

A flexible framework for foliar disease modelling for profitable fungicide management

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Abstract

The benefits derived from fungicide application can vary greatly between years, resulting in unnecessary fungicide applications, or unacceptable losses to disease. While the economic returns from fungicide application are dependent on a complex combination of factors, application decisions often rely on simple decision thresholds and the intuition of growers and agronomists.

Department of Primary Industries and Regional Development (DPIRD) research, supported by investments from the Grain Research Development Corporation (GRDC) has been working for several years to develop foliar disease decision support tools. These tools assist growers in making cost-effective fungicide decisions through integration of field trial research data and the extensive domain specific knowledge of expert plant pathologists. This presentation demonstrates the flexible software framework developed for modelling of polycyclic foliar diseases, and the simulation of possible outcomes to estimate the probability of economic returns. The framework uses the software design principals of modularity and abstraction to allow a single codebase to be configured for multiple diseases. This significantly reduces the replication of code for different diseases and crops, reduces maintenance burden of legacy code, and allows for more rapid deployment of updates and enhancements. This talk demonstrates this framework using the example of net blotch (*Pyrenophora teres*) of barley to show the process of model calibration using available field data and expert interpretation.

Keywords

Disease modelling, decision support tools, fungicide management, integrated disease management

Introduction

Foliar pathogens in cropping systems can cause significant losses in yield if not managed effectively. Conversely conservative management of foliar disease through application of fungicides in excess of requirement can reduce profitability and compromise the long-term effectiveness of fungicides through the promotion of fungicide resistance. Integrated Disease Management (IDM) strategies consider all aspects of the cropping system to minimise disease impacts in a profitable and sustainable way. However, cropping systems are complex and dynamic, therefore balancing the competing requirements of the system as a whole requires significant understanding and experience. Plant pathology in itself is a unique discipline in which expertise is limited to only a subset of the population of growers, agronomists and researchers. However, all growers are required to make decisions about the management of plant pathogens, and update decisions in a dynamic way, in order to maintain a profitable business. The purpose of a Decision Support Tool (DST) is to aid growers and agronomists in making evidence-based choices by integrating knowledge from multiple sources to provide recommendations or predictions tailored to the specific context of the user.

Central to the concept of IDM is the idea of the economic injury level (EIL) and economic threshold (ET). When adapted for foliar diseases, the economic injury level is the disease occurrence that will result in crop injury that exceeds the cost of control measures. The EIL therefore defines the point at which it becomes profitable to intervene. IDM recognises that effective management requires intervention prior to disease pressure reaching the EIL. The ET defines a threshold value at which management action should be taken to prevent the disease exceeding the EIL. Therefore, effective IDM strategy involves being able to predict the likely impact of disease, within a timeframe which allows for effective management intervention. In addition, the EIL, and ET are a function of the value of the crop being managed, as well as the cost and efficacy of the management intervention. In practice growers often use a combination of intuition, experience, trusted advisers, and simple heuristics derived from research trials in order to make these

decisions. A fungicide DST must help decision makers balance these complex inter-acting variables in an evidence-based way without requiring subject matter expertise.

The Department of Primary Industries and Regional Development (DPIRD) in Western Australia, working with the GRDC, have developed a series of DSTs in collaboration with pathologists and agronomists across Australia. These DSTs aim to reduce the manageable impact of fungal diseases, resulting in improved profitability and reduced financial risk. The tools are delivered to end users through a range of technology platforms including desktop and mobile apps, with both off-line and online functionality, and web-based APIs for integration into third-party farm management software.

Tools have been produced for seven high impact diseases affecting cereal, canola and pulse crops at a national level. The tools have been developed by range of people over time, but share similar structure for both inputs and outputs:

- Users enter a range of paddock specific risk factors which are tailored to the specific disease of interest.
- Users enter the possible fungicide application scenarios to be evaluated.
- A disease model is used to estimate the likely yield impact from disease under each scenario, including a baseline of no-action.
- Users estimate their expected yield potential, paddock gate price, including a probable range for each estimate.
- Monte Carlo simulation is used to determine the profitability of each fungicide scenario considering the input values and the uncertainty associated with each variable.
- The profitability of 10,000 random simulations is summarised to provide users with the most likely profit margin of each scenario.

Each tool follows this basic structure however, slight differences exist between tools reflecting the iterative nature of development, pathogen specific modifications, expertise and preferences of the developers, resourcing, etc. The result is that maintenance requirements for existing tools increases with each new disease, which slows the pace of development and release of new tools. Recent work has focussed on unifying the model structure through adopting established software design principals to simplify the creation and upkeep of the suite of tools as well as work towards combining models for each crop to create crop-specific disease management tools rather than a series of disease specific tools. This paper illustrates the relevance of software engineering principals to crop foliar disease modelling, with reference to the recently developed DST for management of net blotches in barley caused by the pathogen *Pyrenophora teres*.

Methods

Model Selection

Plant disease modelling, and modelling in general, is a diverse discipline. A wide range of modelling techniques exist, each suited to different circumstances, including: the purpose of the model, the quantity and type of data available, and the understanding of the underlying system, among other factors. A model that is fit-for-purpose must balance: *feasibility*; possible within the available constraints; *reliability*; accuracy of the model outputs; and *usefulness*; alignment with end-user requirements (Hamilton et al. 2021). Building a predictive foliar disease model which is applicable nationally provides many constraints, the model should: generalise to different regions and climates and also require uniform input data available in all regions. Furthermore, in order to adapt a similar model to different pathosystems the model should be able to cope with systems with low data availability by incorporating expert opinion and transferable knowledge when data is lacking.

Mechanistic models are typically used to achieve this level of flexibility, rather than empirical models. These models aim to describe the underlying disease development process using parameters which are linked to the underlying biology of the pathosystem, e.g., latent period, optimum temperature range, number of infective sites, or number of infective propagules produced. In this way, models can be parametrised for different pathosystems based on variable data sources, including elicitation of expert knowledge. This has distinct advantages in systems where little data is available because it allows the transfer of knowledge of the underlying disease development process from one system to another. Similar flexible disease modelling concepts have been discussed by others e.g., Audsley et al. 2005; Magarey and Sutton 2007.

Model parameterization is a type of abstraction that aligns with fundamental principles of software design.

Abstraction in software design involves creating simplified representations of complex systems, enabling developers to manage complexity by focusing on high-level operations. Parameters in mechanistic models serve as abstractions of complex biological processes, making it easier to develop and implement models that can be applied to various pathosystems.

In software engineering, modularity involves breaking a program or algorithm into separate interchangeable components or modules. This allows developers to modify, replace, or upgrade individual modules without affecting the entire system. Similarly, parameterizing mechanistic models allows individual parameters to be adjusted or replaced without overhauling the entire model.

Framing these concepts in the software engineering paradigm is useful because abstraction and modularity are core principles of software design, and we can leverage a large body of theory and practice and design patterns. Also, effective communication and delivery of DSTs to non-technical end users typically requires adaptation of scientific or statistical models into a software framework.

An example using net blotches of barley (NetBlotchBM)

The NetBlotchBM model uses a flexible risk-index approach similar to that described Magarey and Sutton (2007). The model uses a linear combination of risk factors to calculate a disease severity index (DSI).

In the net blotch context, we calculate a DSI using:

$$DSI = aSN + bSB + cR$$

The parameters SN, SB and R, are functions of: the predicted seasonal outlook (SN), the age / quality of stubble inoculum (SB) and crop variety disease resistance (R). The parameters a, b, c are scale factors which assign relative importance to each risk factor.

The polycyclic nature of net blotch development is expressed using a simple logistic growth model. The DSI value is combined with daily weather data (W_d) to create a daily DSI (DSI_d). This value is scaled by a parameter e so that DSI_d is expressed as a unit of time (Growing Degree Days, GDD) which becomes the growth rate parameter in the logistic growth model.

$$DSI_d = aSN + bSB + cR + dW_d / e$$

The logistic growth model is then run using a daily time-step to predict progression of disease from the current growth stage, terminating at Z75. Disease severity at Z75 is used to calculate grain yield impact, using a linear function based on a relationship established by Jayasena et al. 2007.

A simplified flow diagram representing the NetBlotchBM DST illustrates how this mathematical disease representation is expressed diagrammatically and how these components form discrete modules within the larger DST structure (Figure 1).

Abstraction can also be built at multiple layers creating a nested structure. This allows for the system to be adapted at different levels depending on the similarity of the pathosystems being compared. For example, net blotch (*Pyrenophora teres*) is modelled using a similar structure to an earlier DST model for yellow leaf spot in wheat (YellowSpotWM), caused by the related fungal pathogen, *Pyrenophora tritici-repentis*. The primary changes are slight differences in the risk factors used and the underlying parameters. On the other hand, *Sclerotinia sclerotiorum*, which causes Sclerotinia stem rot disease in canola, is a monocyclic disease. Using a modular structure, Sclerotinia stem rot can be modelled with an almost identical model (SclerotiniaCM), replacing only the polycyclic disease module, for a monocyclic disease module (in addition to a unique set of risk factors and associated parameters).

The overlap in the ways of abstracting both plant disease models description of the real world and software engineering best-practices provide an ideal situation for creating DSTs for new pathosystems and making maintenance of existing DSTs simpler. This provides benefits to the maintainers of the DSTs in time and ability, and future benefits to industry by providing quicker responses with new, robust DSTs.

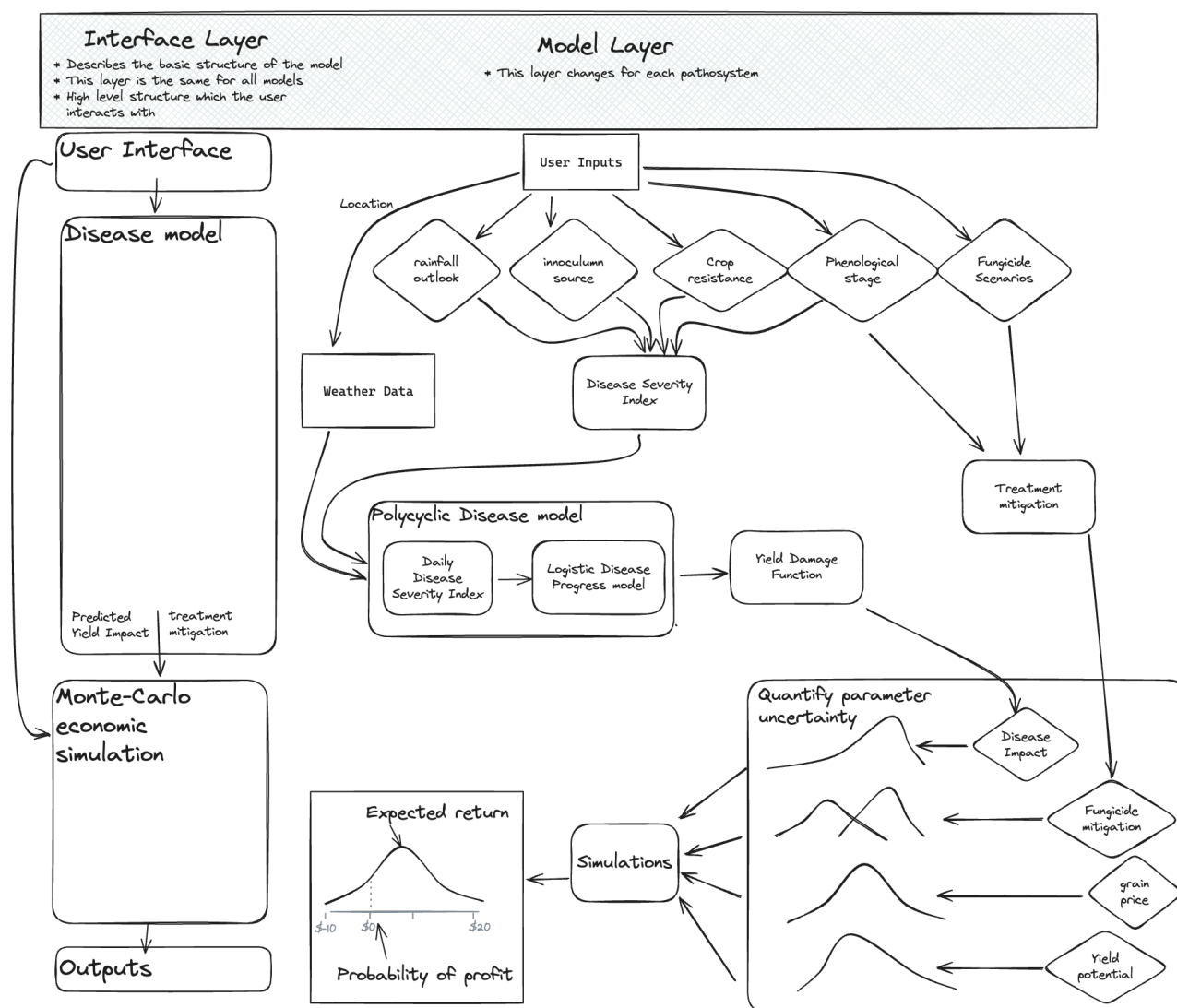


Figure 1: A simplified flow diagram of the NetBlotchBM model showing the two main layers of abstraction (the interface layer and model layer) and modular structure.

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