## Using *ipmr* output

### ipmr further analyses

### Other options

```
# For stochastic IPMs
mean_kernel()

# Extract for calculation
# manual or other packages
my_ipm$sub_kernels

my_ipm$pop_state
```

### General IPMs

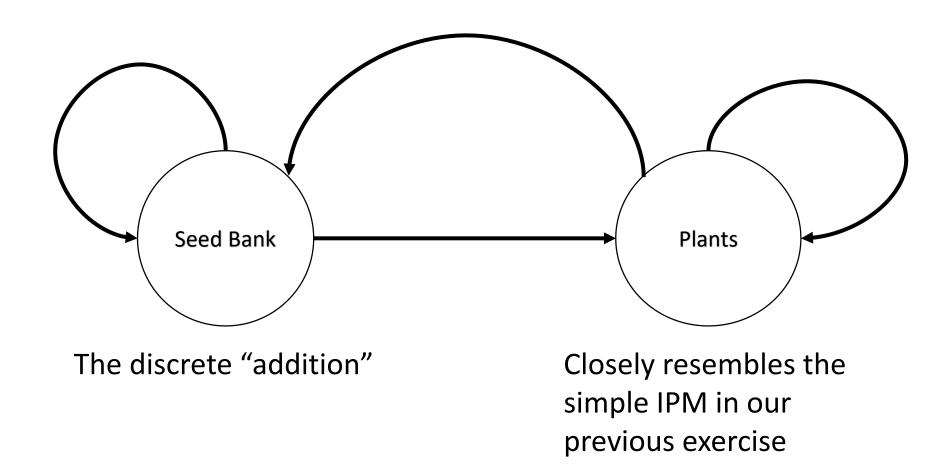
### What are general IPMs

Incorporate ≥ 2 continuous state variables and/or

include transitions between continuous and discrete states

- Height (C) and diameter at breast height (C) of trees
- Developmental stage(s) (D) and body size (C) of animals

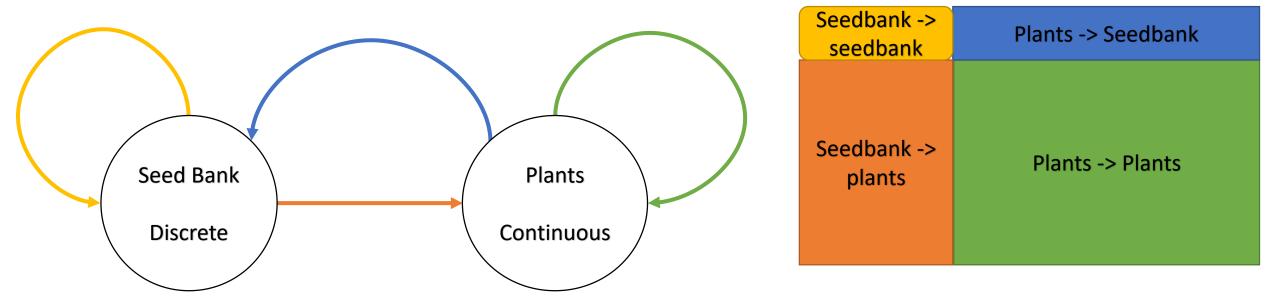
### Example: discrete + continuous state variable



### Example: discrete + continuous state variable

• 
$$n(x', T+1) = p_{germ} * size_{at germ} * B(T) + \int_{L}^{U} [P(x', x)] n(x, T) dx$$

• 
$$B(T+1) = (1 - p_{germ}) * B(T) + \int_{L}^{U} [F] n(x,T) dx$$



# Changes & additions for general IPMs with *ipmr*

```
my_ipm <- define_kernel(</pre>
                               = "CC",
                        family
                     states = list(c('dbh')),
my_ipm <- define_kernel(</pre>
                                  = "CD", # or "CC", "DD", "DC"
                        family
                                   = list(c('dbh', 'seedlings')),
                        states
```

```
my_ipm <- define_kernel(
  family = "CC",

formula = s * g,
...,
)</pre>
```

```
my_ipm <- define_kernel(
  family = "CC",

formula = s * g * d_dbh,
)</pre>
```

```
my_ipm <- define_impl(</pre>
  proto_ipm = my_ipm,
  kernel_impl_list = list( ...,
    F = list(..., state_start = "dbh", state_end = "dbh")
my_ipm <- define_impl(</pre>
  proto_ipm = my_ipm,
  kernel_impl_list = list(...,
    F = list(..., state_start = "dbh", state_end = "seedling")
```

```
my_ipm <- define_pop_state(my_ipm,
n_dbh = rep(1/200, 200))
```

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