

# The PhenoMeNals Approach for Grapevine Yield and Quality Forecasting

Simone Bregaglio, Sofia Bajocco

## Table of contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
----------	---------------------	----------

## 1 Introduction

Grapevine (*Vitis vinifera* L.) is one of the most widely cultivated fruit crops globally, with high economic value and strong sensitivity to climatic variability. Accurate forecasting of yield and quality is essential for decision-making in viticultural management, allowing producers to anticipate harvest volume, allocate labor and inputs efficiently, and adapt wine production strategies accordingly [fraga2019; vanleeuwen2022]. The need for robust forecasting tools is particularly pressing under current climate change scenarios, which are increasing the frequency of extreme events, phenological shifts, and yield variability in perennial crops [chuine2017; santos2020].

Various modeling approaches have been proposed to predict grapevine yield and quality. These include empirical models based on historical correlations with meteorological variables [goulet2019], process-based models incorporating phenological and physiological processes [keller2010], and machine learning approaches trained on large multivariate datasets [oliveira2021]. While each class of models has shown utility under specific conditions, several limitations persist. Empirical models often lack generalizability and physiological interpretability. Mechanistic models are constrained by data requirements and calibration complexity. Data-driven methods can capture nonlinear relationships but frequently act as black boxes, with limited transparency and interpretability for agronomic decision-making.

Moreover, most forecasting models treat phenology in a static or coarse-grained way—e.g., as discrete BBCH stages—and tend to aggregate agrometeorological predictors over fixed calendar or phenophase periods [grifoni2006]. This limits their capacity to capture the dynamic, continuous interaction between plant development and environmental stressors throughout the

season. Additionally, a growing body of evidence indicates that grapevine yield and quality are influenced not only by the climatic conditions of the current growing season but also by those of the previous year [santesteban2011; greer2013; keller2010]. These carry-over effects, mediated by reserve accumulation, bud differentiation, and adaptation mechanisms, are rarely incorporated explicitly into forecasting models.

To our knowledge, no previous approach has operationalized this concept of *phenological memory* using dynamic, time-resolved agrometeorological indicators in a predictive framework. In particular, no existing model applies rolling correlation analyses across the phenological continuum—spanning dormancy and active growth—and accumulates statistically weighted signals from both current and previous years as predictors for yield or quality.

In this study, we introduce **PhenoMeNals (Phenology Memory Signals)**, an innovative, open-source R package and forecasting approach for grapevine production modeling. The PhenoMeNals method integrates:

1. A self-calibrating phenological model simulating the dormancy (0–100%) and growing season (100–200%) using chill/anti-chill and forcing functions aligned with BBCH observations;
2. Eight agrometeorological indicators (phenomenals) reflecting key physiological and pathological risk drivers (e.g., thermal response, water stress, heat/cold extremes, disease-conducive conditions);
3. A novel use of rolling Pearson correlations between these indicators and the target variable, computed over current and prior years, normalized via sigmoid scaling and statistical significance;
4. A final multiple regression model based on selected predictors, evaluated for collinearity, significance, and temporal stability.

The overall goal of this work is to advance forecasting methodology for perennial crops by incorporating climate-driven memory effects into a transparent and reproducible framework. The approach is implemented as a fully open R package available on GitHub, supporting further applications across cultivars and regions.