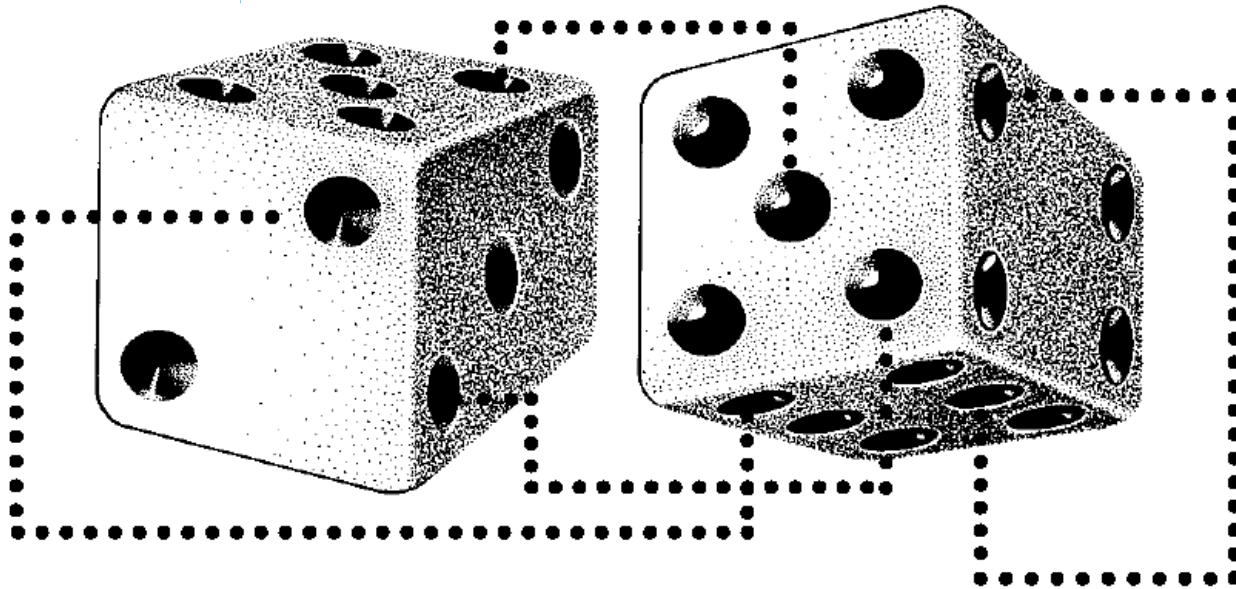


# Bayesian Networks

## Part 2



QB course

**Imperial College**  
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# Constructing a Bayesian Network - Guidelines

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- **Step 1:** converting influence diagram to BN
  - Literature review and expert help
  - influence diagram : Who's the parent? Who's the child?
  - Given the graph and some expert knowledge fill in the CPT for each node
  
- **Step 2:** Peer review
  
- **Step 3:** Testing and Learning from observations
  - Data validation
  - Updating structure and probabilities to match data

# Constructing a Bayesian Network - Guidelines

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- Step 1: converting influence diagram to BN
  - Influence diagram:
    - To illustrate the “ecological causal web” of environmental factors affecting species or outcome of interest (e.g.)
    - Simple figure with boxes and arrows showing relevance and influence amongst variables
    - Several diagrams may be constructed at various spatial scales
    - Needs: literature review and expert knowledge (i.e. list environment factors influencing specific species)
  - BN
    - Give states to variables (T/F, low medium high, range..)
    - Give conditional probabilities for each state of child node for all combinations of their parent states.
    - CP can be specified by experts, or functions found in the literature, or be given a uniform distribution if unknown
  - Goal of step 1: get the model to tell you what you think it should tell you
    - i.e. represent expert judgment and any initial empirical data (or equations) on how the system works

# Constructing a Bayesian Network - Guidelines

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- Tips:

- Keep number of parents below 3 where possible, and number of states low (but enough to ensure precision) (eg by splitting nodes->adding nodes)  
The number of probabilities in CPTs =  $\text{nbstate\_child} \times \text{nbstate\_p1} \times \text{nbstate\_p2} \times \text{nbstate\_p3}..$
- Parentless nodes (input) – typically represents predictor habitat / environment factors – should be evaluated from data (e.g. satellite images)
- Use intermediate nodes to summarise the inputs into major themes
- BNs can be broken up, with the output of one being the input of another
- all nodes should be observable and quantifiable or testable entities
- Keep depth of the model low if possible (e.g. no more than 4 steps between input and output) bigger networks may propagate unnecessary uncertainty. (exception when modelling complex process with measurable intermediate steps)

# Constructing a Bayesian Network - Guidelines

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- Tips:
  - The model, including the rationale for each node and each linkage, should be fully documented
  - Link input nodes if they are likely to be correlated (an assumption of BNs is that prior probabilities associated with unlinked input nodes are uncorrelated).
  - Use proxy nodes for inputs (e.g. habitat size for habitat suitability) and express degree of confidence in proxy
  - Test the model by inputting values

# Constructing a Bayesian Network - Guidelines

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- Step 2
  - Consult other expert not involved in modelling
  - Reconcile the 2 models if changes

# Constructing a Bayesian Network - Guidelines



- Step 3: Testing, calibrating, validating, updating  
(critical so model does not only reflect existing theory but is grounded from field data and can help develop new theories)
  - Testing BN with case data
    - Confusion matrix: compares predicted outcome with actual outcomes (with baselines..)
    - Include the probability of the outcome state, not just the state (reset baseline, e.g. very rare events)
    - When testing BN with data, no need to have data for the whole BN, just some nodes
  - Updating BN
    - Typical Bayesian thinking, revise prior given evidence (using both model and validation data)
      - 1) calibrate model states to align outcome to data (using test results to determine thresholds in discretizing),  
i.e. adjust baseline (e.g.  $P(o) > 30$  may indicate a positive outcome)  
determine more appropriate probability cut-off values in interpreting model predictions
      - 2) adjust CPT to get better data fit, using EM for instance (several learning algorithms here)
- The updated model has a known success rates and is calibrated to provide the best interpretation of results.
- Calibrating and updating Bayesian models – structure and/or CPT - can be an on-going, iterative process as new case data are gathered.

# BN - Tools

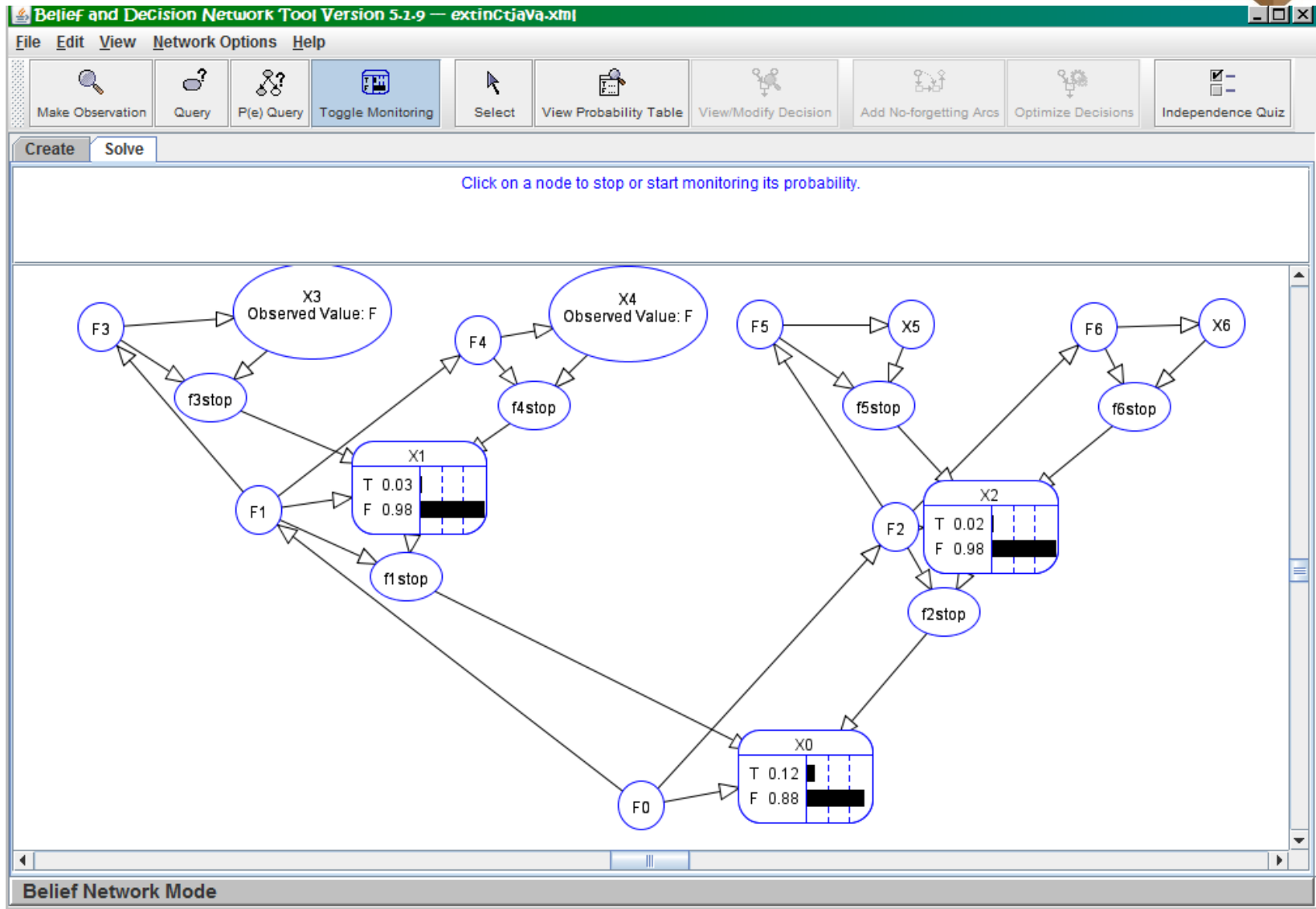
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- R packages
  - <http://www.r-bayesian-networks.org/cookbook>
  - <http://www.bnlearn.com/>
  - <http://cran.r-project.org/web/views/Bayesian.html>
  - <http://www.r-project.org/conferences/DSC-2003/Proceedings/BottcherDethlefsen.pdf>
- Python: <http://www.bayespy.org/intro.html>
- Free Java software with GUI:
  - Belief and Decision Networks <http://aispace.org/bayes/>
- Netica (free version available)
  - <http://www.norsys.com/netica.html>
  - The free version cannot save large models



# Belief and Decision Networks <http://aispace.org/bayes/>



# Netica (free version) <http://www.norsys.com/netica.html>



Netica

File Edit Layout Modify Table Network Cases Report Style Window Help

Most Probable Expl  
✓ Automatic Updating  
Update  
Update by Sampling Ctrl+U  
Remove Findings Ctrl+F8  
Compile  
Compile Optimized  
Expand Time  
Sensitivity to Findings  
Optimize Decisions

BBex +

**Bacteria B**

high	65.0
low	35.0

**Deforestation**

high	30.0
low	70.0

**Habitat Alteration**

high	61.3
low	38.7

**Penguin abundance**

high	46.3
low	53.8

**Hedgehog abundance**

high	38.5
low	61.5

**HA Table (in net BBex)**

Node: HA

Apply Okay

Chance % Probability Reset Close

Bacteria B	Deforestation	high	low
high	high	97	3
high	low	72	28
low	high	75	25
low	low	7	93

# Advantages and limitations of BN

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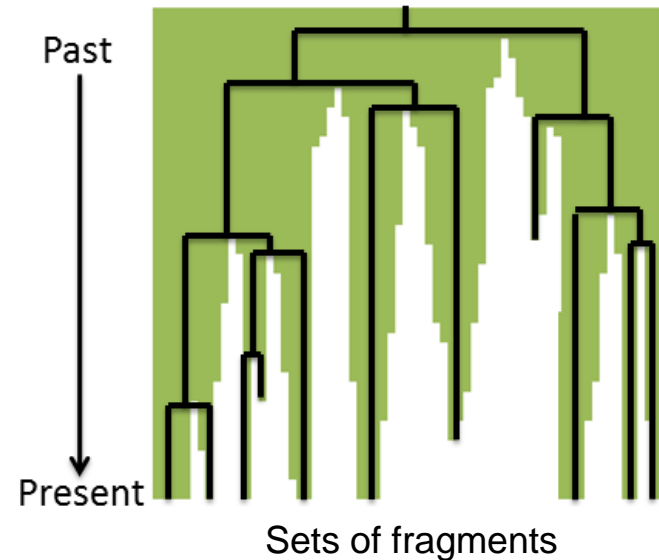
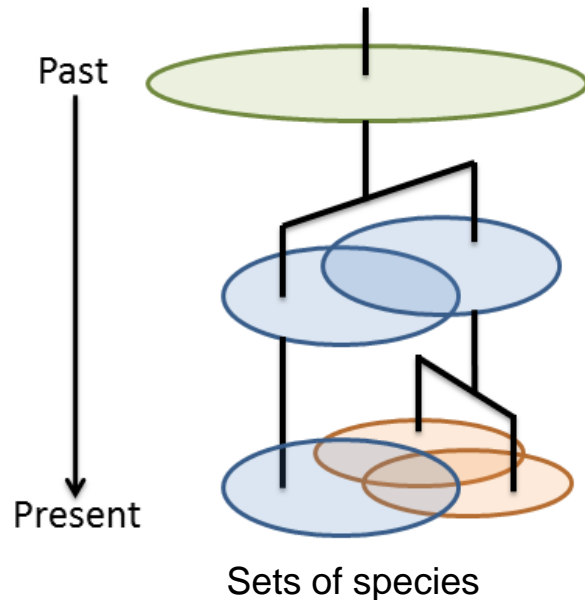
- The advantages of Bayesian Networks :
  - It is easy to recognize the dependence and independence between various nodes.
  - Bayesian networks can handle situations where the data set is incomplete since the model accounts for dependencies between all variables.
  - Bayesian networks can map scenarios where it is not feasible/practical to measure all variables due to system constraints (costs, not enough sensors, etc.)
  - Can be used for any system model - from parameters all known to none
- The limitations of Bayesian Networks:
  - The quality of the results of the network depends on the quality of the prior beliefs or model. A variable is only a part of a Bayesian network if you believe that the system depends on it (although this is true for many models)
  - Calculation of the network is NP-hard (nondeterministic polynomial-time hard), so it is very difficult and possibly costly. (but there are solutions)
  - Calculations and probabilities using Bayes' rule and marginalization can become complex and are often **characterized by subtle wording**, and care must be taken to calculate them properly.
  - Subtle wording is essential, words description of some “tool” nodes used can be very tricky!
  - Discrete states
  - No loop

# Current example: The Terragenesis model

Using landscape history to predict biodiversity patterns in fragmented landscapes

- Theory:

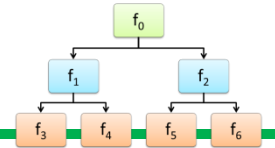
- Through a succession of deforestation events a forest becomes split into fragments
- The family tree of such fragments is named the terrageny
- Reduction in size of local habitat results in species extinction
- Fragments that are recently separated may have more species in common
- The Terragenesis model can help predict biodiversity in human-modified landscapes



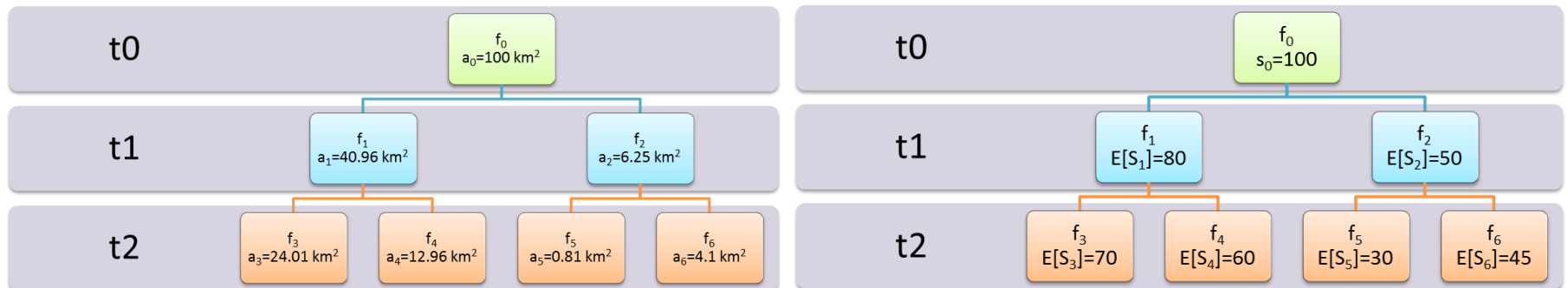
- Hypotheses:

- The terrageny and fragment sizes can be learned from satellite images
- The expected number  $N$  of species in a fragment is a function of fragment area  $A$ :  $N = A^z$  (Species Area Relationship)
- Persistence of a species in a fragment does not affect other species and they all have equal chances
- The species composition of a fragment is determined by the species in its ancestors, but not in its siblings (no dispersal)

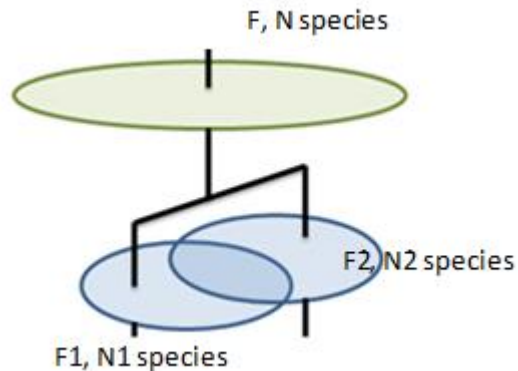
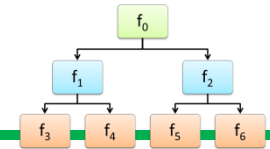
# The Terragenesis BN



- The BN represents the presence/absence of a single species  $i$  in all the fragments of the terrageny
- The nodes of the terrageny are the fragments and the links between them represent their transformation into smaller fragments. The graph of the BN is the terrageny.
- Each node (corresponding to a fragment  $k$ ) is the binary random variable “presence of species  $i$  in the fragment  $k$ ”  
 $F_{ki}$  : binary variable describing the event “species  $i$  is present in  $f_k$ ”
- Species  $i$  is one of the  $s_0$  present in the original fragment  $f_0$
- The probability of species  $i$  to persist after a splitting event is the proportion of “species places” (species capacity) in the new fragment out of the number of species places in the current fragment (they have equal chances)
- The number of species in a fragment randomly varies and is not necessarily equal to the species capacity (except for the original landscape which is fixed).
- The species capacity is the expected value of the number of species given by the species area relationship.
- Conditional independence:** the probability of species  $i$  to be in a fragment given it is in its parent is independent to all other fragments.



# The Terragenesis BN



The Terragenesis BN gives us

- the distribution of species  $i$  in the terrageny,
- the probability for all fragments to contain species  $i$ ,  $P(F_{ki})$

All  $s_0$  species are have equal chances to persist and are mutually independent

→ For all fragments:

The events  $F_{k1}, F_{k2}, \dots, F_{ks_0}$  for all species are mutually independent and identically distributed.

Their sum for a fragment  $f_k$  corresponds to the number  $S_k$  of species in  $f_k$ :

$$S_k = \sum_{i=1}^{s_0} F_{ki}$$

E.g.:

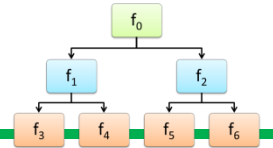
in  $f_0$ :  $F_{01}=1, F_{02}=1, F_{03}=1, F_{04}=1 \rightarrow s_0 = 4$

in  $f_1$ :  $F_{11}=1, F_{12}=0, F_{13}=1, F_{14}=1 \rightarrow S_1 = 3$

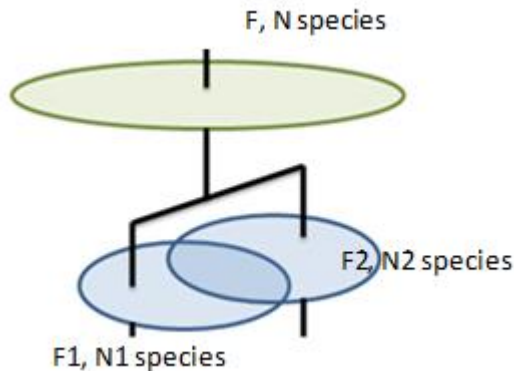
# Bernoulli and Binomial

- The  $Fk_i$  are Bernoulli variables
  - $P(Fk_i = 1) = p$
  - $P(Fk_i = 0) = 1 - p$
  - Their expected value is their probability to be true.
  - $E[Fk_i] = 0 \cdot (1 - p) + 1 \cdot p = p$
  - Variance
  - $\text{Var}(Fk_i) = E(Fk_i^2) - E(Fk_i)^2 = E(Fk_i) (1 - E(Fk_i)) = p(1 - p)$
- $S_k$  the sum of the  $Fk_i$ 
  - The expected value of their sum, for  $i=1 \rightarrow N$ :
  - $E[S_k] = E[\sum_{i=1}^N Fk_i] = \sum_{i=1}^N E(Fk_i) = N \times p$
  - The  $Fk_i$  independent for all  $i$  ( $\text{cov} = 0$ ) so the variance of their sum:
  - $\text{Var}(Fk_i) = N \cdot \text{Var}(Fk_i) = N \times p(1 - p)$
  - $S_k$  is a binomial variable of parameters  $N$  and  $p$
  - A sum of  $N$  i.i.d. (independent and identically distributed) Bernoulli variables with probability  $p$ , is a binomial variable of parameters  $N$  and  $p$

# Fragments similarity



- From the Terragenesis BN we have the probability of species  $i$  to be in each fragment
- And from the Binomial distribution we have the expected values of the number of species in each fragment, and the probability that the number of species is  $x$ .
- We are interested in the similarity between 2 fragments:
- The amount of species shared between 2 fragments (intersection) over the total number of species in the 2 fragments (union).
- To compute this for all fragments we can first compute the probability for a single species  $i$  to be in the 2 fragments (intersection), and in one or the other or both (union)



Independence

$$P(A \cap B) = P(A) \times P(B)$$

Inclusion-exclusion principle

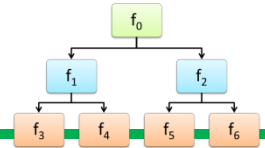
$$P(A \cup B) = P(A) + P(B) - P(A \cap B)$$

Disjoint events

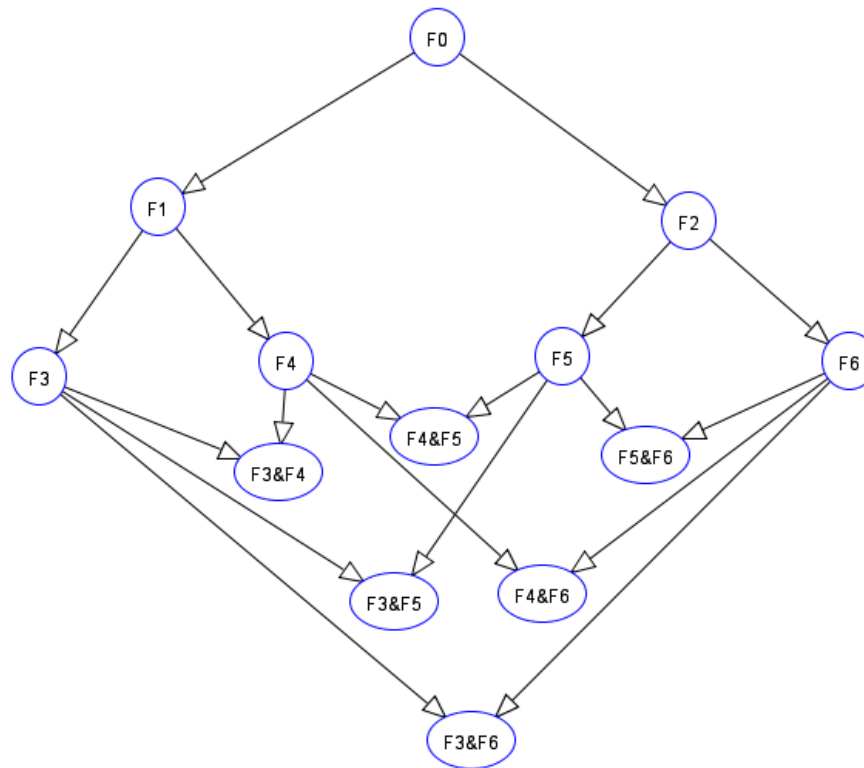
$$P(A \cup B) = P(A) + P(B)$$



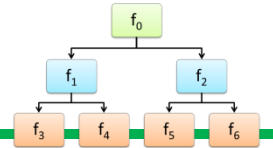
# Fragments similarity



- We can add functional 'AND' nodes in the graph, to represent the variable species  $i$  is present in both fragments, (and then sum for all species) to obtain the expected number of shared species.
- Species  $i$  presence in a fragment is conditionally independent to its presence in another given it is present in their most recent common ancestor
- Expected number of shared species will be a question in the practical

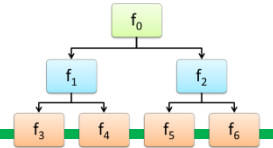


# Extinct species (Not part of practical)

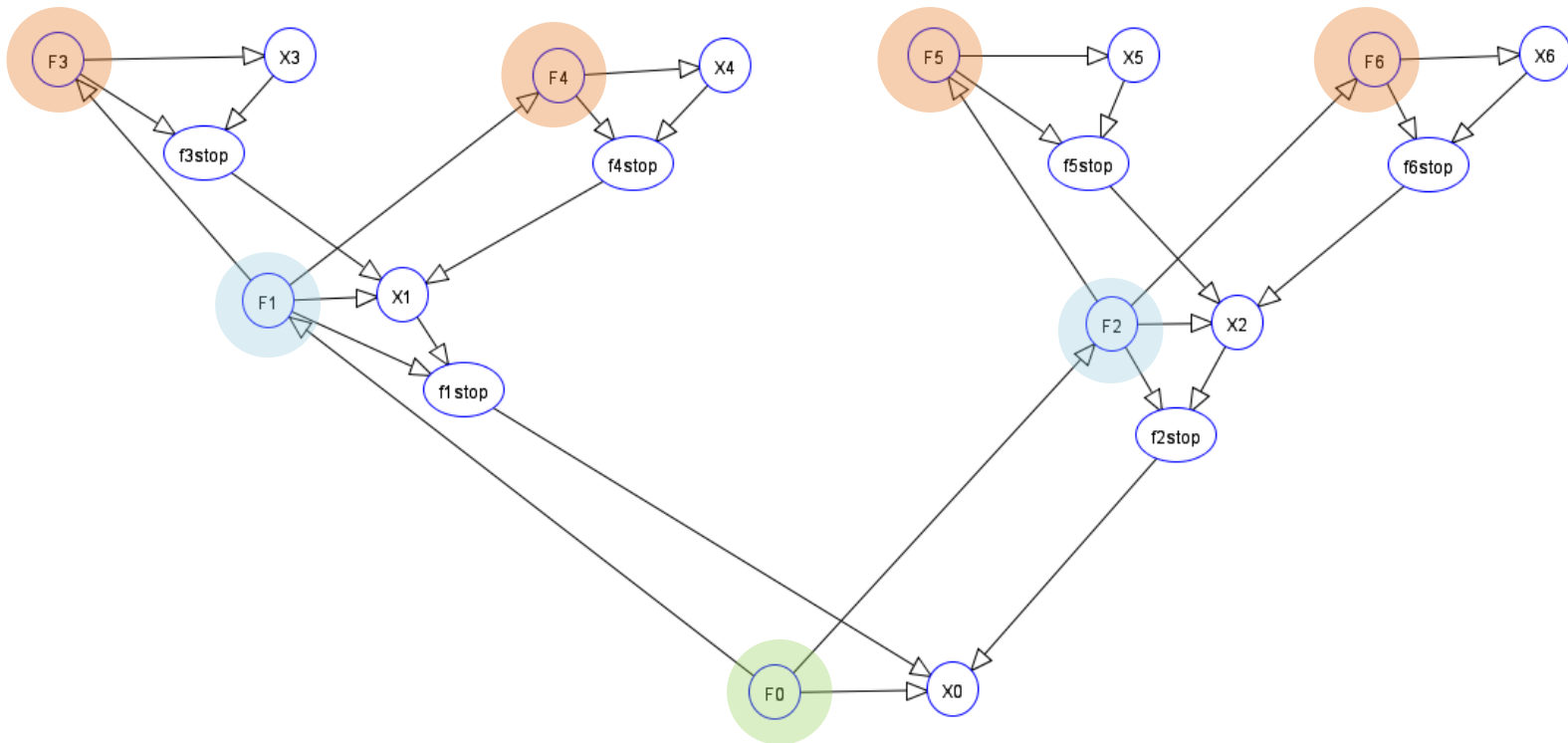


- Species can become extinct after splitting events
- A species in f1 is extinct from f1 if it did not persist in f3 and it did not persist in f4 (descendants)
- A species in f1 is extinct from f2 if it did not persist in f5 and it did not persist in f6
- A species in f0 is extinct from f0 if:
  - It did not persist in f1 OR it did AND is extinct from f1
  - And it did not persist in f2 OR it did AND is extinct from f2
- A species in f3,f4,f5 or f6 cannot be extinct

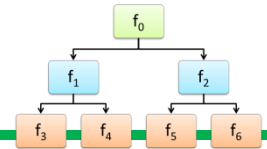
# Extinct species



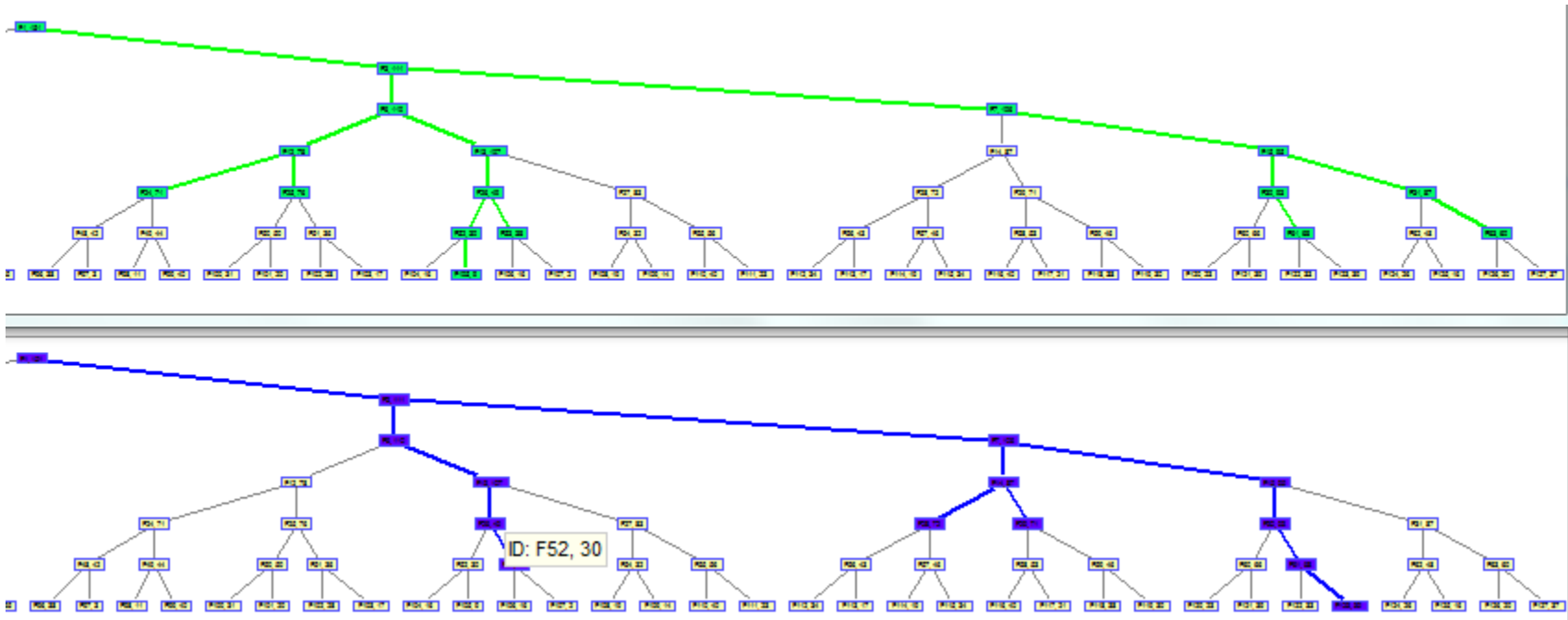
- We can add in the BN the variables “Xk: species i is extinct from fk” and logical nodes to relate them to the Fki following the “extinction” rules.
- Then we can predict the expected number of extinct species in a landscape, given a terrageny.



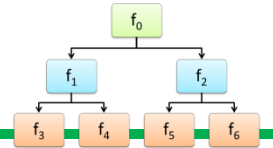
# Endemic species (Not part of practical)



- A species is endemic to the landscape if it is present in only 1 present day fragment
- It is linked to extinct species and also require a recursive definition
- We define a species to be “dominated” by a fragment  $f_k$  if it is in  $f_k$  and the only present day fragment that contains the species (if any) is a direct descendant of  $f_k$  (subtle wording !)
- If  $f_k$  is a present-day fragment then dominated is the same as endemic



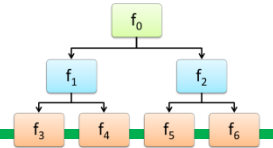
# Endemic species



- A species is dominated by  $f_k$  (given that it is dominated by its parent) if:
    - It is in  $f_k$
    - AND
    - It is not present in his siblings or is but got extinct from it (similar to extinct but it starts from the top)
- All species are dominated by  $f_0$

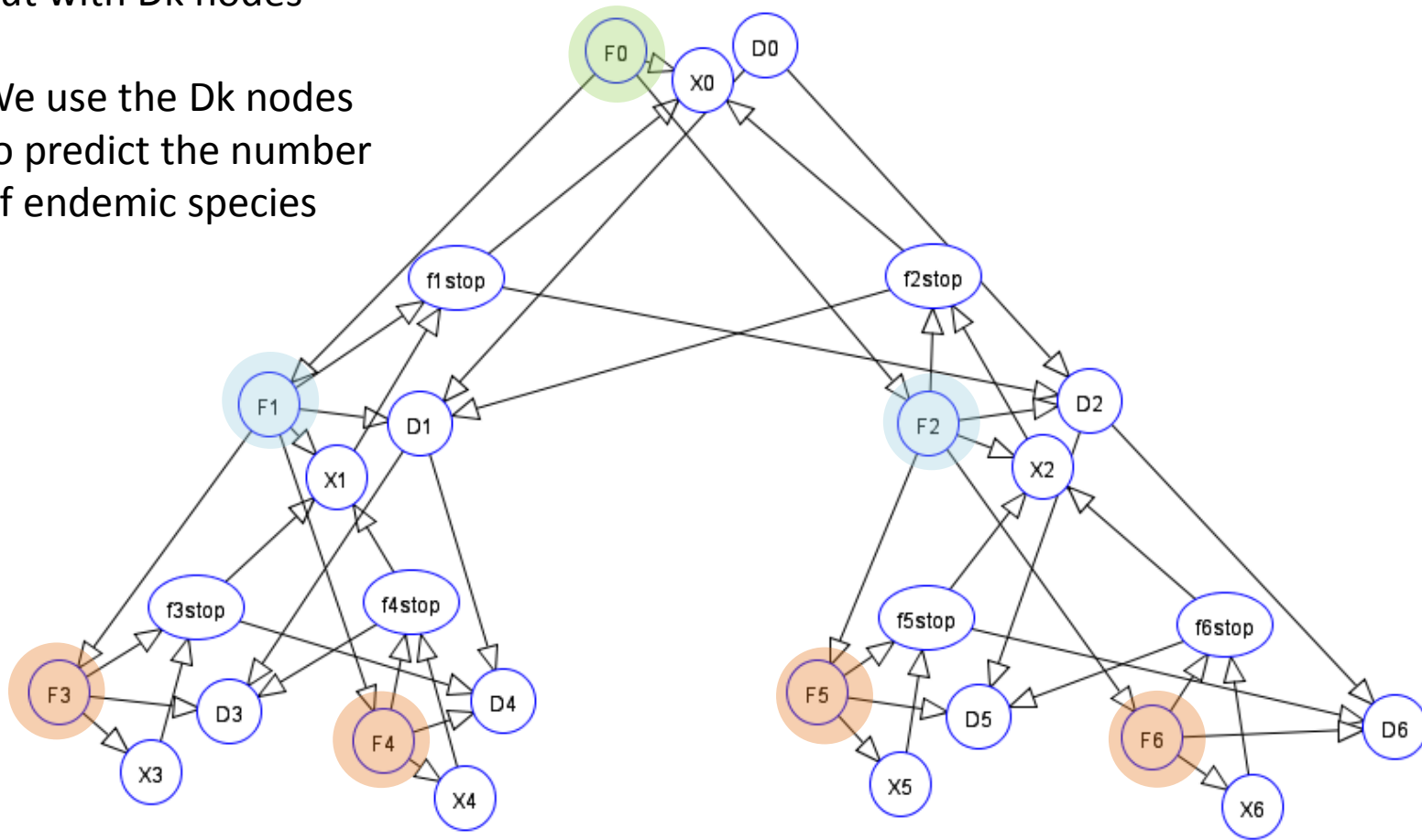
We can add another layer of nodes to represent it:

# Endemic species



Same as extinct BN,  
but with Dk nodes

We use the Dk nodes  
to predict the number  
of endemic species



# Practical :

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- Finding equations of terrageny model
  - As a review of random variables and BN
  - All rules and theorems will be given
  - Needs pen and paper
- Solving simple example BNs manually
- Implementing the Terragenesis model or other examples with a BN GUI software

# Bibliography / suggested readings



## Articles:

- Charniak, Eugene. "Bayesian networks without tears." AI magazine 12.4 (1991): 50.
- Guidelines for developing and updating Bayesian belief networks applied to ecological modeling and conservation – Marcot et al., 2006 Canadian Journal of Forest Research
- Koller, Daphne, et al. "2 Graphical Models in a Nutshell." Statistical relational learning (2007): 13.
- Nicholson, O. Woodberry and C. Twardy (2010). The "Native Fish" Bayesian networks.  
<http://bayesian-intelligence.com/bwb/2012-03/how-to-model-with-bayesian-networks/>

## Web resources:

- An Intuitive Explanation of Bayes' Theorem - by Eliezer Yudkowsky  
<http://yudkowsky.net/rational/bayes>
- Fallacies about probabilities - by Norman Fenton  
[http://www.agenarisk.com/resources/probability\\_puzzles/Making\\_sense\\_of\\_probability.html](http://www.agenarisk.com/resources/probability_puzzles/Making_sense_of_probability.html)
- A Brief Introduction to Graphical Models and Bayesian Networks - by Kevin Murphy  
<http://www.cs.ubc.ca/~murphyk/Bayes/bnintro.html>
- Machine Learning course by Doina Precup  
<http://www.cs.mcgill.ca/~dprecup/courses/ML/lectures.html>
- Virtual Laboratories in Probability and Statistics  
<http://www.math.uah.edu/stat/>
- Bayes nets library:  
<http://www.norsys.com/netlibrary/index.htm>

