

Stratifying an SIR model by two risk groups using AlgebraicPetri.jl

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Introduction

This example serves as a ‘Hello World’ to stratifying Petri net models, where an SIR model is stratified by another model - in this case, two risk groups, H and L, with high and low contact rates respectively. The stratification is done using two manually specified models. At the end, we use Catlab’s imperative interface to construct the risk group model programmatically; while this is more useful for models with many groups, it serves as a good test case.

Libraries

```
using AlgebraicPetri, AlgebraicPetri.TypedPetri
using Catlab, Catlab.CategoricalAlgebra, Catlab.Programs
using Catlab.WiringDiagrams, Catlab.Graphics
using AlgebraicDynamics.UWDDynam
using OrdinaryDiffEq
using LabelledArrays
using Plots
```

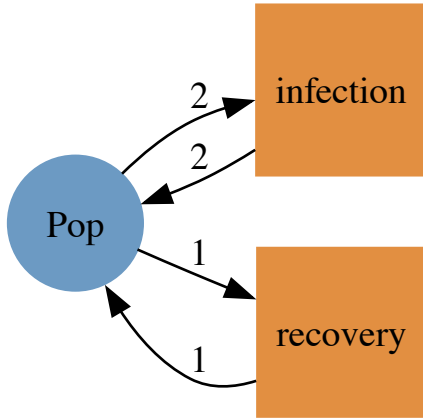
Transitions

We first define a labelled Petri net that has the different types of transition in our models. The first argument is an array of state names as symbols (here, a generic :Pop), followed by the transitions in the model. Transitions are given as `transition_name=>((input_states)=>(output_states))`. In this model, we consider the groups as fixed (i.e. no changes between strata), so we just need to have infection and recovery in the model.

```

epi_transitions = LabelledPetriNet(
    [:Pop],
    :infection=>((:Pop, :Pop)=>(:Pop, :Pop)),
    :recovery=>(:Pop=>:Pop)
)
to_graphviz(epi_transitions)

```

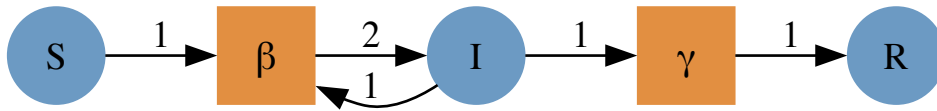


We create a labelled Petri net of the SIR model using the above transitions (or alternatively, we could compose from infection and recovery submodels).

```

sir_uwd = @relation () where (S::Pop, I::Pop, R::Pop) begin
    infection(S, I, I, I)
    recovery(I, R)
end
sir_acst = oapply_typed(epi_transitions, sir_uwd, [: , :])
sir_lpn = dom(sir_acst)
to_graphviz(sir_lpn)

```



We then define a second model with two groups with different contact rates. This also has infection and recovery terms defined in terms of within- and between-group interactions.

```

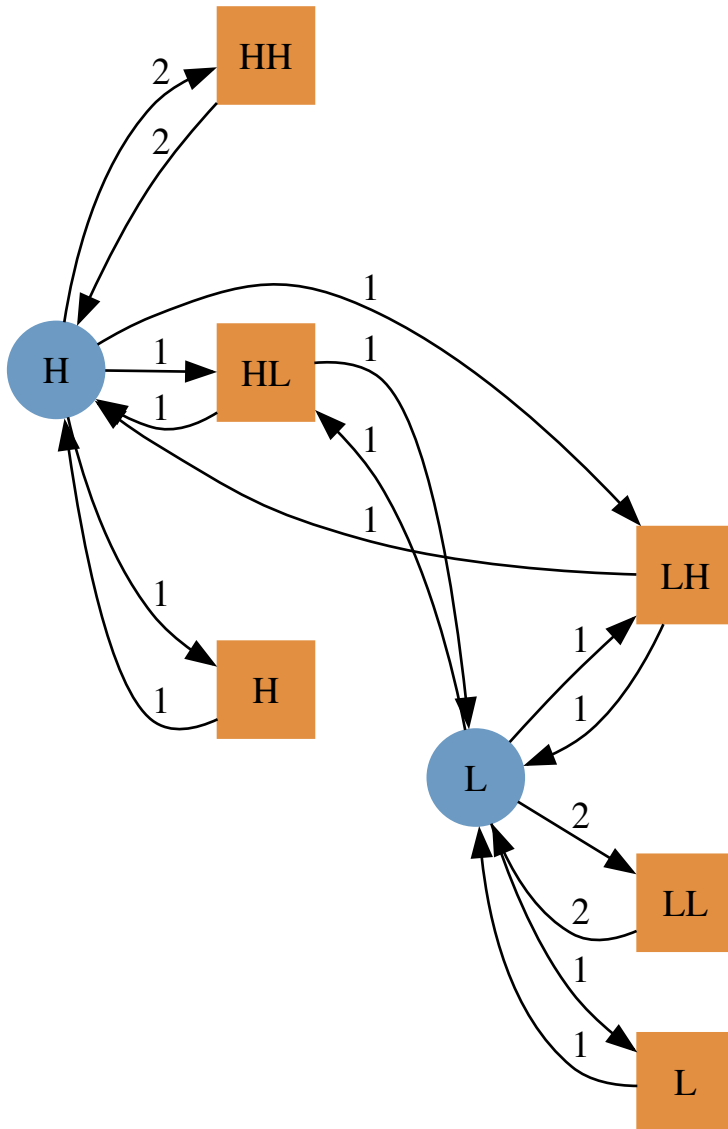
risk_uwd = @relation () where (H::Pop, L::Pop) begin
    infection(H,H,H,H) # Within H infection
    infection(H,L,H,L) # Infection of S_H by I_L
    infection(L,H,L,H) # Infection of S_L by I_H

```

```

infection(L,L,L,L) # Within L infection
recovery(H,H) # H recovery
recovery(L,L) # L recovery
end
risk_acst = oapply_typed(epi_transitions, risk_uwd, [:HH, :HL, :LH, :LL, :H, :L])
risk_lpn = dom(risk_acst)
to_graphviz(risk_lpn)

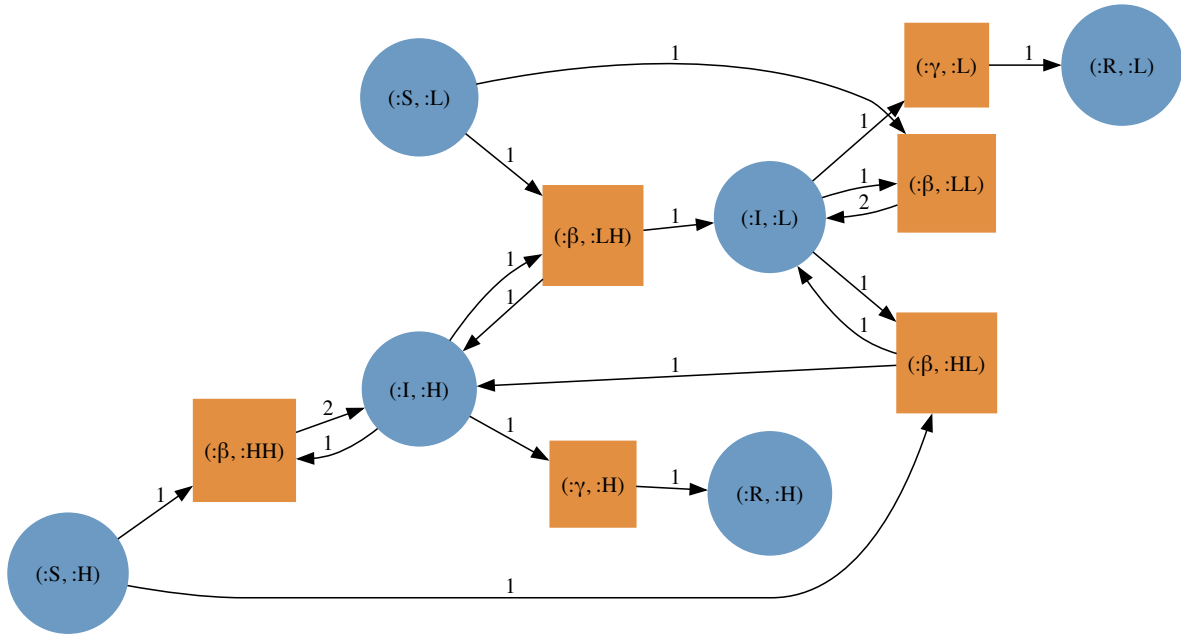
```



We create a stratified model by using a typed product between the SIR model and the risk model, to generate an `ACSetTransformation`, from which we subsequently extract a labelled

Petri net.

```
sir_risk_acst = typed_product(sir_acst, risk_acst)
sir_risk_lpn = dom(sir_risk_acst)
to_graphviz(sir_risk_lpn)
```



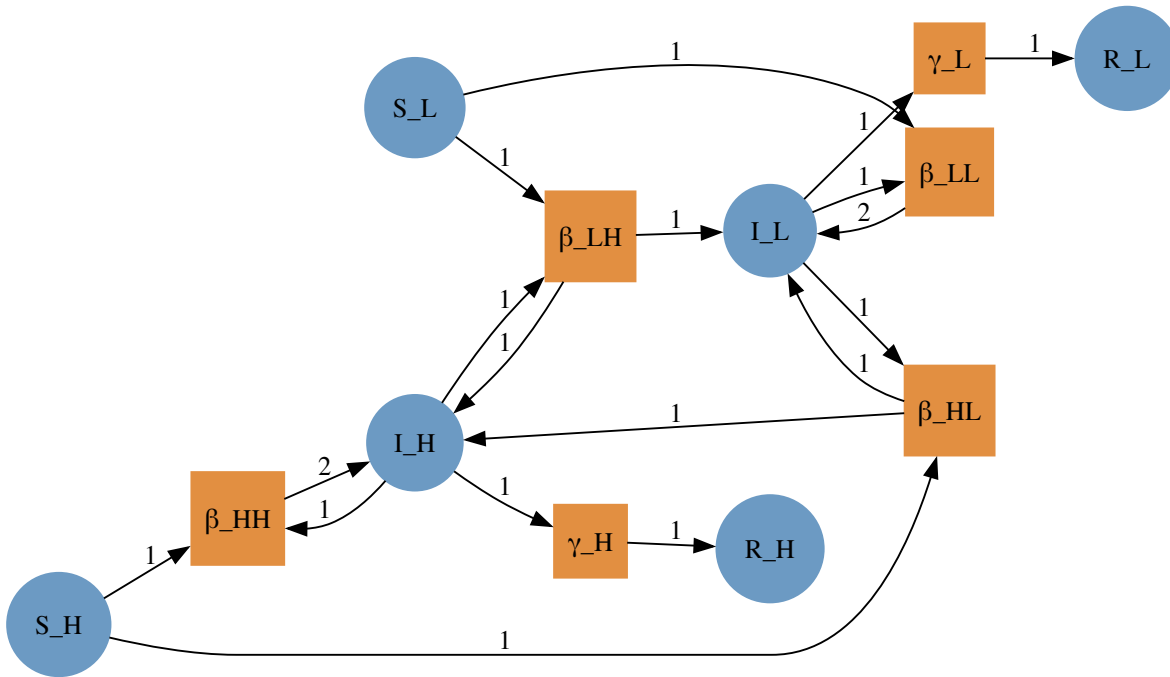
The state names of the resulting stratified model are tuples of symbols:

```
snames(sir_risk_lpn)
```

```
6-element Vector{Tuple{Symbol, Symbol}}:
 (:S, :H)
 (:I, :H)
 (:R, :H)
 (:S, :L)
 (:I, :L)
 (:R, :L)
```

The solvers in `OrdinaryDiffEq.jl` do not work with these state names, so we use `flatten_labels` to obtain a vector of symbols (of the form `:S_H`, `:I_H`, etc.).

```
sir_risk_lpn_flatlabels = flatten_labels(sir_risk_lpn)
to_graphviz(sir_risk_lpn_flatlabels)
```



Running the model

To run the model, we need to choose specific group sizes and parameter values. We define two groups of equal size and initial composition.

```
K = 2
S = [495.0, 495.0]
I = [5.0, 5.0]
R = [0.0, 0.0]
N = [S[i]+I[i]+R[i] for i in 1:K]
```

```
2-element Vector{Float64}:
 500.0
 500.0
```

The model above is defined in terms of transmission rates between the two groups, which is a combination of (a) the contact rates between the two groups and (b) the probability of

transmission per infectious contact. We assume that the two groups have different overall contact rates, c , and that the fraction of contacts between groups i and j , π_{ij} , follows a proportional mixing assumption.

```

= 0.05
c = [20.0, 5.0]
pij = hcat([c[j]*N[j]/sum([c[k]*N[k] for k in 1:K]) for j in 1:K] for i in 1:K...)
betas = ( .* (c .* pij) ./ N)
= 0.25;

```

We now define the initial conditions and parameter arrays as labelled arrays.

```

u0 = @LArray vec([S I R]')[1] Tuple(snames(sir_risk_lpn_flatlabels))
p = @LArray [vec(betas); ; ] Tuple(tnames(sir_risk_lpn_flatlabels))
tspan = (0.0, 40.0);

```

We then compute the vector field from the labelled Petri net (with flatten labels), define the ODEProblem, and solve.

```

sir_risk_vf = vectorfield(sir_risk_lpn_flatlabels)
sir_risk_prob = ODEProblem(sir_risk_vf, u0, tspan, p)
sir_risk_sol = solve(sir_risk_prob, Rosenbrock32());

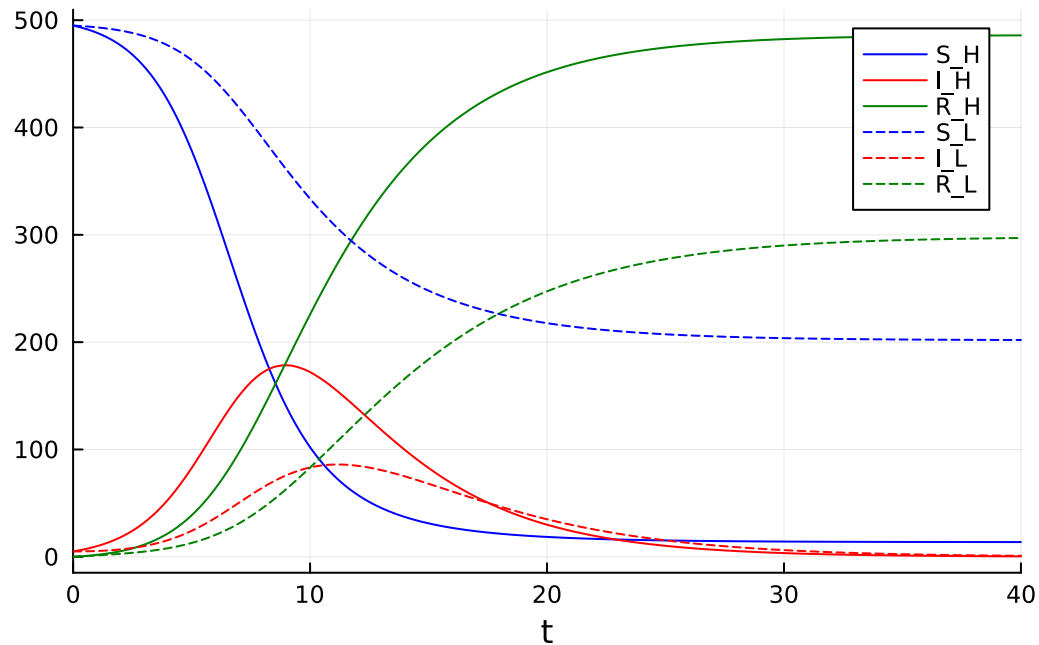
```

Plotting

```

plot(sir_risk_sol, linecolor=[:blue :red :green], linestyle=[:solid :solid :solid :dash :dash]

```



Automating the generation of risk groups

We can also build the risk model using Catlab's imperative interface.

```
function make_risk_groups()
    # Start with a blank UWD with 2 populations
    uwd = RelationDiagram(repeat([:Pop], 2))
    # Specify the names of the groups
    names = ["H", "L"]
    # Build junctions (just a `Dict`), with the side effect of updating the UWD
    # `junctions` will be as follows
    # Dict{Symbol, Int64} with 2 entries:
    #   :H => 1
    #   :L => 2
    junctions = Dict{Symbol, Int64}()
    for (i, name) in enumerate(names)
        variable = Symbol(name)
        junction = add_junction!(uwd, :Pop, variable=variable)
        set_junction!(uwd, port, junction, outer=true)
        junctions[variable] = junction
    end
    # This generates all combinations of the keys
```

```

# Here, this will be:
# 2x2 Matrix{Tuple{Symbol, Symbol}}:
# (:H, :H) (:H, :L)
# (:L, :H) (:L, :L)
pairs = collect(Iterators.product(keys(junctions), keys(junctions)))
# This creates an empty vector to store the transition names in
tnames = Vector{Symbol}()
## Cycle through pairs and add boxes for infection
for pair in pairs
    # We need 4 entries in the tuple as :infection is defined as infection(S, I, I, I)
    # So for the first pair, ins_outs = (:H, :H, :H, :H)
    ins_outs = (pair[1], pair[2], pair[1], pair[2])
    # In the below, [junction_type(uwd, junctions[p]) for p in ins_outs] is just a vector
    box = add_box!(uwd, [junction_type(uwd, junctions[p]) for p in ins_outs], name=:infection)
    # The below loops through zip((:H, :H, :H, :H), [1, 2, 3, 4])
    for (rgn, port) in zip(ins_outs, ports(uwd, box))
        set_junction!(uwd, port, junctions[rgn])
    end
    # This adds the names (as `Symbol`s) to the vector of transition names
    push!(tnames, Symbol("${pair[1]}${pair[2]}"))
end
## Generate an ACSet transformation using the above `epi_transitions`
act = oapply_typed(epi_transitions, uwd, tnames)
## Add recovery within groups
act = add_reflexives(act, repeat([[:recovery]], 2), epi_transitions)
return act
end;

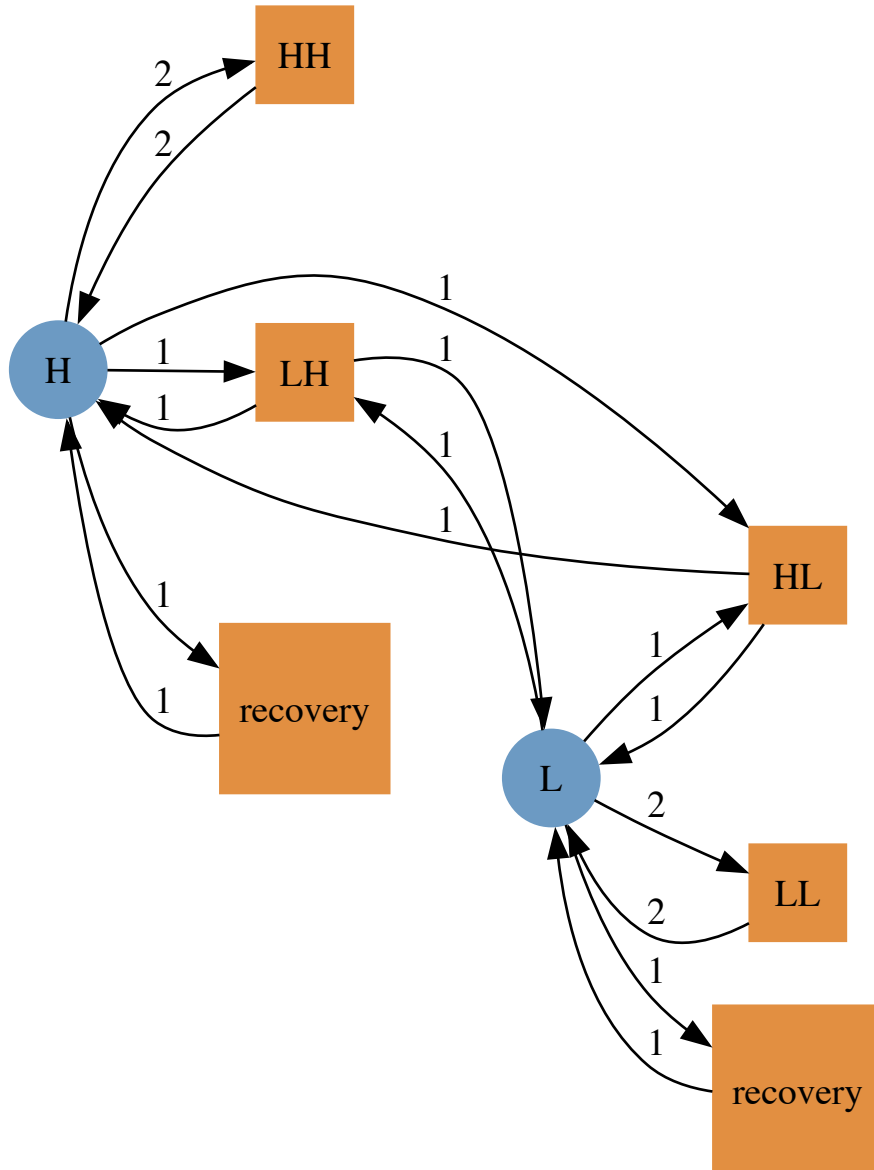
```

We can now generate a LabelledPetriNet as follows.

```

risk_automated_acst = make_risk_groups()
risk_automated_lpn = dom(risk_automated_acst)
to_graphviz(risk_automated_lpn)

```

We stratify the SIR model by the risk model using `typed_product`, as before.

```
sir_risk_automated_acst = typed_product(sir_acst, risk_automated_acst)
sir_risk_automated_lpn = dom(sir_risk_automated_acst)
to_graphviz(sir_risk_automated_lpn)
```

