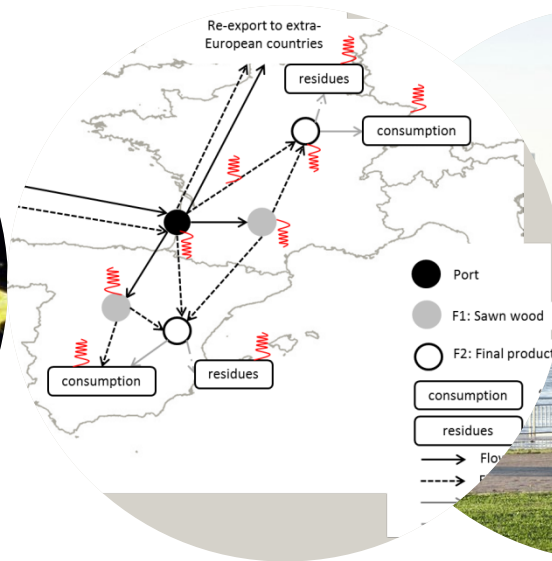


Modelling to predict introduction and spread of forest pests in Europe

Wopke van der Werf, Bob Douma, Monique Mourits, Christelle Robinet



HOMED: Holistic management of emerging pests and diseases

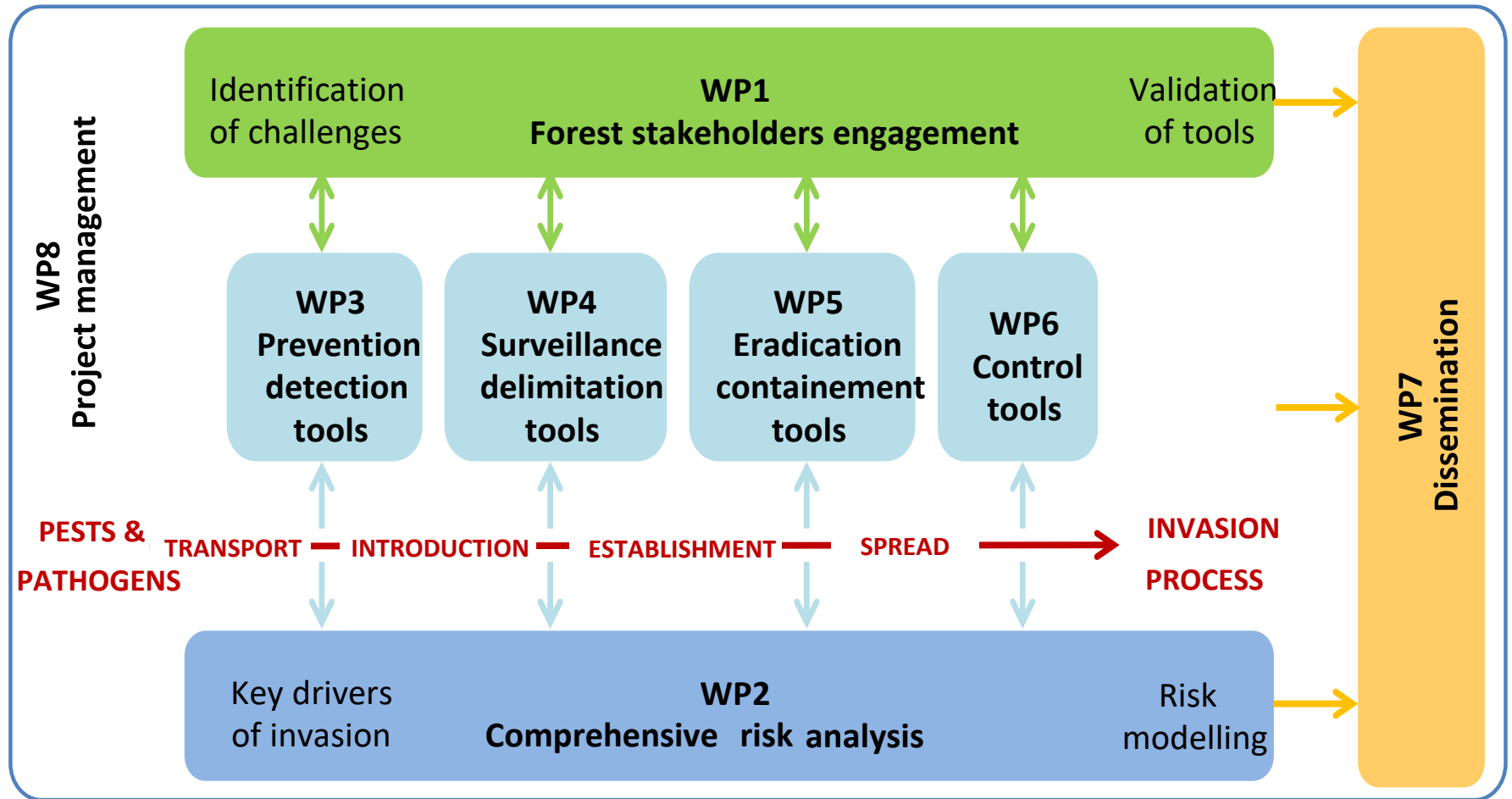
- New EU H2020 project 1 Oct. 2018 – 30 Sept. 2022
- Emerging native and non-native pests and pathogens threatening European forests
- Holistic multi-actor approach
- Trees in forests, nurseries, urban and rural areas
- Science, technology and management (decision) support

- Led by Herve Jactel, INRA Bordeaux
- 23 partners

- | | | |
|-----|--|---------------------------------|
| 1. | Institut national de la recherche agronomique (INRA) | France |
| 2. | Alliance Forêt Bois[®] (AFB) | France |
| 3. | CAB International (CABI) | United Kingdom |
| 4. | Institute of Zoology, Chinese Academy of Science (CAS) | China |
| 5. | Commonwealth Scientific and Industrial Research Organisation (CSIRO) | Australia |
| 6. | Consiglio Nazionale Delle Ricerche (CNR) | Italy |
| 7. | Coventry University (CU) | United Kingdom |
| 8. | Swiss Federal Institute for Forest, Snow and Landscape Research (WSL) | Switzerland |
| 9. | European Forest Institute (EFI) | Finland |
| 10. | INRA Transfert (IT) | France |
| 11. | Instituto Superior de Agronomia (ISA) | Portugal |
| 12. | Mendelova Univerzita v Brne (MENDELU) | Czech Republic |
| 13. | New Zealand Forest Research Institute Limited (SCION) | New Zealand |
| 14. | Pensoft[®] | Bulgaria |
| 15. | Royal Horticultural Society (RHS) | United Kingdom |
| 16. | Sveaskog AB | Sweden |
| 17. | Sveriges Lantbruksuniversitet (SLU) | Sweden |
| 18. | Telespazio[®] (TPZF) | France |
| 19. | The University of Queensland (UQ) | Australia |
| 20. | United States Forest Service (USDA FS) | United States of America |
| 21. | Università degli Studi di Padova (UNIPD) | Italy |
| 22. | University of Pretoria (UP) | South Africa |
| 23. | Wageningen University (WU) | The Netherlands |



Eight workpackages



WP2: Comprehensive risk analysis for emerging and invasive pests

- T2.1 Development of a generic framework for pathway modelling to assess risks of entry (including transfer to host) and effectiveness of entry mitigation
- T2.2 Development of a generic framework for modelling spread (including establishment) and spread mitigation
- T2.3 Development of a generic framework for emergence due to changes in climate, environment and management practices
- T2.4 Development of a generic framework for economic assessment of risk mitigation

WP2: Comprehensive risk analysis for emerging and invasive pests

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Pathway models

- Pathway = Country of Origin + traded commodity
- A pathway model describes mathematically the movement of pest propagules or their vectors (carriers) from a source (area) to a geographic area of concern
- Quantifies the number of pest propagules that come into contact with the host or host habitat
- Uses trade statistics and pest specific parameters
- Uses expert judgement to quantify parameters that are not well established from research (e.g. level of infestation in the trade)

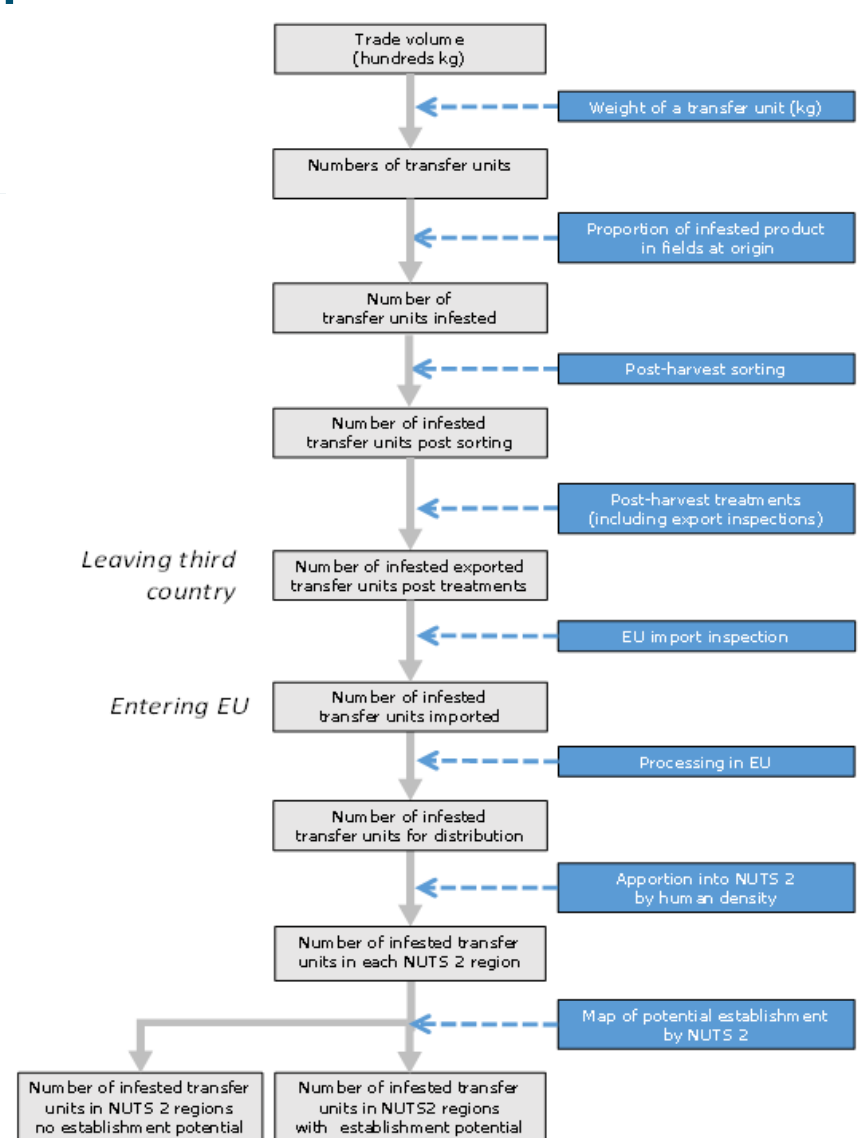
Douma JC, M Pautasso, RC Venette, C Robinet, L Hemerik, MCM Mourits, J Schans, W van der Werf (2016) Pathway models for analysing and managing the introduction of alien plant pests – an overview and categorization. *Ecological Modelling* 339, 58-67. <http://dx.doi.org/10.1016/j.ecolmodel.2016.08.009>

Pathway models

- Unidirectional
- A subset of epidemic network models (multi-directional)
- Make the assessment of entry quantitative
- Enable comparison of pathways and management options
- Enable uncertainty analysis and scenario studies

Douma JC, M Pautasso, RC Venette, C Robinet, L Hemerik, MCM Mourits, J Schans, W van der Werf (2016) Pathway models for analysing and managing the introduction of alien plant pests – an overview and categorization. *Ecological Modelling* 339, 58-67. <http://dx.doi.org/10.1016/j.ecolmodel.2016.08.009>

Pathway modelling for assessing and predicting pest introduction and its mitigation



Some thoughts on quantitative pathway models

- Authorities (e.g. EFSA) are interested in transparent quantification of risk
- International trade relatively well-known, but still problems in the resolution of data collection (tracking and tracing not at the same level as in animals)
- Pest-specific parameters problematic; many are lacking because not seen as scientifically interesting
- Expert elicitation required to parameterize models
- Elicitation and models can include experts' uncertainty
- Need to build familiarity and assess advantages and disadvantages of a quantitative approach

LETTER

Predicting the spread of all invasive forest pests in the United States

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Abstract

We tested whether a general spread model could capture macroecological patterns across all damaging invasive forest pests in the United States. We showed that a common constant dispersal kernel model, simulated from the discovery date, explained 67.94% of the variation in range size across all pests, and had 68.00% locational accuracy between predicted and observed locational distributions. Further, by making dispersal a function of forest area and human population density, variation explained increased to 75.60%, with 74.30% accuracy. These results indicated that a single general dispersal kernel model was sufficient to predict the majority of variation in extent and locational distribution across pest species and that proxies of propagule pressure and habitat invasibility – well-studied predictors of establishment – should also be applied to the dispersal stage. This model provides a key element to forecast novel invaders and to extend pathway-level risk analyses to include spread.

Keywords

Dispersal kernel, habitat invasibility, macroecology, propagule pressure, spatially explicit.

Ecology Letters (2017) 20: 426–435



Hypotheses of the study

- The spread of biological invaders proceeds following similar processes across species, and so we predicted that a single general model of pest spread can fit well for all forest pests in the United States.
- Pest life history, propagule pressure, and habitat invisibility can be meaningfully integrated into a dispersal kernel, and lead to improved predictions in a general model.



Negative exponential (=Laplace) kernel

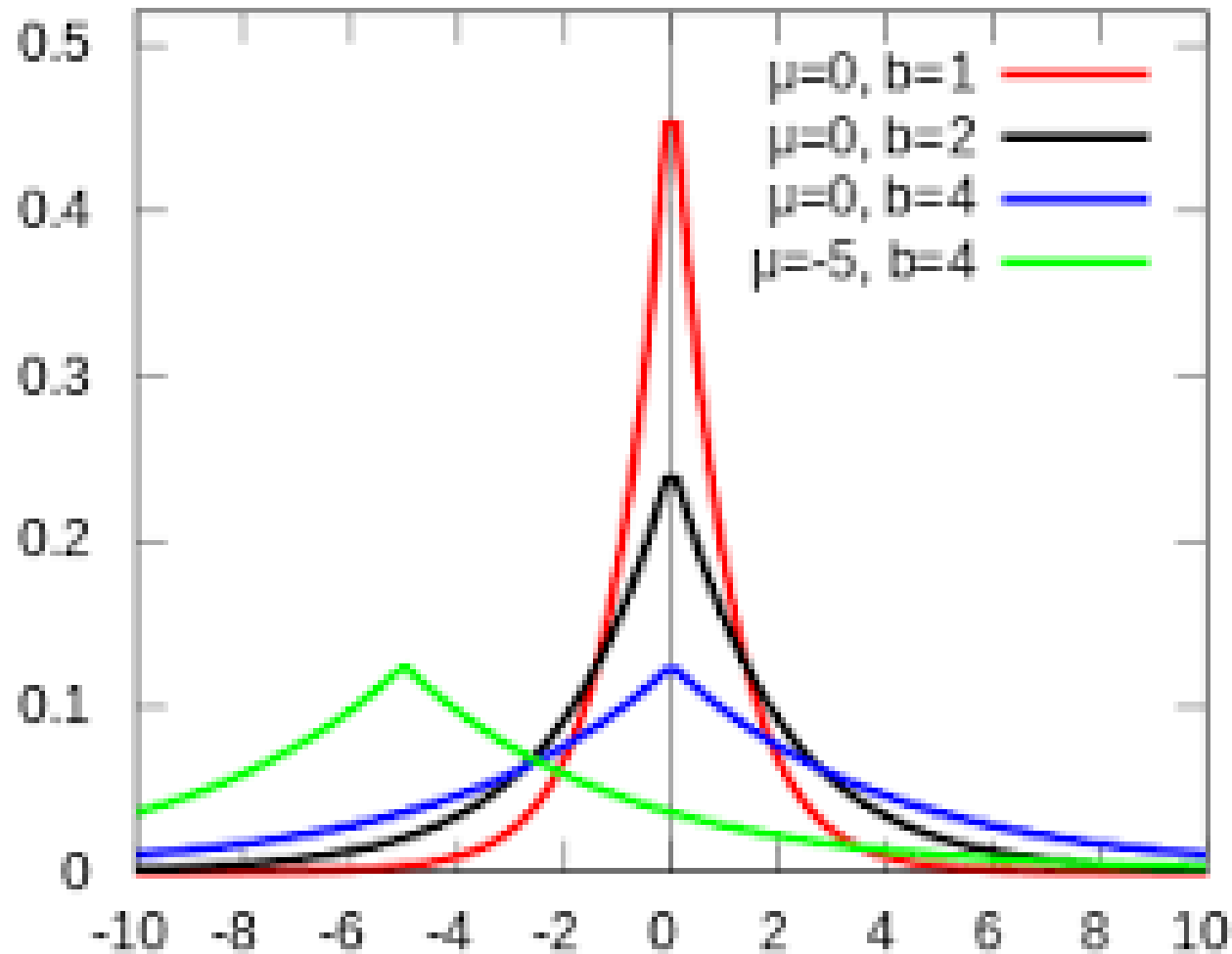


Table 1 Results of stepwise regression for the dispersal kernel model fit to United States data using habitat invasibility (HI), propagule pressure (PP) and pest life history (LH) factors

| Term | Type | Description | Entry order | Estimate (β_p) | MET score (km) | R_{MSE}^2 | Δ MET score (km) |
|---|------|--|-------------|------------------------|----------------|--------------------|-------------------------|
| Intercept | NA | NA | 1 | 1.1248 | 113.07 | 0.6794 | NA |
| Forested land (km ²)* | HI | Sum of land area covered by forest | 2 | -0.8438 | 68.11 | 0.7231 | -44.96 |
| Human population (km ⁻²)* | PP | Current human population density at each time step | 3 | -0.1378 | 60.44 | 0.7560 | -7.67 |
| Forested land (km ²)† | HI | Sum of land area covered by forest | NA | 0.4106 | 57.69 | 0.7519 | -2.75 |
| Host density (km ³ km ⁻³)* | HI | Host tree volume for that particular pest per grid cell | NA | -0.0205 | 60.04 | 0.7558 | -0.40 |
| Host density (km ³ km ⁻³)† | HI | Host tree volume for that particular pest per grid cell | NA | 0.0031 | 60.41 | 0.7517 | -0.03 |
| Host species count* | HI | Number of tree species that are hosts of any pest present in grid cell | NA | -0.0384 | 60.04 | 0.7442 | -0.40 |
| Host species count† | HI | Number of tree species that are hosts of any pest present in grid cell | NA | 0.1186 | 60.28 | 0.7524 | -0.16 |
| Tree density (m ³ km ⁻²)* | HI | Total tree volume by grid cell | NA | 0.3067 | 59.67 | 0.7485 | -0.77 |
| Tree density (m ³ km ⁻²)† | HI | Total tree volume by grid cell | NA | 0.1060 | 60.26 | 0.7488 | -0.18 |
| Body size (mm) | LH | Pest body length (separate intercept fit for fungi) | NA | 0.0011; 0.1464 | 60.24 | 0.7572 | -0.20 |
| Continent of origin | LH | Eurasian vs. Non-Eurasian | NA | 0 | 60.44 | 0.7560 | 0 |
| Feeding guild | LH | Pathogens vs. Arthropods | NA | 0.0163 | 60.25 | 0.7489 | -0.19 |
| Number of hosts | LH | Number of host species possessed by pest | NA | -0.0012 | 60.41 | 0.7557 | -0.03 |
| Human population (km ²)† | PP | Current human population density at each time step | NA | 0.0217 | 60.32 | 0.7527 | -0.12 |
| Income (USD)* | PP | Per capita income in 1999 | NA | 0 | 60.44 | 0.7560 | 0 |
| Income (USD)† | PP | Per capita income in 1999 | NA | 0 | 60.44 | 0.7560 | 0 |
| Road length (km)* | PP | Total length of all major roads in grid cell | NA | -0.0148 | 60.17 | 0.7463 | -0.27 |
| Road length (km)† | PP | Total length of all major roads in grid cell | NA | 0.4935 | 58.64 | 0.7587 | -1.8 |

*Parameters influencing the probability of dispersal into a cell (Z_i).

†Parameters influencing the probability of dispersal out of a cell (Z_{ij}).

Negative estimates indicate positive influences on dispersal and vice versa. Since all variables were standardised, the relative influence of each fitted parameter on dispersal can be determined by its magnitude (magnitude of 'Estimate' in the table). Conversely, the relative importance of each parameter on minimum energy test (MET) is determined by its entry order in our generalised dispersal kernel model (See Fig. S3). Our best model had $\delta = 2.4321$ and $\Phi = 0.0006227$ with a jackknifed MET score of 60.44 km per species and a jackknifed R_{MSE}^2 of 0.7579. Terms with entry order 'NA' did not meet our variable importance threshold for inclusion, and their associated data is for their proposed inclusion as a fourth term in our model.

© Rectangular Spin
(a) Real Data

Constant

GDK



Figure 4 A selection of model predictions for individual species (a. *Coleophora laricella*, b. *Leucoma salicis*, c. *Nuculaspis tsugae*), showing the true presence data (left column), constant dispersal model predictions (centre column) and generalised dispersal kernel predictions (right column) as green areas. These distributions are only a small selection and do not show the full variation in model predictions across species, which are included in Fig. S2.

© Rectangular Spin
(a) Real Data

Constant

GDK



A common constant dispersal kernel model, simulated from the discovery date, explained 68% of the variation in range size across all pests, and had 68% locational accuracy between predicted and observed locational distributions

By making dispersal a function of forest area and human population density, variation explained increased to 76%, with 74% accuracy.

A single general dispersal kernel model was sufficient to predict the majority of variation in extent and locational distribution across pest species and proxies of propagule pressure and habitat invasibility – well studied predictors of establishment – should also be applied to the dispersal stage.

This model provides a key element to forecast novel invaders and to extend pathway-level risk analyses to include spread.

Our deliverables for HOMED

- D2.1 Reports on key drivers of invasiveness and emergence of forest PnPs (M18)
- D2.2 Framework for economic assessment of the impact of invasive or emerging forest PnPs (M24)
- D2.3 Semi-mechanistic models for forest PnPs risk assessment and management (M30)
- D2.4 Database with parameters for semi-mechanistic models for forest PnPs risk assessment and management to use in multi-criteria decision analysis tool for forest PnPs management options (M36)

Thanks!

