# Multi-Hypothesis

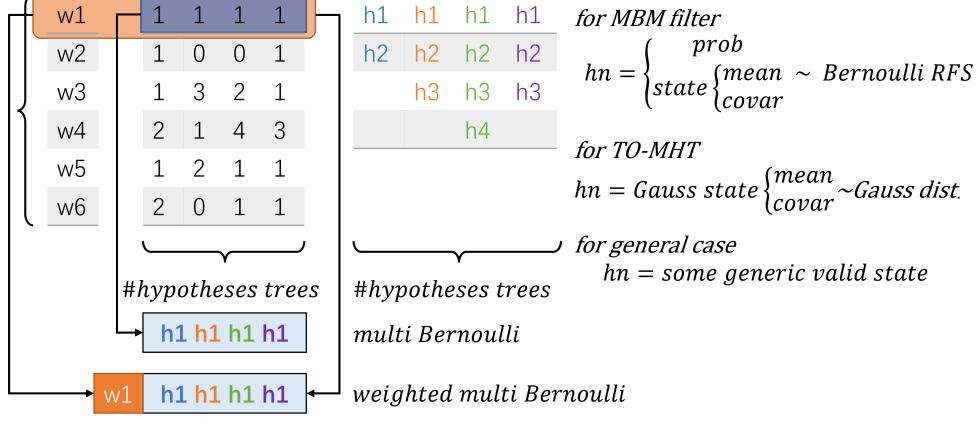
A clear explanation

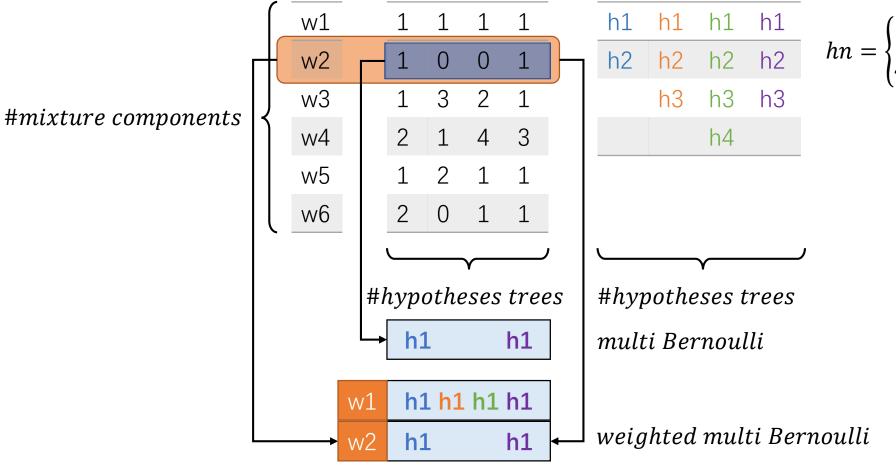
### Multi-Hypothesis representation

- local hypotheses(hypotheses trees) representation
  - global weights
  - hypotheses look-up table
  - local hypotheses forest
- global hypotheses representation
  - global weights
  - global hypotheses

global weights lookup table hypotheses forest w1 h1 h1 h1 h1 w2 h2 h2 h2 h2 0 0 3

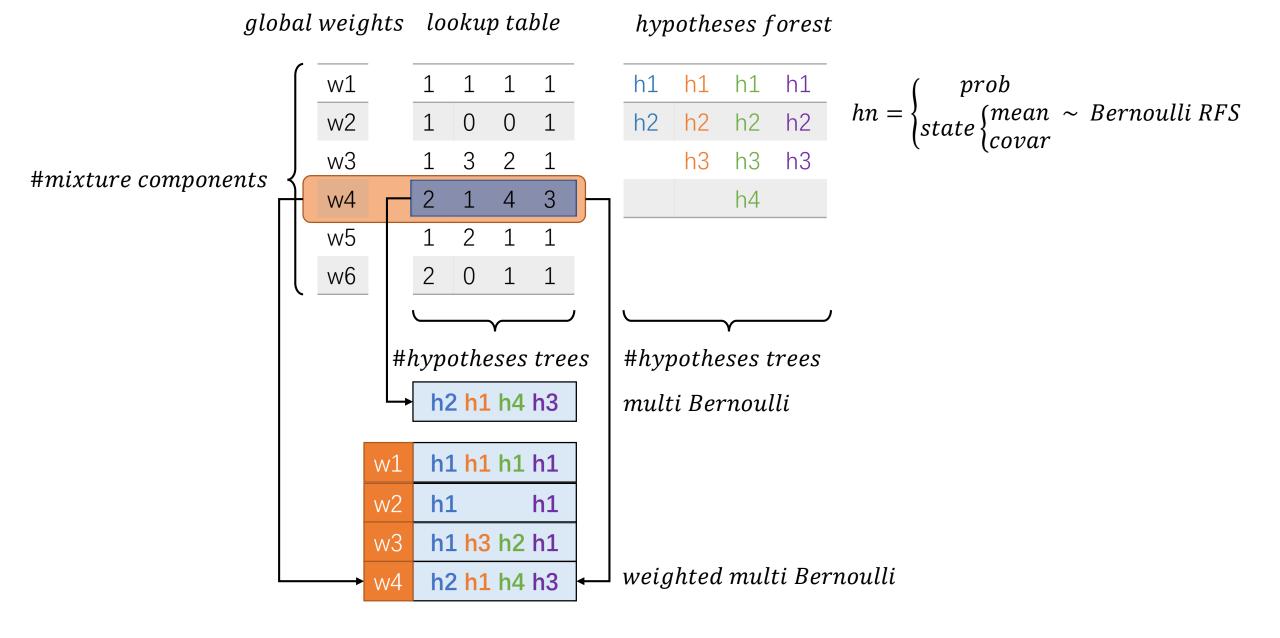
#mixture components

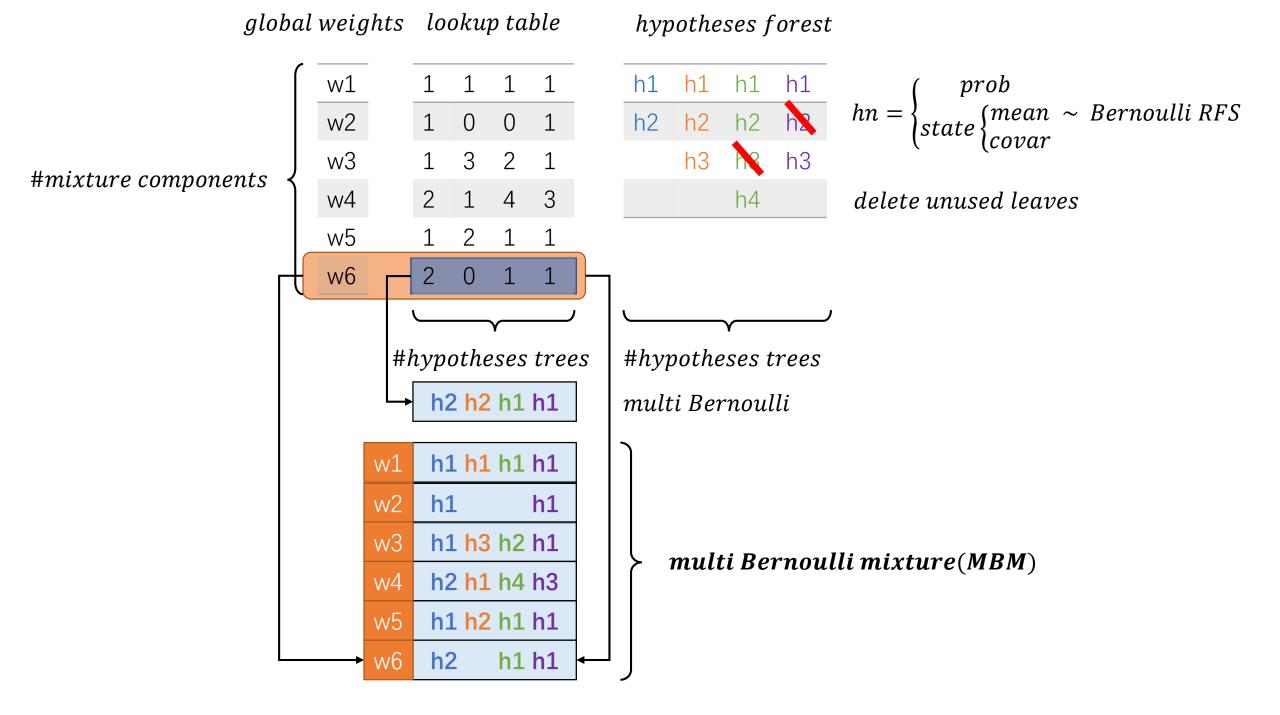




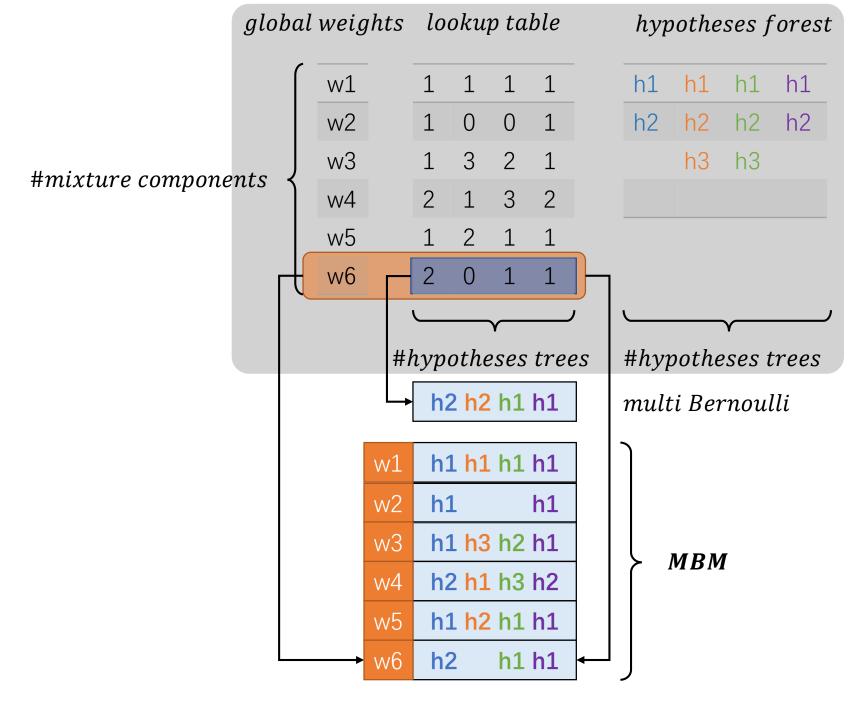
$$hn = \begin{cases} prob \\ state \end{cases} \begin{cases} mean \sim Bernoulli RFS \end{cases}$$

global weights lookup table hypotheses forest w1h1 h1 h1 h1 (mean ~ Bernoulli RFS h2 h2 0 0 h2 h2 w2 w3 h3 h3 h3 #mixture components h4 w4 w5 w6 0 #hypotheses trees #hypotheses trees h1 h3 h2 h1 multi Bernoulli h1 h1 h1 h1 w1 w2 h1 h1 weighted multi Bernoulli h1 h3 h2 h1





global weights lookup table hypotheses forest w1 h1 h1 h1 h1 (mean ~ Bernoulli RFS h2 h2 h2 h2 0 0 w2 h3 3 w3 h3 #mixture components delete unused leaves w4 reassign the forest and the table w5 w6 #hypotheses trees #hypotheses trees h2 h2 h1 h1 multi Bernoulli h1 h1 h1 h1 w1 w2 h1 h1 h1 h3 h2 h1 w3 multi Bernoulli mixture(MBM) h2 h1 h3 h2 w4 h1 h2 h1 h1 w5 w6 h2 h1 h1



$$hn = \begin{cases} prob \\ state \\ covar \end{cases}$$
 Rernoulli RFS

delete unused leaves reassign the forest and the table

MBM has three parts in hypotheses trees representation:

- 1. global weights
- 2. lookup table
- 3. hypotheses forest

global weights lookup table hypotheses forest w1 h1 h1 h1 h1 h2 h2 h2 h2 w2 0 0 h3 w3 3 h3 #mixture components 3 w4 w5 w6 #hypotheses trees #hypotheses trees h2 h2 h1 h1 multi Bernoulli h1 h1 h1 h1 w1 w2 h1 h1 h1 h3 h2 h1 w3 **MBM** h2 h1 h3 h2 w4 h1 h2 h1 h1 w5

h2

w6

h1 h1

potiteses jorest

$$hn = \begin{cases} prob \\ state \\ covar \end{cases} \sim Bernoulli RFS$$

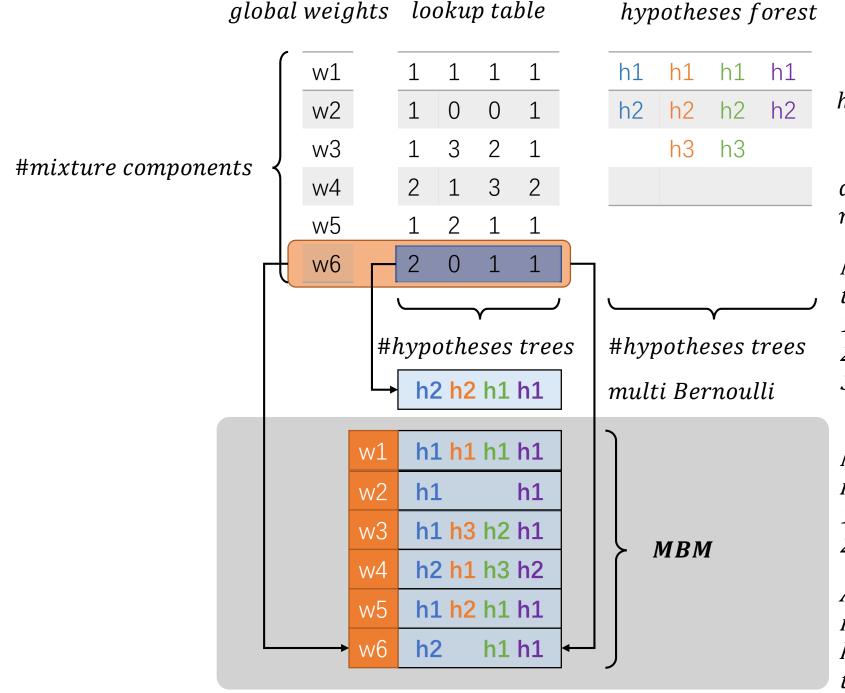
delete unused leaves reassign the forest and the table

MBM has three parts in hypotheses trees representation:

- 1. global weights
- 2. lookup table
- 3. hypotheses forest

MBM has two parts in global hypotheses representation:

- 1. global weights
- 2. global hypotheses



$$hn = \begin{cases} prob \\ state \\ covar \end{cases} \sim Bernoulli RFS$$

delete unused leaves reassign the forest and the table

MBM has three parts in hypotheses trees representation:

- 1. global weights
- 2. lookup table
- 3. hypotheses forest

MBM has two parts in global hypotheses representation:

- 1. global weights
- 2. global hypotheses

As you can see, the global hypotheses representation has many duplicated *local states. So we prefer the hypotheses* trees representation.

## Multi-Hypothesis predict(local hypo. repr.)

- local hypotheses(forest) predict
  - for each local hypo. in each hypo. tree
    - predict local hypo.
  - global weights / look-up table don't change.

### global weights timestamp = k

hypotheses forest

h1

h3

h2 h2 h2 h2

h3

h1

w1	1	1	1	1
w2	1	0	0	1

$$h1$$
  $h1$   $hn = generic state$ 

#mixture components

multi hypotheses

#### global weights

#### timestamp = k + 1

hypotheses forest prediction

w1 0 w2 3 w3 #mixture components w4 w5 w6 0 h1 h1 h1 h1 h2 h2 h2 h2 h3 h3

hn = generic state

multi hypotheses prediction

## Multi-Hypothesis update(local hypo. repr.)

- local hypotheses(forest) update
  - for each local hypo. in each hypo. tree
    - gating(ellipsoidal gating in Gaussian state)
    - update hypo. and associated measurement log-likelihood with missed detection and associated measurements in gate
  - resulted in [#meas in gate + 1(missed hypo)] updated hypos and measurement log-likelihoods correspondingly
- global weights / look-up table / hypo. forest update
  - for each predicted global hypothesis
    - create cost matrix for data association(DA)(use the associated measurement log-likelihoods calculated before)
    - Murty DA
    - update global weights / look-up table / hypo. forest

#### global weights

#### lookup table

#### hypotheses forest

h2

h2

h1 h1

h2

h2

h3

$$timestamp = k$$

hn = generic state

#mixture components

multi hypotheses

#### timestamp = k + 1

#### hypotheses forest

h1	h1	h1	h1
h2	h2	h2	h2
	h3	h3	

new measurements: z1,z2

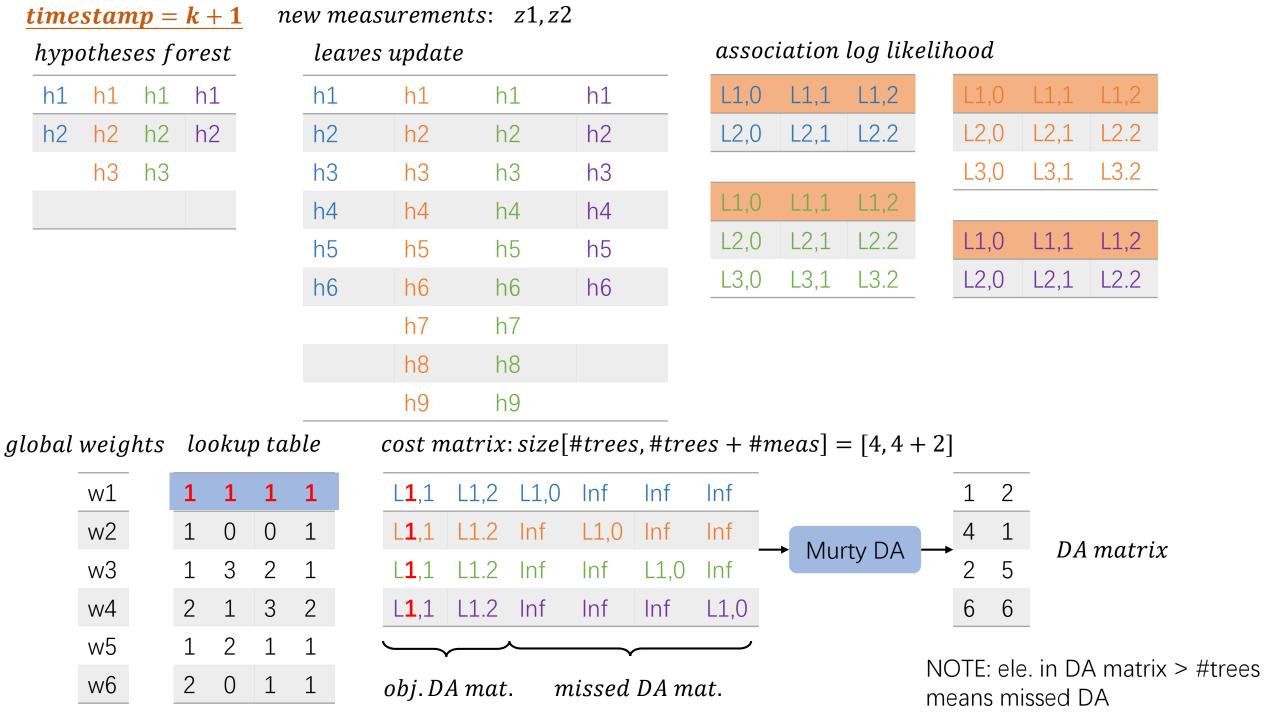
#### leaves update

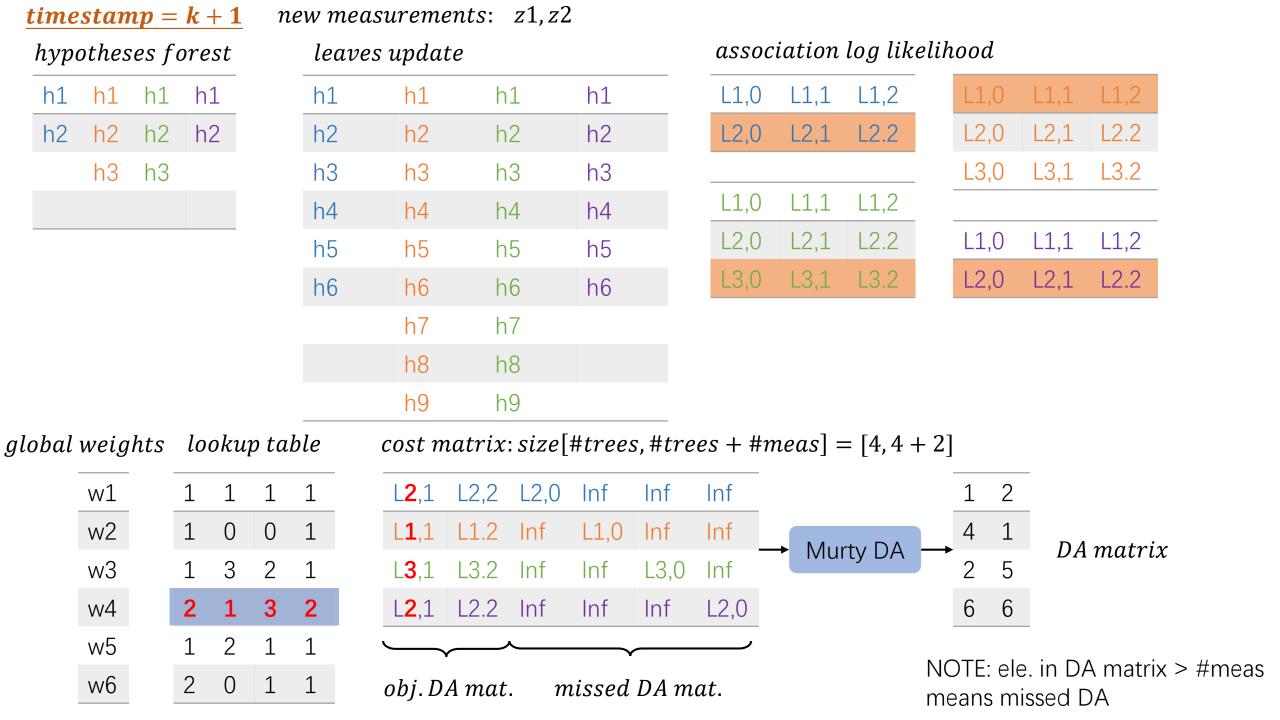
h1,0	h1,0	h1,0	h1,0
h1+z1	h1+z1	h1+z1	h1+z1
h1+z2	h1+z2	h1+z2	h1+z2
h2,0	h2,0	h2,0	h2,0
h2+z1	h2+z1	h2+z1	h2+z1
h2+z2	h2+z2	h2+z2	h2+z2
	h3,0	h3,0	
	h3+z1	h3+z1	
	h3+z2	h3+z2	

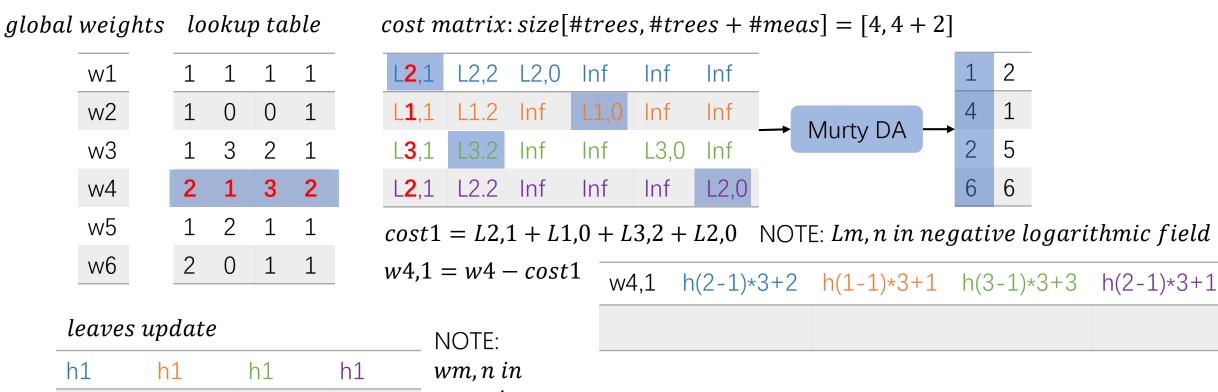
#### association negative log likelihoods

L1,0	L1,1	L1,2	L1,0	L1,1	L1,2
L2,0	L2,1	L2.2	L2,0	L2,1	L2.2
			L3,0	L3,1	L3.2
L1,0	L1,1	L1,2			
L2,0	L2,1	L2.2	L1,0	L1,1	L1,2
L3,0	L3,1	L3.2	L2,0	L2,1	L2.2

*Lm*, *n* means **negative** loglikelihood with the leaf m associated to the meas n at the blue tree, n = 0 means missed hypothesis







h1	h1	h1	h1
h2	h2	h2	h2
h3	h3	h3	h3
h4	h4	h4	h4
h5	h5	h5	h5
h6	h6	h6	h6
	h7	h7	
	h8	h8	
	h9	h9	

wm,n in negative logarithmic field

w4,1 means the 4th tree and the 1st meas DA, h(2-1)\*3+2 means the 2nd leaf (idx is (2-1)\*3,3=#meas+1) in the 4th tree and the 1st meas DA, +1 means the missed DA. +2 means the 1st meas DA. +3 means the 2nd meas DA. and so on...

