of the protection quality, we calculated the corresponding set of indices for the 90-year simulations of the UM plots Rougemont G, used for the validation, and Rougemont LA, used for the calibration. We used the natural hazard profiles for torrents and floods (the detailed profile values are listed in Table S5.1). Both stands are composed almost exclusively of Norway spruce and silver fir. The main difference is that Rougemont G was transformed from a two-layered stand into a single-tree selection forest with a typical inverse J-shaped diameter distribution, while Rougemont LA featured such a diameter distribution over the entire measurement period.

Overall, both stands featured similar protective effects over time (Fig. 7). The indices for **mixture**, **seedlings**, and **saplings and thicket** were very similar or even identical over time in both stands, and always below the minimal profile. The analysis of the underlying subindices revealed that among the trees with $DBH > 12$ (mixture index), the share of spruce was too high and that of beech and sycamore maple too low. The low index values for seedlings resulted from both the species composition (almost no beech and maple) and the relatively stringent requirement in the minimal profile that 80% of all cells without saplings or larger ($H > 40$ cm) need to contain seedlings. The index value for saplings and thicket was always slightly below the minimal profile, again primarily due to species composition, with too much spruce and too little beech, even though the regeneration cover fulfilled the ideal profile.

Vertical structure in Rougemont G was rated better on average than in Rougemont LA, fulfilling the minimal profile during roughly half of the simulated period. Both stands, however, failed to reach the ideal profile at any point because the lowest diameter class was consistently under- and hence the upper classes underrepresented. The index for **horizontal arrangement** is determined by the requirements regarding the natural hazard, i.e., in this case gap length, gap size, and canopy cover. It started out at the ideal value of 1 and dropped slightly below 0 over time, driven by exceedingly long and large gaps due to the spatially random harvesting that was applied. Finally, the index for **“support trees”**, which is assessing the mean crown length of the most stable trees, increased in both simulations over time from the minimum to the maximum; this was due to increasing mean crown lengths of silver fir, with the change happening earlier in Rougemont LA.

4. Discussion

4.1. Model structure and development

The purpose of ProForM is to investigate the effects of management on the protective function of mountain forest stands. The model is process-based, including submodels for regeneration, growth, and mortality, which were developed largely independently of each other using different sets of empirical data. The main data sources were a combination of regeneration growth data across large parts of Switzerland (Brüllhardt et al., 2020; Schmid et al., 2021), the Swiss NFI (Brändli et al., 2020; WSL, 2020), and forest reserve data from Switzerland and Germany for the mortality functions (Hülsmann et al., 2018). Only the submodel for the dynamics of the crown base height was developed based on theoretical considerations, but then linked to empirical data in the model calibration. Being partly process-based and partly based on empirical data, ProForM is a hybrid between “pure” process-based stand models such as 3-PG (Landsberg and Waring, 1997) and “pure” empirical models such as BWinPro (Hansen and Nagel, 2014) or SwissStandSim (Zell, 2018; Zell et al., 2020). ProForM is more closely related to other stand-scale models developed for temperate and mountain forests in which at least some submodels were developed and

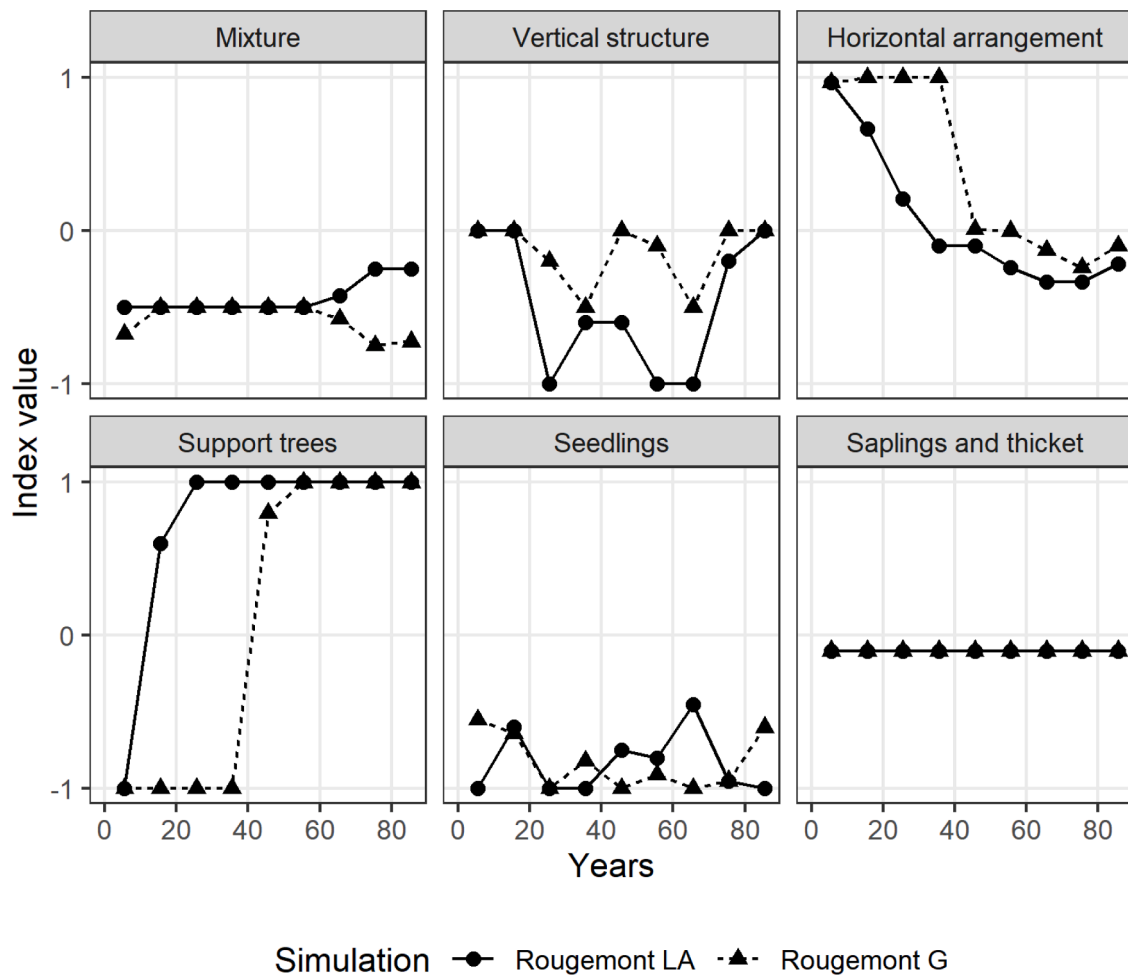


Fig. 7. Protective quality of the simulated UM stands Rougemont G (triangles connected with dotted line) and Rougemont LA (circles connected with solid line) according to the six indices, assuming that these stands are protecting against torrents and floods. An index value of 1 corresponds to the ideal profile, 0 to the minimal profile, whereas -1 indicates that the minimal profile was not met in any of the underlying subindices. The mean index values over each 10-year period are shown.

parameterized based on empirical data, e.g., ForClim (Bugmann, 1996), PICUS (Lexer and Hönninger, 2001; Seidl et al., 2005), or Samsara2 (Courbaud et al., 2015).

The main design principles underlying ProForM are (1) the use of cohorts of identical trees as the main agent, similar to gap models such as ForClim and 4C (Bugmann et al., 1997), and (2) spatial explicitness by assigning each cohort to a cell with known location, thus allowing for interactions among neighboring cells, a concept found, e.g., in PICUS and many empirical single-tree stand models such as SILVA (Pretzsch et al., 2002). Another principle underlying ProForM is (3) that the basic growth equation quantifies growth under optimal conditions, which is then reduced by environmental factors and local competition as experienced by the cohorts. This concept is widespread and applied, e.g., in many gap models (Bugmann, 2001).

A peculiarity of ProForM is the use of two growth equations to be able to simulate the growth of trees starting from very small sizes (here, a height of 10 cm). Similar to a version of ForClim (Wehrli et al., 2007), one equation is used for modeling height growth of regeneration, and one for diameter growth of adult trees, with the transition at 12 cm DBH in our case, dictated by the caliper threshold of the Swiss National Forest Inventory. A different approach was used in SORTIE (Pacala et al., 1996) by modeling stem diameter at 10 instead of 130 cm tree height. Apart from these two examples, only few dynamic stand models include regeneration from such a small size as ProForM. In the context of sustainable protection from natural hazard, a focus on small trees (i.e.,

regeneration) is crucial, however, and ProForM fulfills this requirement well.

ProForM is a relatively simple model: it has low structural complexity, includes only four species and no explicit climate dependency of the demographic functions. However, it is parameterized for four discrete elevational zones to represent typical conditions in Swiss mountain forests. We applied a simple concept to aggregate multiple abiotic and biotic factors that influence tree growth and regeneration occurrence, such as local climate, soil quality, or browsing pressure, into two parameters for site characterization (*site* and *regeneration quality*) which in turn affect simulated growth and regeneration dynamics through pre-factors applied to the respective functions. Implicitly, these qualities and the resulting pre-factors can be used to aggregate different factors depending on the simulated site. This allows the model to be applied to stands along a large environmental gradient and thus under most conditions in the northern and central European Alps. However, to apply the model to sites outside its original geographic range, site-specific parameterization of the environmental factors would be needed. Lastly, even though the model cannot be directly used to simulate forest dynamics under a changing climate, preliminary conclusions by analogy are possible due to the expected upward shift of elevational zones (Frehner and Huber, 2019; Zischg et al., 2021).

4.2. Model parameterization and calibration

Most of ProForM's parameters were not calibrated but determined using empirical data in one of three ways: a) by fitting statistical models, e.g., for the core functions of the height growth of regeneration; b) by deriving single parameter values within more theoretical submodels, e.g., the maximum diameter growth rate of trees > 12 cm DBH; or c) by estimation informed by data analysis, e.g., the time required for bare-ground cells to contain regeneration. In this process, to which we refer as parameterization, outputs of the entire model (at the stand scale) were not compared to empirical data. A similar procedure was followed in the development of SORTIE (Pacala et al., 1996). This approach conserves the process formulations and their respective parameter values as qualitative and quantitative hypotheses regarding the underlying ecological processes.

Only in the subsequent model calibration, simulated patterns emerging at the stand scale were compared to time series of independent data to determine the values of five parameters. A common procedure for parameter selection would have been to conduct a sensitivity analysis (e.g., Huber et al., 2018; Lagarrigues et al., 2015; Lin et al., 2022). Instead, we selected parameters that we deemed important to tie the model even more strongly to empirical data but for which we were unable to make an assessment in the sense of parameterization (cf. above). The minimal values of the three pre-factors used in regeneration (germination and ingrowth) and growth (height and diameter growth) were calibrated because these allow the model to simulate below-optimal growth conditions, which the submodels' core functions are parameterized for. Also, the two competition thresholds determining the onset of crown base lowering or elevation were calibrated to link the purely theory-based submodel for crown dynamics to empirical data.

During calibration, the parameter values were adjusted iteratively and simultaneously “by hand”, similar to the calibration procedure by Pabst et al. (2008) with ZELIG and Risch et al. (2005) with ForClim. We deliberately decided against more sophisticated calibration procedures such as parameter optimization (e.g., Lin et al., 2022; Mina et al., 2016) or Bayesian approaches (e.g., Cailleret et al., 2020; Forrester et al., 2021a; Lagarrigues et al., 2015; van Oijen et al., 2013) that would arguably have led to a closer fit of model results to the data. We had only rather few stand records per stratum available for calibration, which in some cases also lacked information on certain processes relevant to calibration, such as almost no records of sycamore maple or no new regeneration appearing in the stands of the HM zone. Therefore, our simple calibration procedure offered several advantages: it allowed us to avoid overfitting the model to these time series, to take specific emergent patterns in equilibrium simulations into account, and to use parameter values calibrated with higher certainty to estimate values of strata or species with less or no information in the calibration data. Finally, it allowed us to select a set of parameter values that are ecologically consistent across all four strata, something that is rather difficult to achieve with automated procedures (cf. Bircher, 2015).

4.3. Model performance

The stand data from the Swiss EFM network (Forrester et al., 2021b, 2019) used to assess model performance during calibration and validation cover exceptionally long periods, i.e., up to more than a century. The plots selected to assess the performance of ProForM furthermore cover a large environmental gradient in terms of elevation and growth conditions, they comprise a wide range of stand structures and species compositions and can therefore be regarded as a stringent test set. The use of these records posed three main challenges that introduced uncertainties to the assessment process: First, there were unknown quantities of regeneration below the caliper threshold in most plots. Initializing the model with only the recorded trees would have created artificial lags, as encountered, e.g., by Didion et al. (2009). To avoid this problem, assumptions had to be made on the quantity and composition

of regeneration below the caliper threshold. Second, the simulation settings for *site* and *regeneration quality* had to be estimated based on very limited local information on site conditions and the factors influencing regeneration growth, e.g., browsing pressure. Third, no spatial information was available on the initial stand structure and the management interventions. The cohorts at initialization and the location of management interventions were therefore distributed randomly in space.

Various model processes contain stochastic components, most notably regeneration, mortality, and management, that could compromise the meaningfulness of comparing single model runs to empirical data. However, preliminary tests have shown that the influence of these stochastic events on emergent patterns at the stand level is relatively small, as they act on the cohort level and are averaged out over the entire stand. Still, using the RDC harvest algorithm, uncertainties were introduced, as its dependency on the accuracy of the simulated diameter distribution at the time of intervention can augment existing discrepancies between simulated and measured diameter distributions over time.

In spite of these potential sources of error, ProForM performed very satisfactorily. In general, the simulated emergent patterns of basal area, stem numbers, diameter distribution, and species composition agreed well with observations over long periods. Despite it being a relatively simple model, the validation revealed its ability to reproduce the dynamics of managed stands at least as well as much more complex simulation models such as Samsara2 (Courbaud et al., 2015), ZELIG (Pabst et al., 2008), ForClim (Bircher et al., 2015; Didion et al., 2009; Mina et al., 2017; Rasche et al., 2011; Wehrli et al., 2005), PICUS (Irauschek et al., 2017b; Pardos et al., 2015; Seidl et al., 2005), SILVA (Mette et al., 2009; Pretzsch et al., 2002; Schmid et al., 2006) or 4C (Lasch et al., 2005), judging by the validation metrics reported in these studies. Furthermore, most other forest stand models have been validated against considerably shorter time series (e.g., 15 to 30 years for PICUS and SILVA; 40 to 65 years for Samsara2, ZELIG, and 4C). Different versions of ForClim have been validated against EFM plots, and some of them were also used in the present study for calibration. It is noteworthy that the ability of ProForM to reproduce the dynamics of these plots is similar to the performance of recent ForClim versions (Bircher et al., 2015; Mina et al., 2017). It is quite remarkable that in spite of its simplicity and the problems underlying the definition of appropriate settings for model testing, ProForM is performing so well.

4.4. Model limitations and further development

Despite the general success of the model, the calibration and validation revealed some weaknesses and thus indications for further development. The most pronounced discrepancies between observed and simulated data were evident in the diameter distributions in the SM plots Biel East and Biel West, suggesting that the model has a problem capturing the differentiation of a uniform stand into a two-layer structure. This behavior resulted from (1) an incorrect representation of interspecies competition, and (2) an increasing divergence over time caused by the RDC management algorithm. Competition effects across species could certainly be refined by introducing species-specific growth responses to competition and site quality.

Another problem is that the diameter distribution in initially highly uniform young stands remained too narrow over time. This became evident in the HM calibration plot Morissen and, to a lesser extent, in the SA plots Hospental and Realp. The underlying reason is the simplifying assumption that there are no individual differences in growth among trees of the same diameter as they are experiencing the same level of competition.

Furthermore, in the UM plots Buttes LCR and Rougemont G, the timing of new waves of regeneration was evidently delayed. This could be caused by many factors playing important roles in the dynamics of regeneration establishment that are not represented in the model, such

as masting cycles or fluctuations in browsing pressure. However, the amount and in Buttes LCR also the species composition of the regeneration wave matched the observations well, and we therefore do not consider this a major problem. Still, the species selection procedure at germination could be improved by including, e.g., the local competition level and species-specific shade tolerance.

Finally, growth and therefore basal area in the UM plot Le Chenit, which features extremely poor growth conditions, was always overestimated. This indicates that the calibrated minimal value of the growth reduction factor is not low enough as a result of attributing the same site quality instead of a slightly higher one to the more favorable site of Sigriswil lower, which was used for calibration.

Even though the applied management algorithm with its spatially random selection of single trees produced good results for most plots, further options should be added to the model to represent the spectrum of current management practices in mountain forests (Brang et al., 2006; Streit et al., 2009). This could include locally clustered interventions (round or slit-shaped gaps), the species-specific promotion of regeneration through appropriate gap sizes, or the enhancement of collective stand stability by promoting stable trees with long crowns. In addition, the model can be used to simulate the dynamics of unmanaged stands; however, the plausibility of such simulation results (especially over long periods) would first need to be assessed thoroughly, as this was not the scope of our study.

4.5. Assessments of the protective quality of forest stands

The assessments of the protective quality of the two UM plots at Rougemont revealed that these stands do not satisfy the requirements for protection forests against torrents and floods, as the minimal profile was not met across all indices at any point in time. This can be attributed mainly to the management schemes applied at these two plots, which was not focused on maximizing the protective effect, and its representation in the model. The protective function in these two stands would greatly benefit from an active promotion of beech and sycamore maple as well as spatially clustered interventions instead of the random removal of single trees that resulted at some point in oddly shaped but large and/or long gaps, as small openings were becoming connected over time in the simulation.

Still, these two case studies illustrate the holistic approach of NaiS (Frehner et al., 2005) and its implementation in ProForM. The major model features enabling this are (1) the model's spatially explicit nature and (2) the explicit modeling of regeneration starting from very small height. Gap models such as ForClim or 4C, and distance-independent growth simulators such as BWinPro or SwissStandSim lack the spatial information required to assess gaps and usually model ingrowth with a size threshold well above a height of 1.3 m (but cf. Wehrli et al. (2007) for ForClim). While these shortcomings are not present in Samsara2, this model is currently parameterized for Norway spruce and silver fir only. Among the stand-scale forest models applicable to European mountain forests, PICUS in connection with the regeneration submodel described in Woltjer et al. (2008) is, to our knowledge, the only other model with which an assessment of the protective function of similar breadth could be achieved. While PICUS is among the most complex forest stand models (Bugmann and Seidl, 2022), ProForM is located on the opposite side of the complexity-spectrum. Hence, it occupies its own niche for possible model applications, as, for example, comparatively little input data and site characterizations are needed to run the model.

Possible further developments of ProForM to improve the assessment of the protective function would be to include (1) lying deadwood as a favorable seedbed for spruce at high elevations and as obstacles to rock and snow movements, (2) ground vegetation influencing local germination probabilities, and (3) further tree species.

5. Conclusions

With the development and testing of ProForM, we have shown that it is possible to provide a relatively simple dynamic model that captures the dynamics of mountain forest stands accurately. The model is mostly based on empirical data yet describes the demographic processes in an ecologically interpretable way, which makes its projections more robust compared to “pure” empirical approaches.

Furthermore, the features of ProForM make it possible to represent most of the criteria used in many European countries to assess the protective function of mountain forest stands, integrating both the protective function of the current stand structure as well as the stand's resistance and resilience to large disturbances. Thus, ProForM can be used to assess the long-term sustainability of the protective function of mountain forest stands.

Lastly, the high accuracy and level of detail in the assessment of the protective function embedded in ProForM render this tool valuable for investigating the complex effects of current and alternative management schemes on the provisioning of the ecosystem service “protection against natural hazards” of temperate mountain forests in practical forest management.

CRedit authorship contribution statement

Ueli Schmid: Conceptualization, Methodology, Software, Investigation, Writing – original draft, Visualization. **Monika Frehner:** Conceptualization, Methodology, Writing – review & editing, Supervision, Funding acquisition. **Jonas Glatthorn:** Data curation, Writing – review & editing. **Harald Bugmann:** Conceptualization, Methodology, Resources, Writing – review & editing, Supervision, Funding acquisition.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

ProForM v1.02 (Original data) (github) **The Experimental Forest Management network** (Reference data) (Envidat)

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at [doi:10.1016/j.ecolmodel.2023.110297](https://doi.org/10.1016/j.ecolmodel.2023.110297).

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