Modular Probabilistic Models
via Algebraic Effects

Minh Nguyen, Roly Perera, Meng Wang, Nicolas Wu

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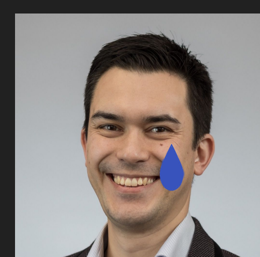

Probabilistic model: a set of relationships between random variables

$$x \longrightarrow \boxed{\text{model}(\theta)} \longrightarrow y$$

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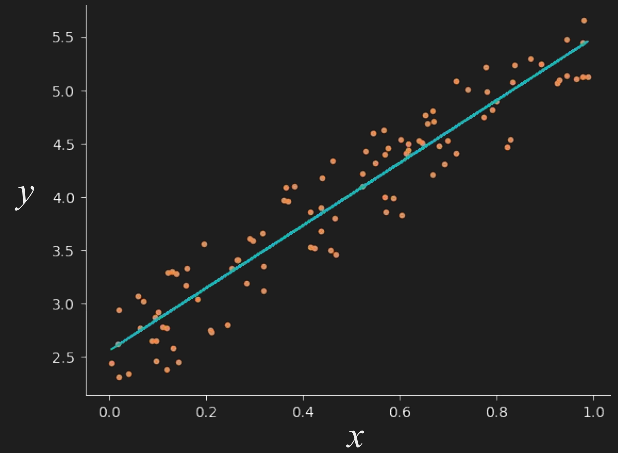
Linear regression

input $\left\{ \lambda x. \right.$

parameters $\left\{ \begin{array}{l} \mu \sim \text{Normal}(0, 3) \\ c \sim \text{Normal}(0, 2) \\ \sigma \sim \text{Uniform}(1, 3) \end{array} \right.$

output $\left\{ \; y \sim \text{Normal}(\mu * x + c, \sigma) \right.$



PPLs: Probabilistic models as programs

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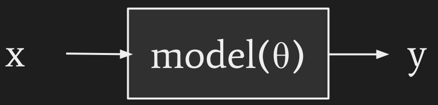

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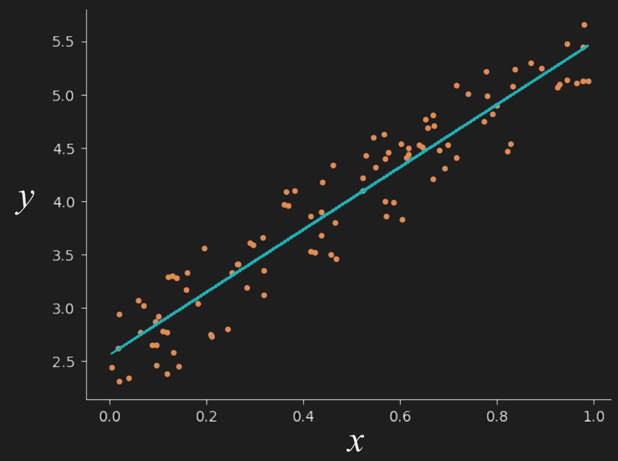

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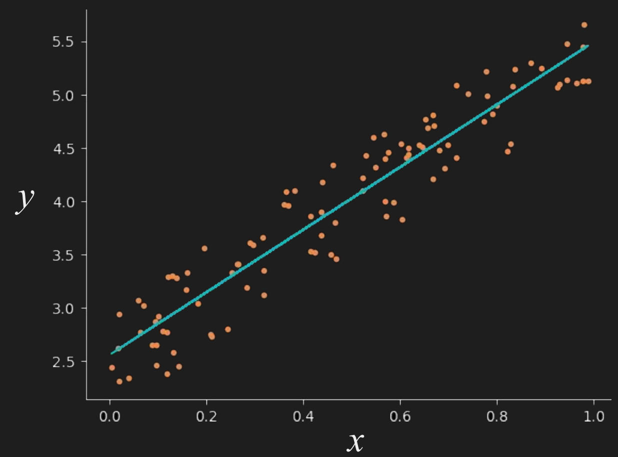

What might linear regression look like as a probabilistic program?

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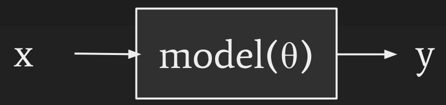

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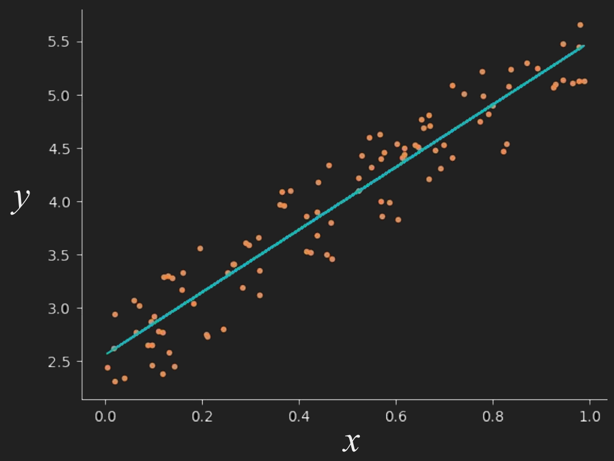

What might linear regression look like as a probabilistic program?

[Monad Bayes**]**

A possible simulation

```
linRegr x μ c σ = do
  y ← sample (normal (μ * x + c) σ)
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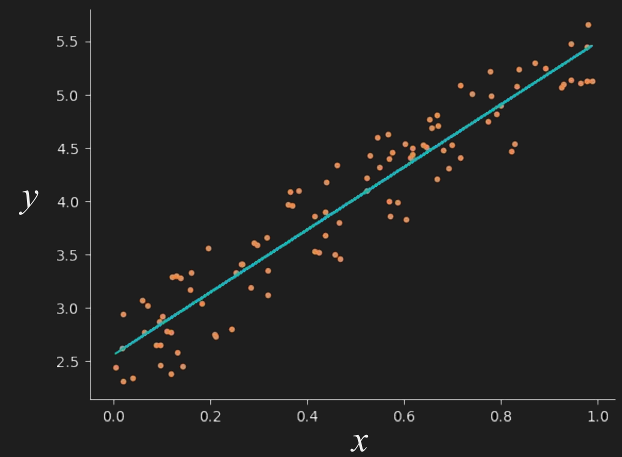

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A possible inference

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linRegr x y = do
  μ  ← sample (normal 0 3)
  c  ← sample (normal 0 2)
  σ  ← sample (uniform 0 3)
  observe (normal (μ * x + c) σ) y
  return (μ, c, σ)
```

PPLs: Probabilistic models as programs

[WebPPL]

A possible simulation

```
var linRegr = function(x, mu, c, σ) {
 y = sample(Normal(mu * x + c, σ), y)
 return y
}
```

A possible inference

```
var linRegr = function(x, y) {
  mu     = sample(Normal(0, 3))
  c      = sample(Normal(0, 2))
  σ      = sample(Uniform(0, 2))
  observe(Normal(mu * x + c, σ), y)
  return (mu, c, σ)
}
```

[Anglican]

A possible simulation

```
(defquery linRegr [x, mu, σ, c]
(let [y (sample(normal (c + (* mu) x)) σ)]
 {:output y}))
```

A possible inference

```
(defquery linRegr [x mu-prior σ-prior c-prior y]
(let [mu    (sample mu-prior)
      c     (sample c-prior)
      σ     (sample σ-prior)
      pred (fn [x] (normal (c + (map (* mu) x)) σ))]
      (observe (predictive x) y)
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How about just one general-purpose model?

Motivation 1: Multimodal models

Multimodal model: a model whose random variables can be specialised to `sample` or `observe` modes

ProbFX: a Haskell PPL supporting multimodal models

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Interacting with a ProbFX model

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do -- | Simulation
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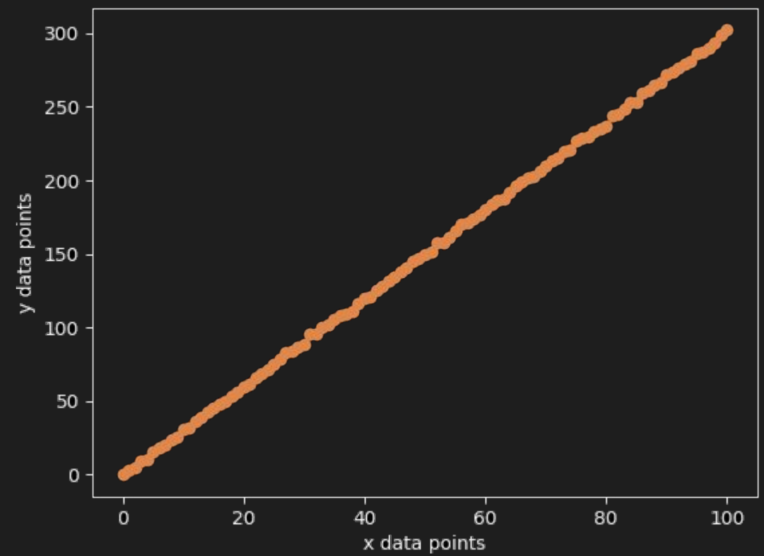

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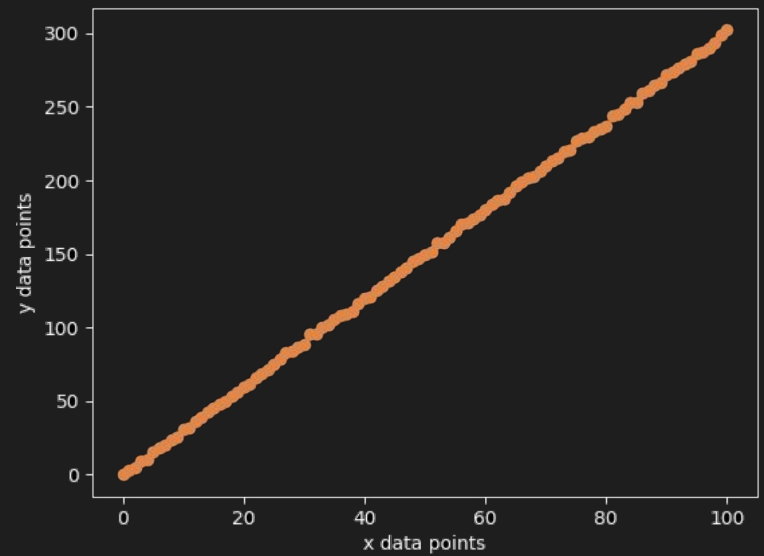

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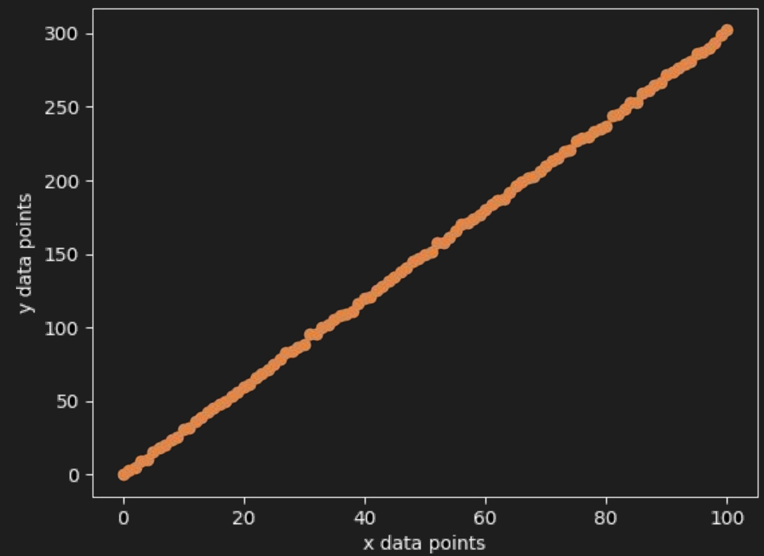

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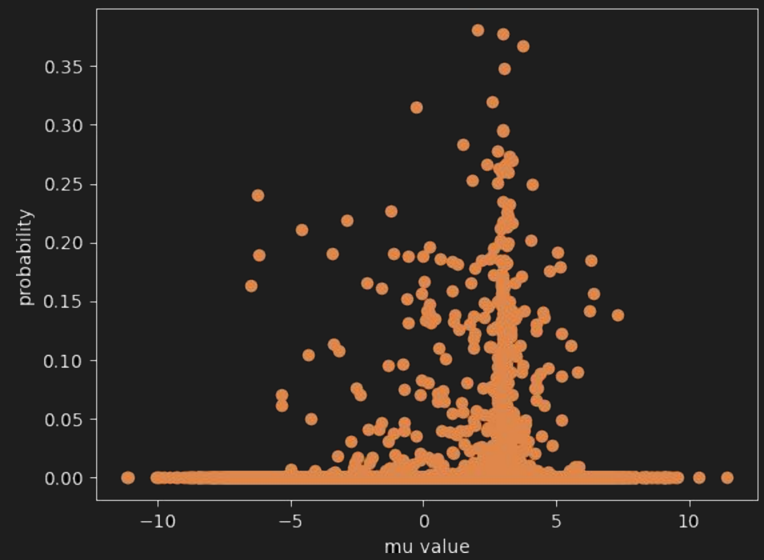

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   (env_outs, weights) ← lw 1000 (linRegr xs) env_in
   let μs = map (get #μ) env_outs
   return (μs, weights)
```

We **observe** μ, c, σ
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Motivation 2: Compositional models

Support for multimodal models already exists…

Supported model features	ProbFX	Gen	Turing	Stan	Pyro
Multimodal	●	●	●	●	●
Modular	●	●	●	○	●
Higher-order	●	◐	○	○	◐
Type-safe	●	○	○	●	○

● Full support
◐ Partial support
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But models are generally not first-class citizens

[Turing]

```
@model function linRegr(x, mu, c, σ, y)
  y ~ Normal(mu * x + c, σ)
end
```

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Type-safe	●	○	○	●	○

● Full support
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But models are generally not first-class citizens or are not statically typed

[Turing]

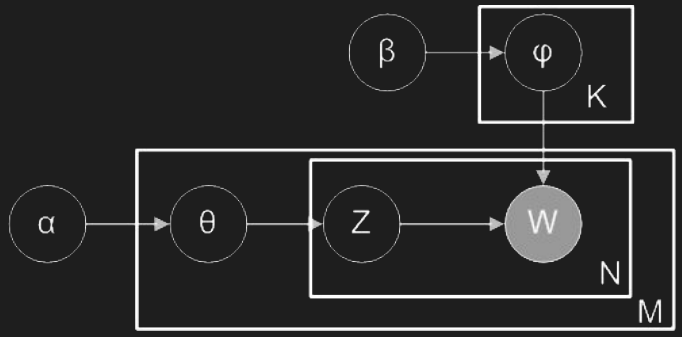
```
@model function linRegr(x, mu, c, σ, y)
  y ~ Normal(mu * x + c, σ)
end
```

[Pyro]

```
def linRegr(x, mu, c, σ):
  pyro.sample("y", dist.Normal(mu * x + c, σ))
  return y

pyro.condition(linRegr, {"hotdog" = True}) ??
```

What about compositional, higher-order models?



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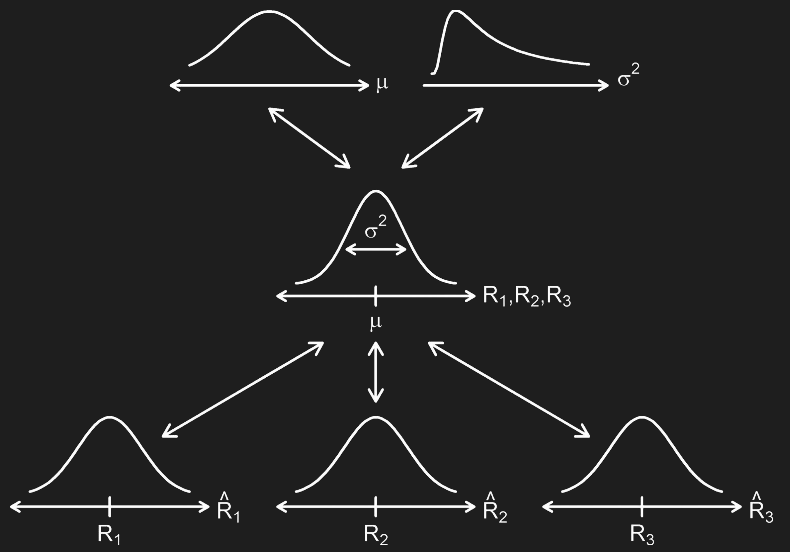
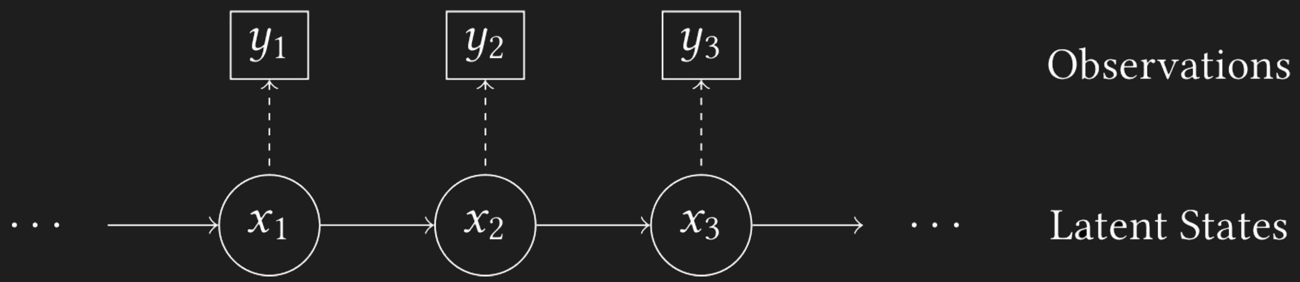


Motivation 2: Compositional models

Hidden Markov Model (HMM)



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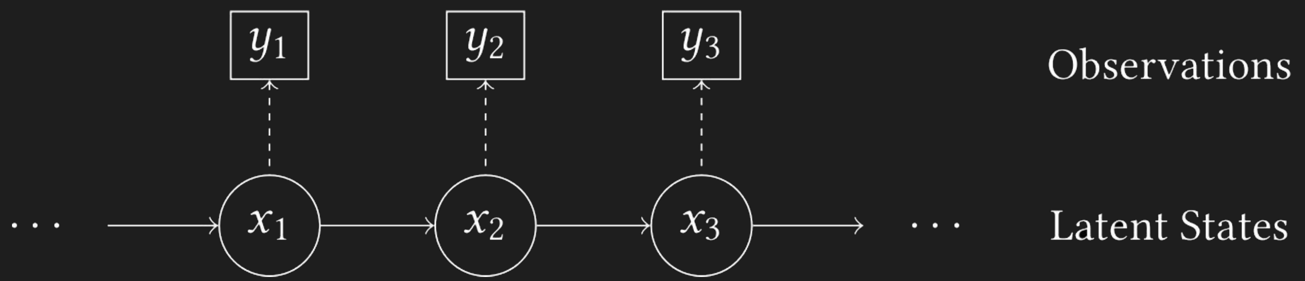

We can decompose this into two sub-models:

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type TransModel env x   = x -> Model env x
type ObsModel   env x y = x -> Model env y
```

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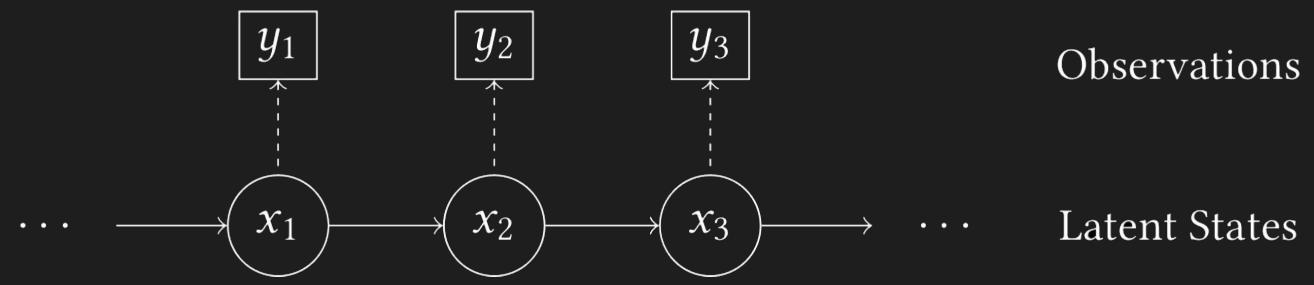

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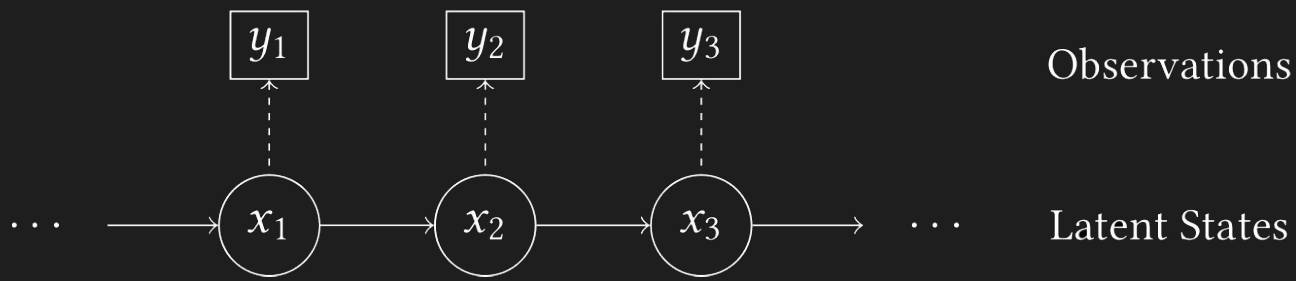

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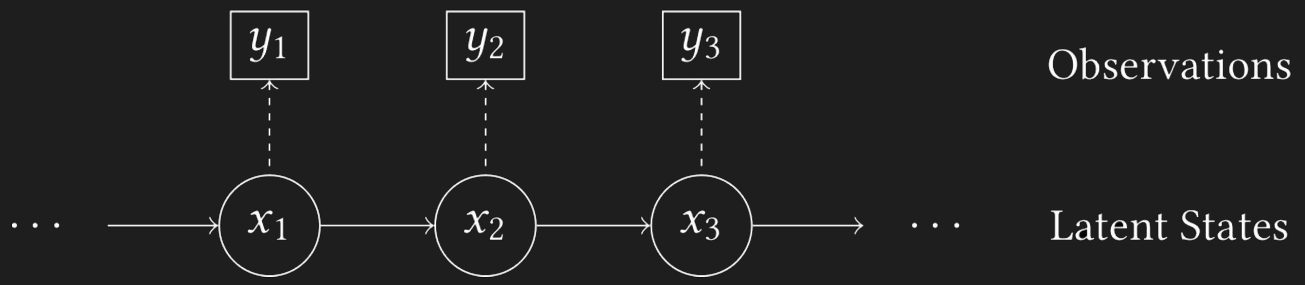

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  let hmmNode x = do x' <- transModel x
                     y' <- obsModel x'
                     return x'
  foldl (>=>) return (replicate n hmmNode) x0
```

```
(>=>) :: (a -> Model env b)
      -> (b -> Model env c)
      -> (a -> Model env c)
```

Modelling an Epidemic: the SIR model

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Setting: We assume a fixed total population of **S**usceptible, **I**nfected, and **R**ecovered individuals.

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The SIR model: During an epidemic, how do these populations vary over time (days)?

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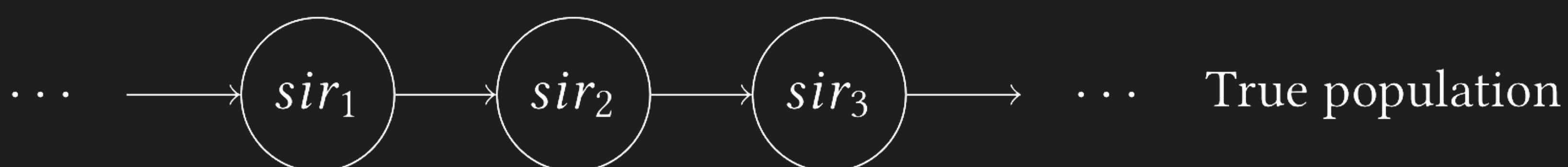
```
data Population  = Population { s :: Int,
                                i :: Int,
                                r :: Int }
```

The SIR model: During an epidemic, how do these populations vary over time (days)?



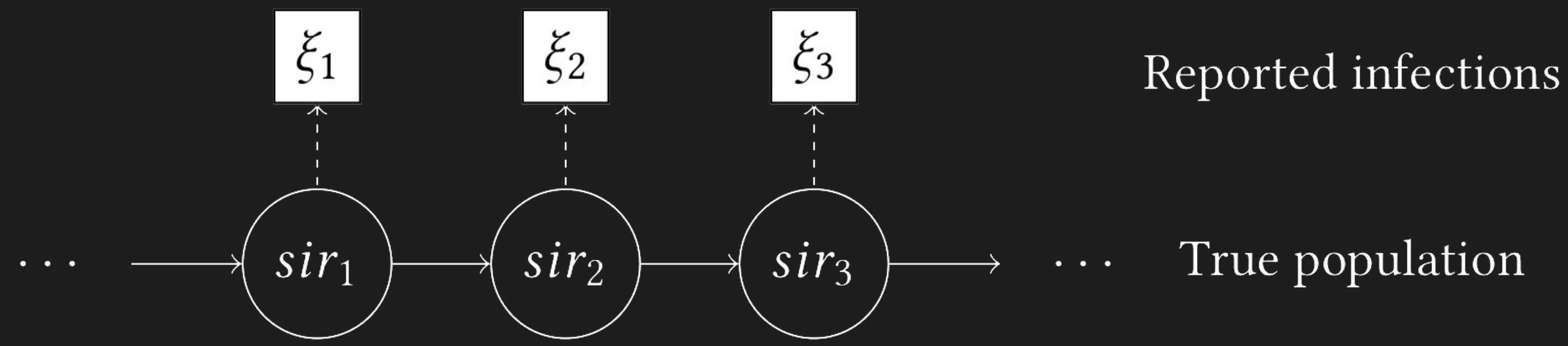
Modelling an Epidemic: the SIR model

Setting: We assume a fixed total population of **S**usceptible, **I**nfected, and **R**ecovered individuals.


```
type ReportedInf = Int

data Population  = Population { s :: Int,
                                i :: Int,
                                r :: Int }
```

The SIR model: During an epidemic, how do these populations vary over time (days)?



Modelling an Epidemic: the SIR model

SIR observation model


```
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data Population  = Population { s :: Int,
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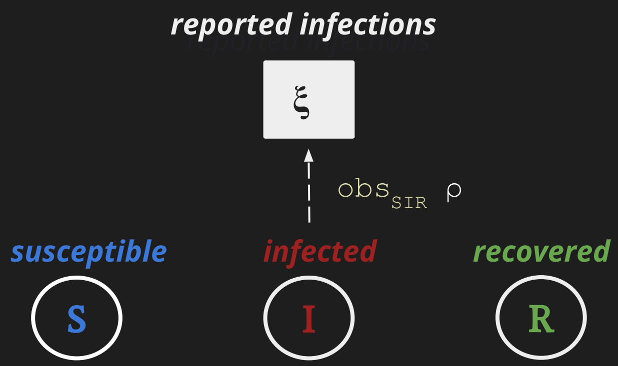
```
type ObsModel env x y = x -> Model env y
```

Modelling an Epidemic: the SIR model

SIR observation model

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type ReportedInf = Int
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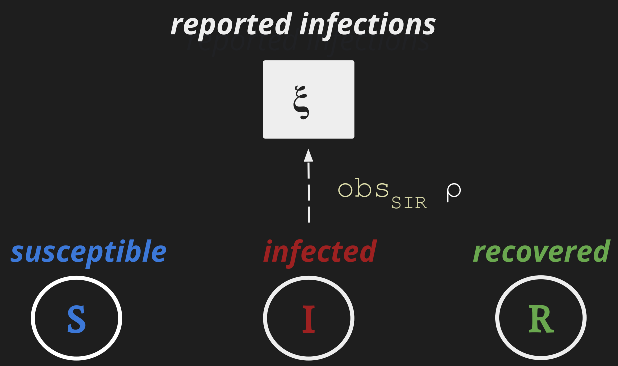
```
data Population  = Population { s :: Int,
                                i :: Int,
                                r :: Int }
```

```
type ObsModel env x y = x -> Model env y
```

```
obsSIR :: Observable env "ξ" Int => Double -> ObsModel env Population ReportedInf
obsSIR ρ (Population _ i _)  = poisson (ρ * i) #ξ
```

Modelling an Epidemic: the SIR model

SIR transition model

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type TransModel env x = x -> Model env x
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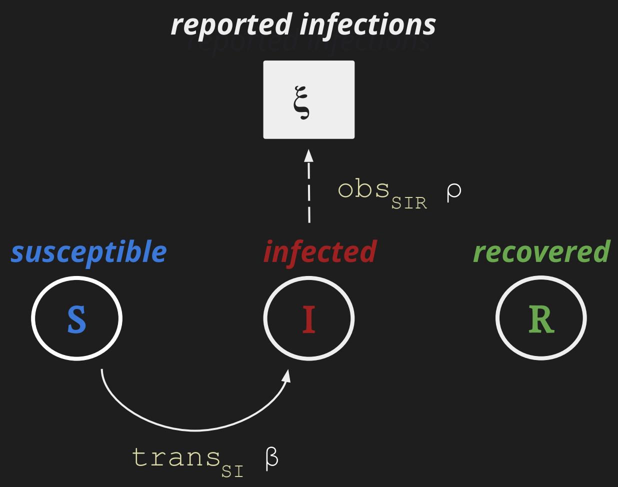
Modelling an Epidemic: the SIR model

SIR transition model

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data Population  = Population { s :: Int,
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                                 r :: Int }
```
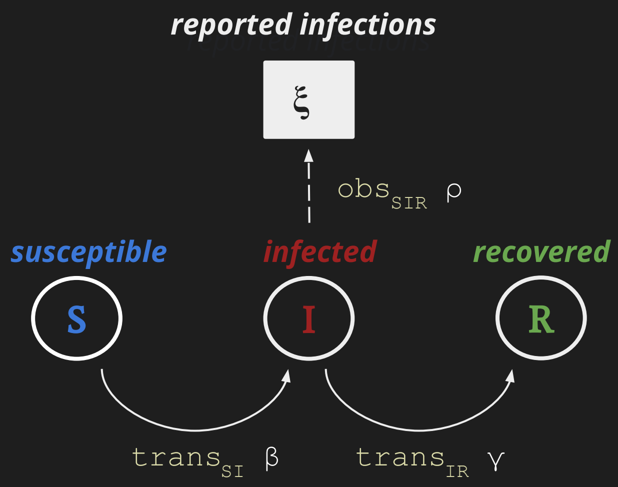

```
type TransModel env x = x -> Model env x
```

```
trans_SI :: Double -> TransModel env Population
trans_SI β (Population s i r) = do
  δ_SI ← binomial' s (1.0 - exp (-β * i / s + i + r))
  return $ Population (s - δ_SI) (i + δ_SI) r
```

Modelling an Epidemic: the SIR model

SIR transition model

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transIR :: Double -> TransModel env Population
transIR γ (Population s i r) = do
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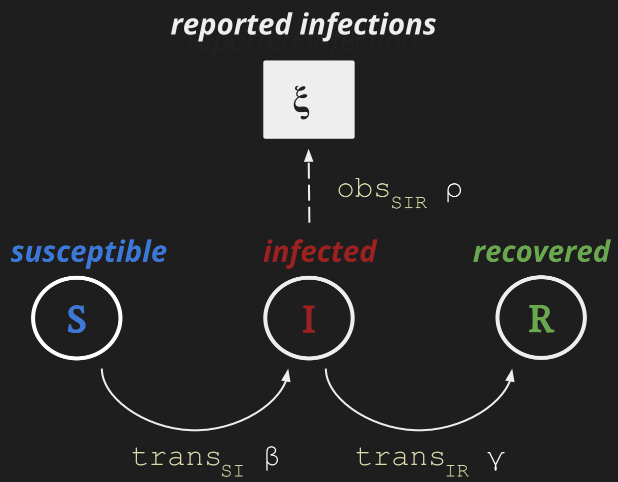
  return $ Population s (i - δIR) (r + δIR)
```

Modelling an Epidemic: the SIR model

SIR transition model

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  return $ Population (s - δSI) (i + δSI) r

transIR :: Double -> TransModel env Population
transIR γ (Population s i r) = do
  δIR ← binomial' i (1.0 - exp (-γ))
  return $ Population s (i - δIR) (r + δIR)
```
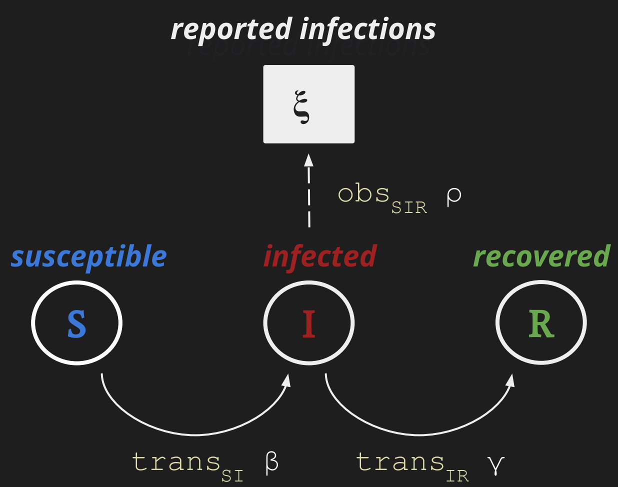

```
transSIR :: Double
         -> Double
         -> TransModel env Population
transSIR β γ = transSI β >=> transIR γ
```

Modelling an Epidemic: the SIR model

SIR as a Hidden Markov Model




```
hmm :: TransModel env x -> ObsModel env x y -> Int -> x -> Model env x
```

```
obsSIR ρ (Population _ i _)
  = poisson (ρ * i) #ξ

transSIR β γ
  = transSI β >=> transIR γ
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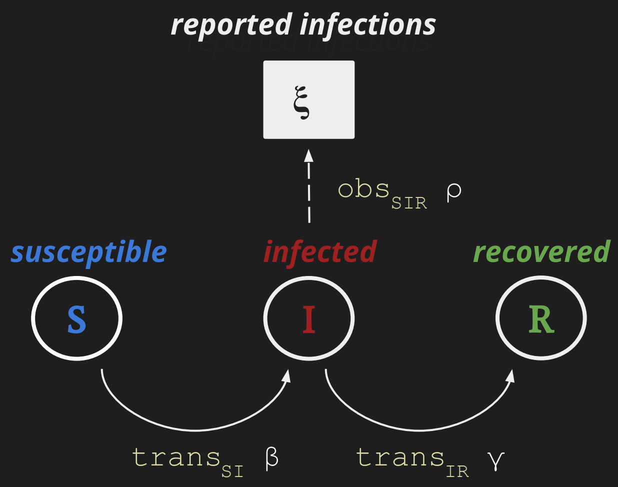
Modelling an Epidemic: the SIR model

SIR as a Hidden Markov Model

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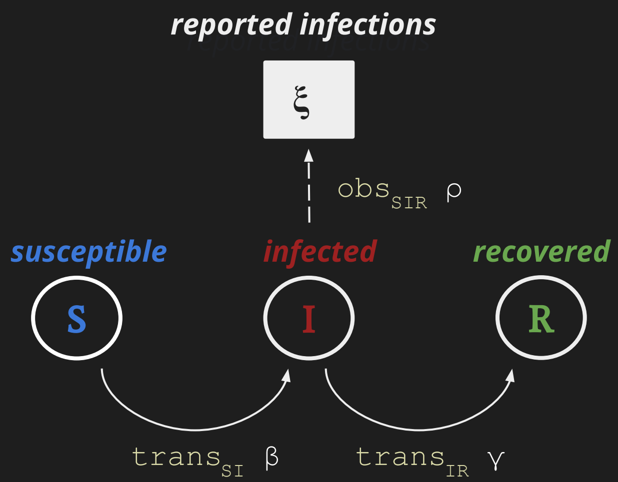
$$\left.\begin{aligned}&\mathtt{obs}_{SIR}\ \rho\ \mathtt{(Population\ \_\ i\ \_)}\\&\quad = \mathtt{poisson}\ (\rho\ *\ \mathtt{i})\ \#\xi\\&\mathtt{trans}_{SIR}\ \beta\ \gamma\\&\quad = \mathtt{trans}_{SI}\ \beta\ \mathtt{>=>}\ \mathtt{trans}_{IR}\ \gamma\end{aligned}\right\}\quad \mathtt{sirModel} = \mathtt{hmm}\ (\mathtt{trans}_{SIR}\ \beta\ \gamma)\ (\mathtt{obs}_{SIR}\ \rho)$$

Modelling an Epidemic: the SIR model

SIR as a Hidden Markov Model

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  = trans_SI β >=> trans_IR γ
```
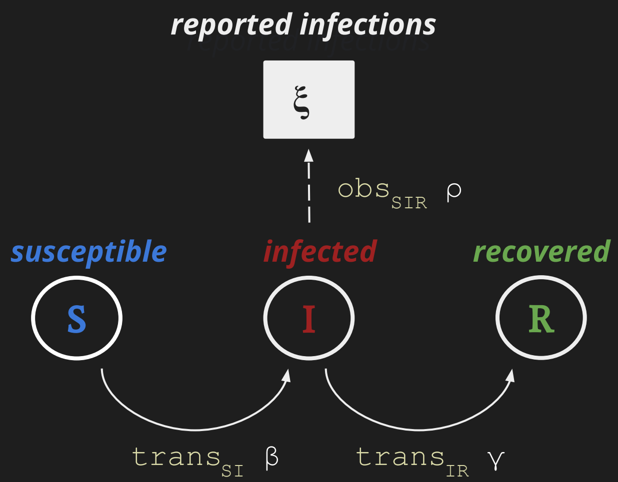
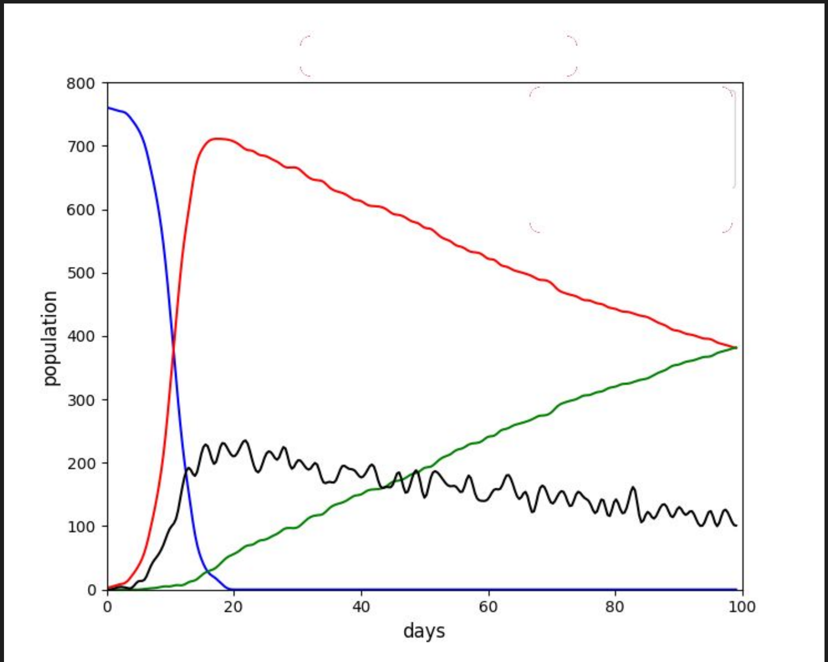

```
sirModel = hmm (trans_SIR β γ) (obs_SIR ρ)
                 100 (Population {s = 762, i = 1, r = 0})
```

Modelling an Epidemic: the SIR model

SIR as a Hidden Markov Model



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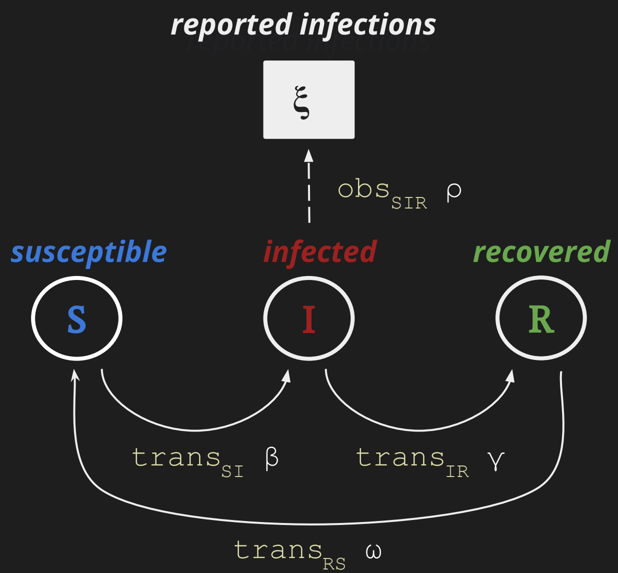
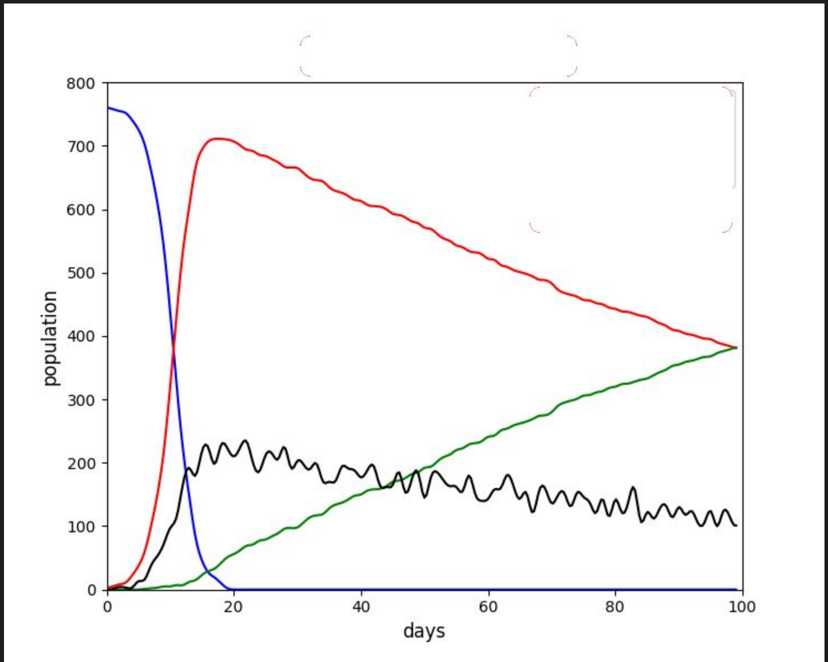
Modelling an Epidemic: the SIR model

SIR as a Hidden Markov Model



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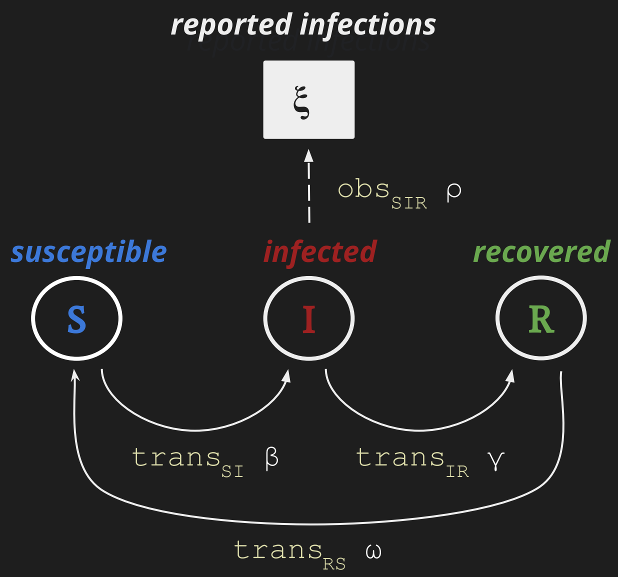
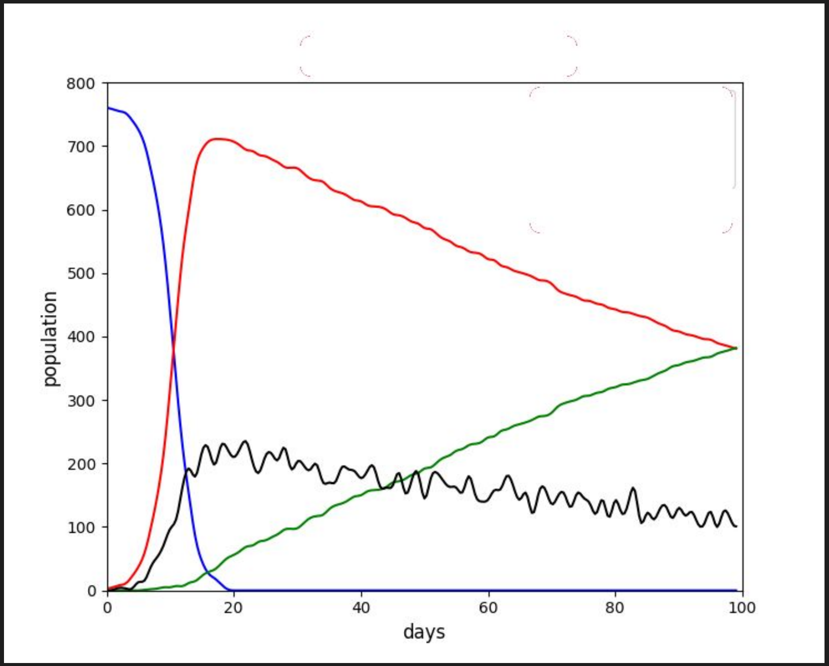
Modelling an Epidemic: the SIR model

SIR as a Hidden Markov Model



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obs_SIR ρ (Population _ i _)
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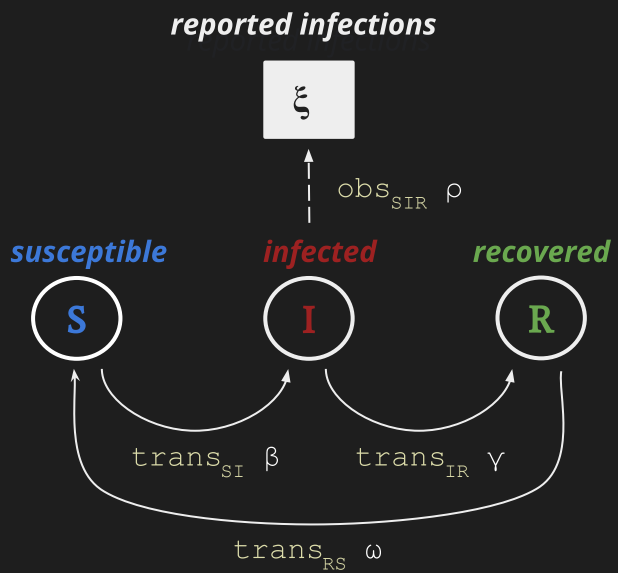
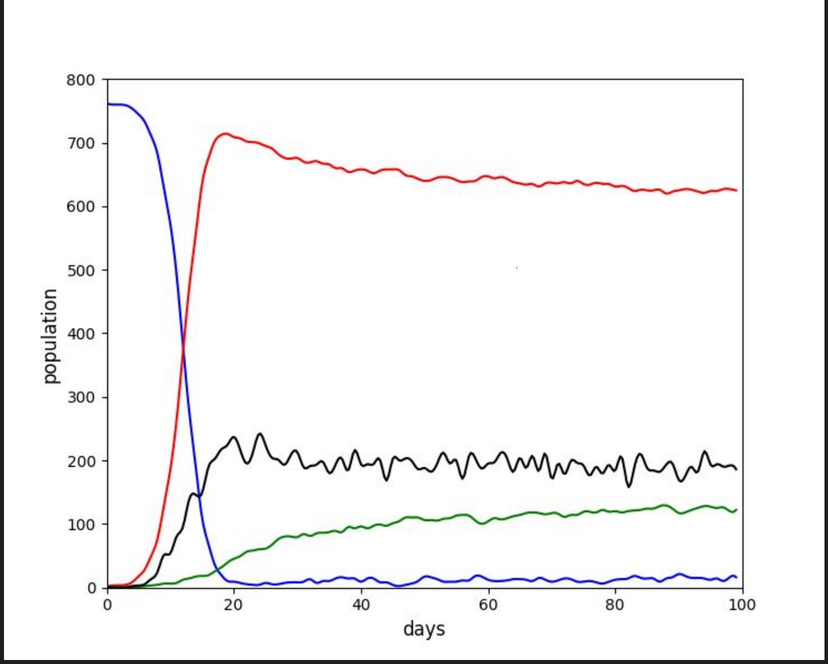
Modelling an Epidemic: the SIR model

SIR as a Hidden Markov Model



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Modelling an Epidemic: the SIR model

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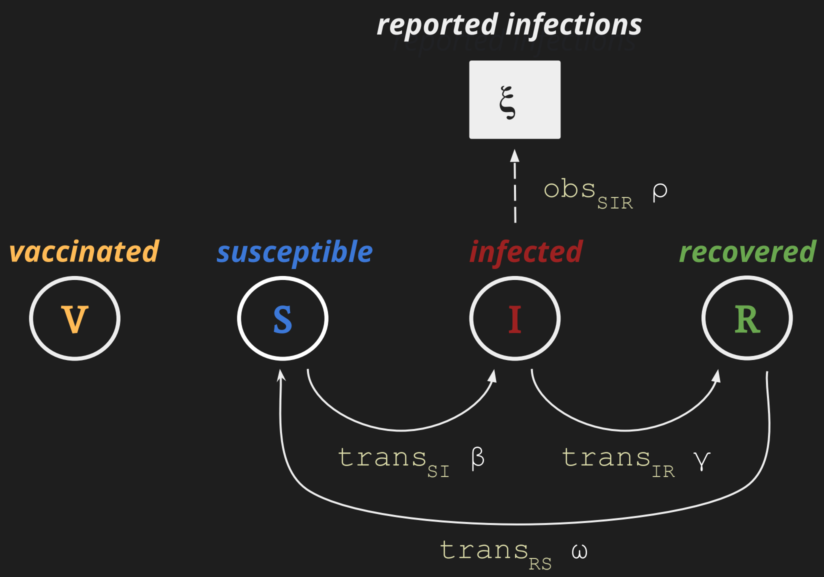

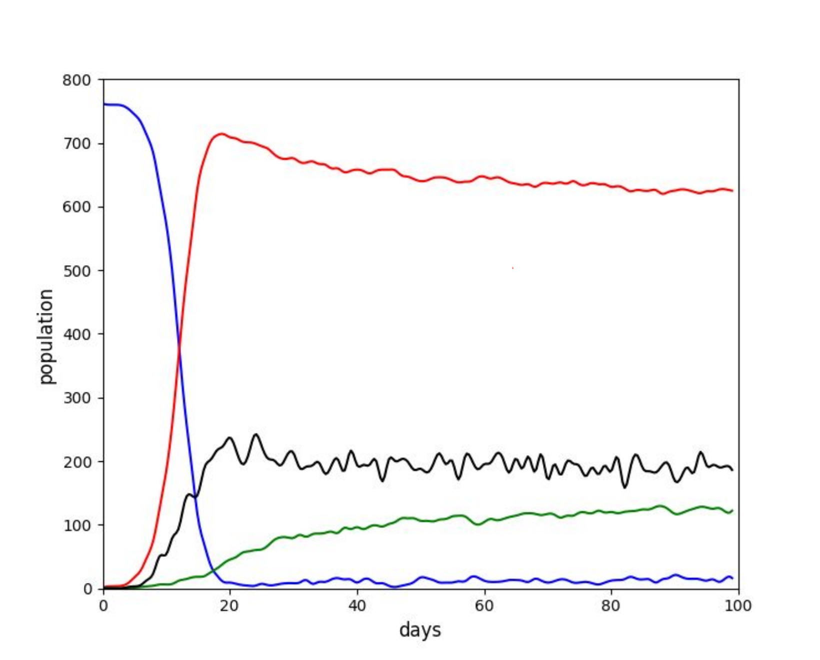


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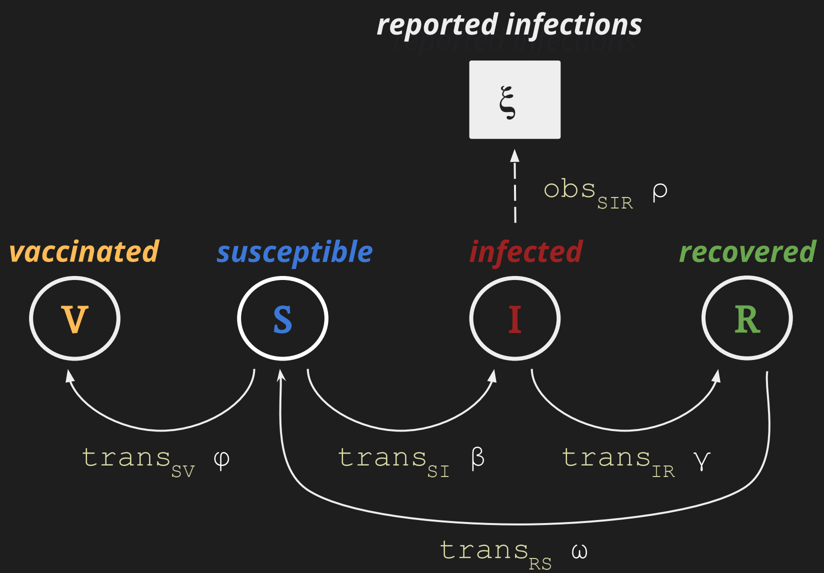
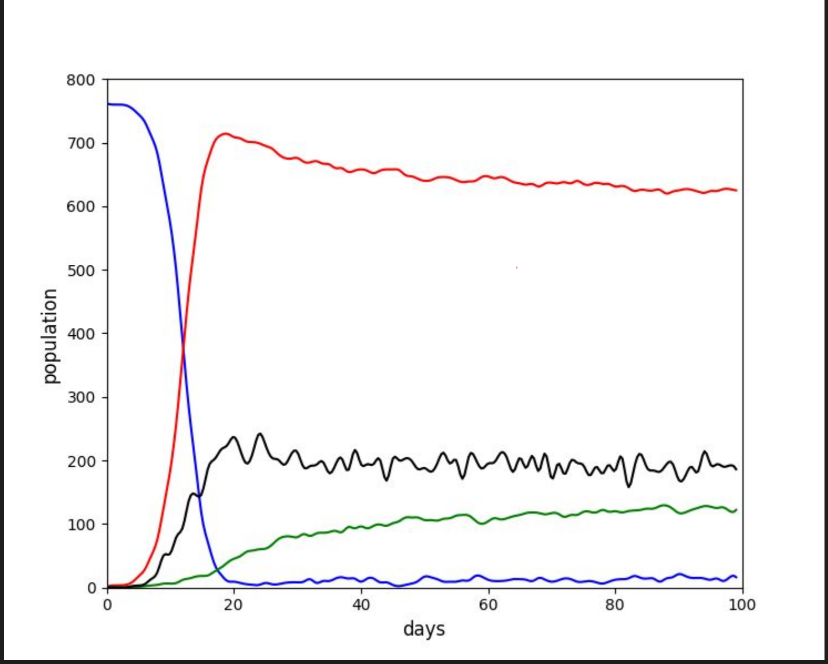
Modelling an Epidemic: the SIR model

SIR as a Hidden Markov Model



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Modelling an Epidemic: the SIR model

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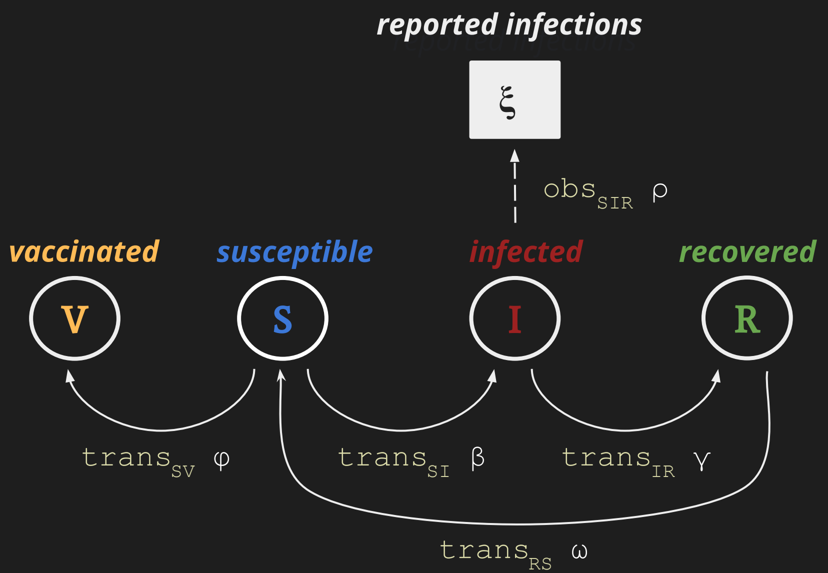
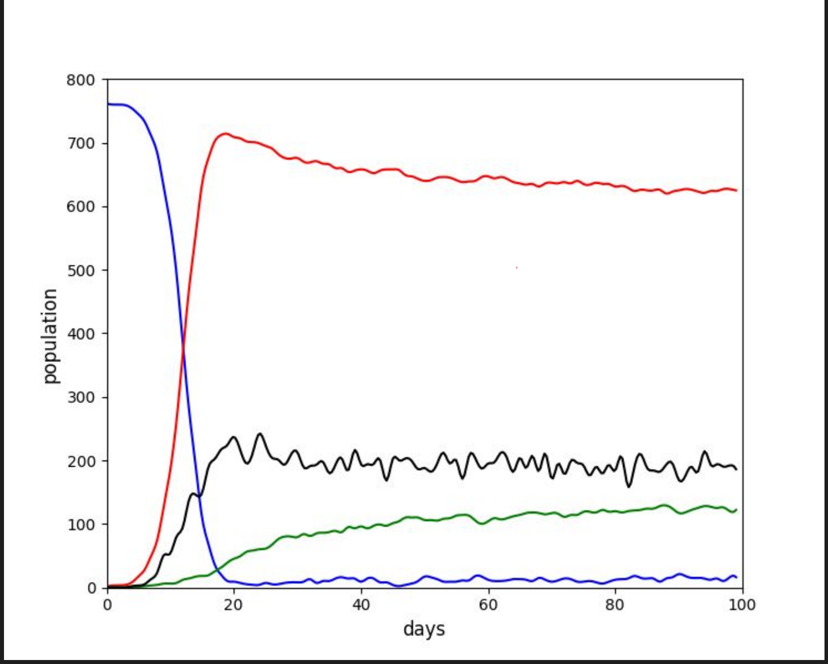




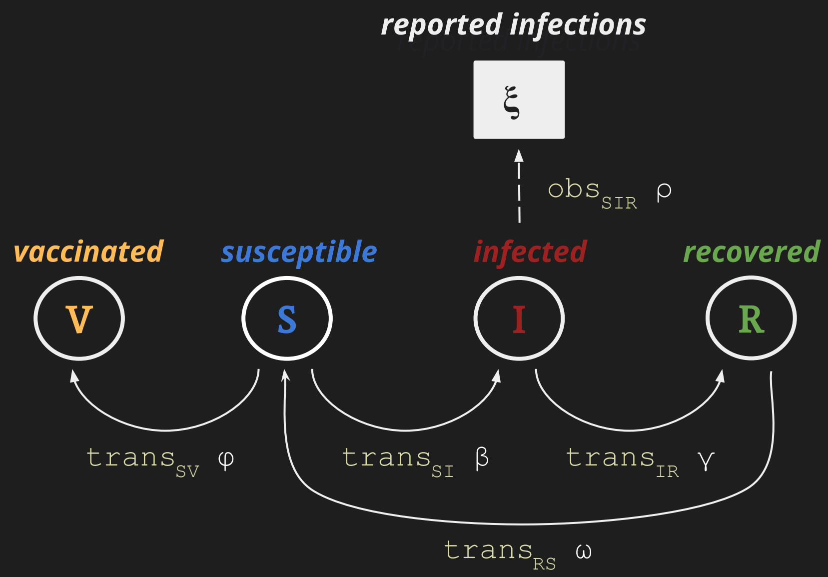

```
hmm :: TransModel env x -> ObsModel env x y -> Int -> x -> Model env x
```

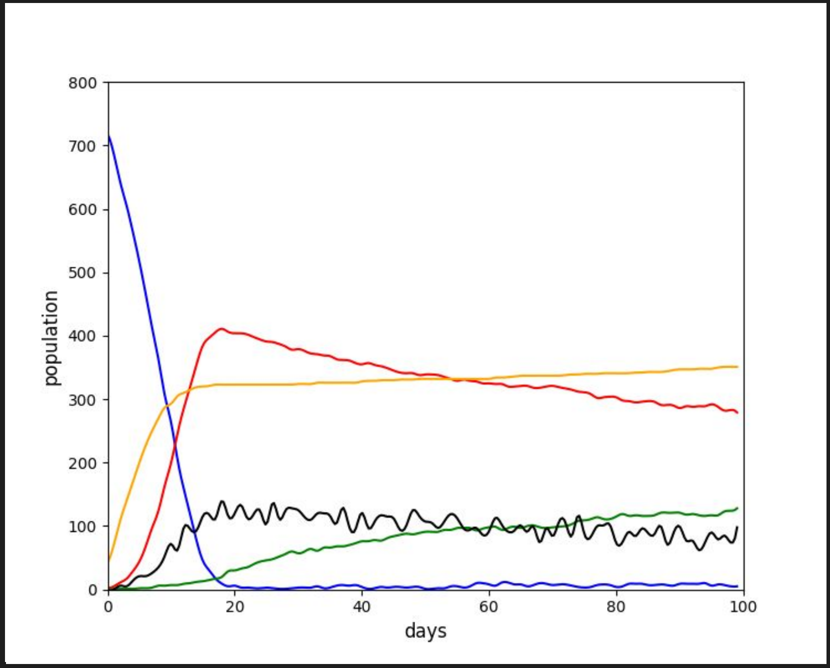
```
obs_SIR ρ (Population _ i _ _)
  = poisson (ρ * i) #ξ

trans_SIR β γ ω φ
  = trans_SI β >=> trans_IR γ
               >=> trans_RS ω
               >=> trans_SV φ
```

```
sirModel = hmm (trans_SIR β γ ω φ) (obs_SIR ρ)
                 100 (Population {s = 762, i = 1, r = 0, v = 0})
```

Modelling an Epidemic: the SIR model

SIR as a Hidden Markov Model



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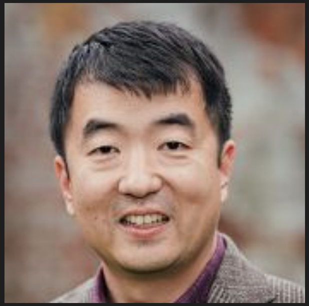
Minh Nguyen, Roly Perera, Meng Wang, Nicolas Wu






[github.com/min-nguyen/prob-fx]

Models

```
type Model env es a = (Member Dist es, Member (ObsReader env) es) => Prog es a
```

Primitive distributions

Reading observable variables

Effect signature

Smart constructors for primitive distributions

```
coinFlip :: (Observable env "p" Double,
             Observable env "y" Bool)
         => Model env es Bool
coinFlip = do
  p <- uniform 0 1 #p
  y <- bernoulli p #y
  return y
```

desugars to

```
coinFlip = do
  maybe_p <- call (Ask #p)
  p       <- call (Uniform 0 1 maybe_p)
  maybe_y <- call (Ask #y)
  y       <- call (Bernoulli p maybe_y)
  return y
```

handles to

```
(#p := [])
(#y := [True])
```

```
coinFlip = do
  p       <- call (Sample (Uniform 0 1))
  y       <- call (Observe (Bernoulli p) True)
  return y
```

Model environments

```
data Env env where
  ENil  :: Env '[]
  ECons :: [a] -> Env env -> Env ((x := a) : env)

data Assign x a = x := a

-- For example:
(#μ := [3.0]) • (#c := [0.0]) • (#σ := [1.0]) • (#y := []) • nil
  :: Env ["μ" := Double, "c" := Double , "σ" := Double, "y" := Double]
```

Observable variables

```
data ObsVar (x :: Symbol) where
 ObsVar :: KnownSymbol x => ObsVar x


-- For example:
#foo :: ObsVar "foo"
```