

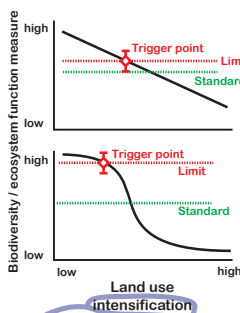
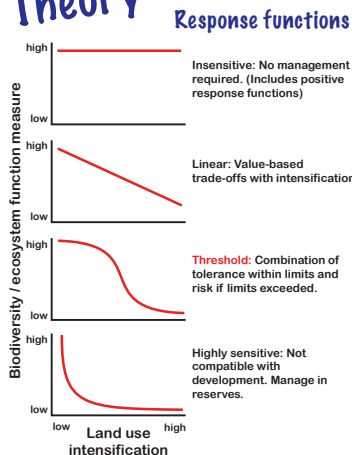
# Next generation biodiversity assessment across gradients of land-use intensification

Ian A. Dickie<sup>1,2</sup>, Robert J. Holdaway<sup>1</sup>, Jamie R. Wood<sup>1</sup>, Kate H. Orwin<sup>1</sup>, Catriona MacLeod<sup>1</sup>  
<sup>1</sup>Landcare Research, <sup>2</sup>Bio-Protection Research Centre



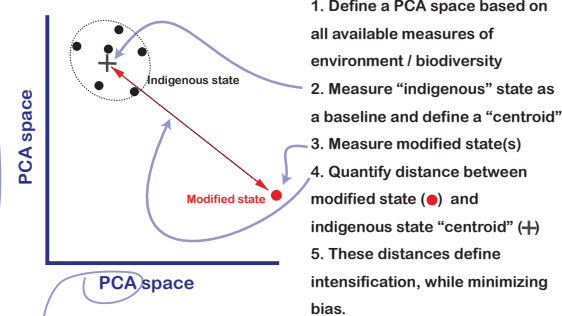
## Goal: Define environmental limits, thresholds, and trigger points for biodiversity across gradients of land-use intensification

### Theory



For linear and threshold responses set **trigger points** to achieve standards that incorporate **uncertainty and risk**

### An objective measure of intensification: intensification = distance from indigenous



### but how do you define "intensification"?

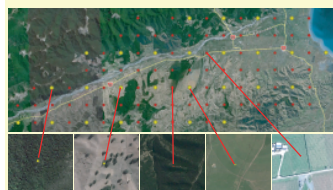
Need a metric that:

- applies equally well to all major land-uses
- minimizes bias in choice of measurements

PCA stands for "Principle component analysis" -- we use it as way to remove correlations among variables reducing bias based on what is measured.

### Methods

#### Land-use gradient



Wairau Valley with 30 plots spanning all major land-uses:

- Indigenous forest
- Pine plantation
- Low producing grasslands
- High producing grasslands (e.g., dairy)
- Vineyards

#### Field measurements

Build on traditional, 20 x 20 m plots

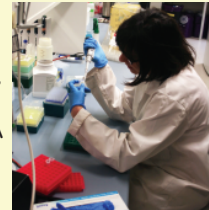
- All plant species
- 10 min bird counts
- Extensive (24 locations within plot) sampling of soil for DNA and ecosystem function measurement



#### Next-generation DNA methods for Biodiversity

Using a pooled soil sample, divide into sequential extractions:

- All fungi and microbes from soil DNA extracts
- Root DNA to measure plant community
- Live and dead extractions of mites, nematodes, and other invertebrates
- Low-copy DNA extraction techniques to detect birds and other animals from environmental DNA
- Multiple extracts then combined



#### Ecosystem function

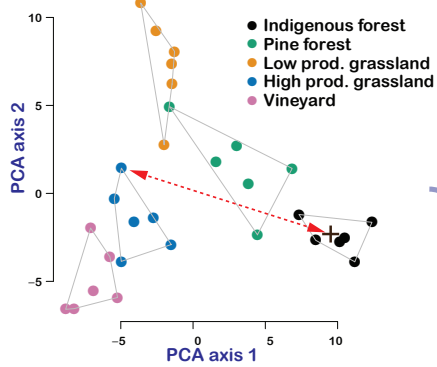
Using soil samples measure various aspects of function:

- Soil nutrients and availability
- Microbial resistance / resilience
- Microbial composition using fatty acid marker profiling
- Decomposition rates of standard substrates



- Using suite of PCR primers detect all bacteria, archaea, plants and animals from DNA extracts.
- **Current status:** we have DNA extracted and primers working
- Next step is next-generation sequencing on 454 platform
- Flexible to adapt to emerging technology

### Results so far

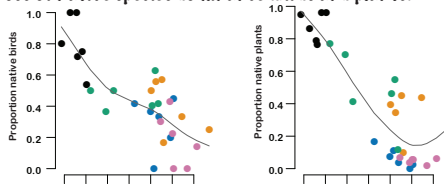


Combine all variables to develop metric of intensification (including all axes)

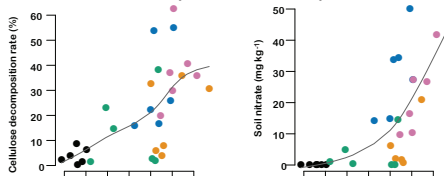
#### Acknowledgements

We thank the land-owners who permitted us to access and sample on their farms, forests, and vineyards, the Marlborough District Council, and the many staff of Landcare Research who contributed to this work, particularly Chris Morse, Karen Boot, Nicola Bolstridge, Kev Drew, Geoff Walls, Sarah Kruijs, Ella Hayman, Matt McGlone, Peter Bellingham, and Gwen Grellet. This work is funded by a Smart Ideas grant from the Ministry of Business, Innovation and Employment (C09X1205).

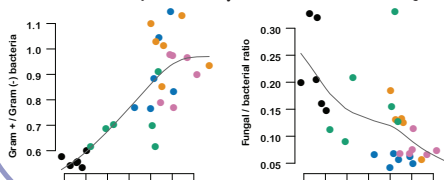
#### Loss of native species dominance (birds and plants)



#### Changes in ecosystem processes (decomposition, nitrate)

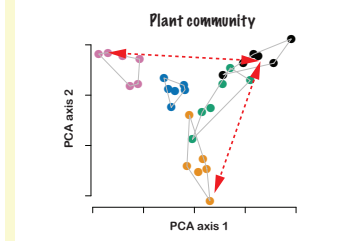
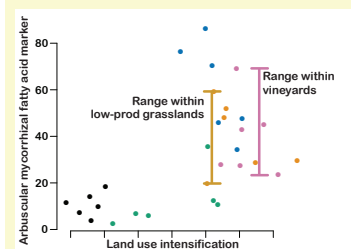


#### Shifts in soil ecosystem composition (bacteria, fungi)



Land use intensification

Even within a given land use, we observe large variation in response metrics, suggesting opportunities to enhance ecosystem function and biodiversity within land use



It is also curious that low-producing grasslands can be considered equally "intense" as vineyards or dairy. This is largely driven by a strong, orthogonal PCA separation of plant communities and our value-free inclusion of all aspects of change, not just "negative" aspects

Stay tuned for DNA results in early 2014