### Metabolite-Flow Variability Analysis (MFVA) or Flux-Sum Variability Analysis (FSVA)



Categories of Flux-Sum Intervals between Cancer/Normal Model and Mutant/Normal Model



- The black line indicates the fluxsum interval of the normal model, and the red line indicates that of the mutant/cancer model.
- The categories are a qualitative measure to determine the trend of flux change between mutant and normal case, not quantitative.

#### Computational Procedures of Fuzzy Equal Membership Grade

• The FSVA problems for the cancer model and basal model in Step (A) are respectively applied to compute the minimum and maximum synthesis rate for each metabolite. Such interval flux-sum are expressed as shown in Step (B):

Minimum/Maximum flux-sum for each metabolite of cancer cell:

 $\left[r_{m,\min}^{CA}, r_{m,\max}^{CA}\right]$ 

Minimum/Maximum flux-sum for each metaboliteof basal cell:

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\left[r_{m,\min}^{BL}, r_{m,\max}^{BL}\right]
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Minimum/Maximum flux-sum for each metabolite of the i<sup>th</sup> mutant:  $\left[r_{m,\min}^{MU}, r_{m,\max}^{MU}\right]_{i}$ 

 Using interval arithmetic, log2 interval fold changes of the template and mutants are computed as shown in Step (C):

Differentiall Expression Flux-Sum	Differentiall Expression Flux-Sum
of the template:	of each mutant:
$\begin{bmatrix} \mathbf{LFC}_{m}^{CABL} \end{bmatrix} = \begin{bmatrix} LFC_{m,\min}^{CABL}, LFC_{m,\max}^{CABL} \end{bmatrix}$	$\left[\mathbf{LFC}_{m}^{MUBL}\right]_{i} = \left[LFC_{m,\min}^{MUBL}, LFC_{m,\max}^{MUBL}\right]_{i}$

• The computation and definition of the interval arithmetic are expressed as follows:

# Computation of log2 interval fold changes of the template and mutants

• From Step (B), we have the interval flux-sum of each metabolite for cancer, basal and each mutant



• The interval fold changes of the template and each mutants are computed by interval arithmetic as

The interval fold change of the template:

$$\left[CABL_{m,\min}, CABL_{m,\max}\right] = \left[\min\left\{\frac{r_{m,\min}^{CA}}{r_{m,\min}^{BL}}, \frac{r_{m,\min}^{CA}}{r_{m,\max}^{BL}}, \frac{r_{m,\max}^{CA}}{r_{m,\min}^{BL}}, \frac{r_{m,\max}^{CA}}{r_{m,\max}^{BL}}\right\}, \max\left\{\frac{r_{m,\min}^{CA}}{r_{m,\min}^{BL}}, \frac{r_{m,\min}^{CA}}{r_{m,\max}^{BL}}, \frac{r_{m,\max}^{CA}}{r_{m,\max}^{BL}}, \frac{r_{m,\max}^{CA}}{r_{m,\max}^{BL}}\right\}\right]$$

The interval fold change of the  $i^{th}$  mutant:

$$\left[MUBL_{m,\min}, MUBL_{m,\max}\right]_{i} = \left[\min\left\{\frac{r_{m,\min}^{MU}}{r_{m,\min}^{BL}}, \frac{r_{m,\min}^{MU}}{r_{m,\max}^{BL}}, \frac{r_{m,\max}^{MU}}{r_{m,\min}^{BL}}, \frac{r_{m,\max}^{MU}}{r_{m,\max}^{BL}}\right\}, \max\left\{\frac{r_{m,\min}^{MU}}{r_{m,\min}^{BL}}, \frac{r_{m,\max}^{MU}}{r_{m,\max}^{BL}}, \frac{r_{m,\max}^{BL}}{r_{m,\max}^{BL}}, \frac{r_{m,\max}^{BL}}{r$$

# Computation of log2 interval fold changes of the template and mutants

• The log2 interval fold changes of the template and each mutant are obtained, respectively, as

Template:

$$\begin{bmatrix} \mathbf{LFC}_{m}^{CABL} \end{bmatrix} = \begin{bmatrix} LFC_{m,\min}^{CABL}, LFC_{m,\max}^{CABL} \end{bmatrix} = \log 2 \left( \begin{bmatrix} CABL_{m,\min}, CABL_{m,\max} \end{bmatrix} \right) = \begin{bmatrix} \log 2 \left( CABL_{m,\min} \right), \log 2 \left( CABL_{m,\max} \right) \end{bmatrix}$$
  
i<sup>th</sup> mutant:  
$$\begin{bmatrix} \mathbf{LFC}_{m}^{MUBL} \end{bmatrix}_{i} = \begin{bmatrix} LFC_{m,\min}^{MUBL}, LFC_{m,\max}^{MUBL} \end{bmatrix}_{i} = \log 2 \left( \begin{bmatrix} MUBL_{m,\min}, MUBL_{m,\max} \end{bmatrix}_{i} \right) = \begin{bmatrix} \log 2 \left( MUBL_{m,\min} \right), \log 2 \left( MUBL_{m,\max} \right) \end{bmatrix}_{i}$$

 Define the interval fuzzy membership function to be applied as a quantitative measure to determine how closeness of the mutant interval fold changes to the template.

Membership function

The user provides the lower and upper bounds of the left and right membership function:  $\int LEC^{CABL} + S \ LEC^{CABL} > 0$ 

$$LFC_{m,LB} = \begin{cases} LFC_{m,\min}^{CABL} / \delta, LFC_{m,\min}^{CABL} \ge 0\\ \delta LFC_{m,\min}^{CABL}, LFC_{m,\min}^{CABL} < 0 \end{cases}$$
$$LFC_{m,UB} = \begin{cases} LFC_{m,\max}^{CABL} / \delta, LFC_{m,\max}^{CABL} \le 0\\ \delta LFC_{m,\max}^{CABL}, LFC_{m,\max}^{CABL} > 0 \end{cases}$$
where  $\delta = 4$ 



# Evaluation of Interval Fuzzy Equal Membership Grade for each Mutant to the Template

• The interval left and right membership functions are defined as follows:

• The minimum and maximum values of interval left and right membership functions are computed by interval arithmetic as follows:

$$\begin{bmatrix} \eta_{m,\min}^{L}, \eta_{m,\max}^{L} \end{bmatrix}_{i} = \begin{bmatrix} \min\left\{\frac{\left(LFC_{m,\min}^{MUBL} - LFC_{m,LB}\right)}{\left(LFC_{m,\min}^{CABL} - LFC_{m,LB}\right)}, \frac{\left(LFC_{m,\min}^{MUBL} - LFC_{m,LB}\right)}{\left(LFC_{m,\min}^{CABL} - LFC_{m,LB}\right)}, \frac{\left(LFC_{m,\max}^{MUBL} - LFC_{m,LB}\right)}{\left(LFC_{m,\min}^{CABL} - LFC_{m,LB}\right)}, \frac{\left(LFC_{m,\max}^{MUBL} - LFC_{m,LB}\right)}{\left(LFC_{m,\max}^{CABL} - LFC_{m,LB}\right)}, \frac{\left(LFC_{m,\max}^{MUBL} - LFC_{m,LB}\right)}{\left(LFC_{m,\max}^{Rax} - LFC_{m,LB}\right)}, \frac{\left(LFC_{m,\max}^{Rax} - LFC_{m,LB}\right)}{\left(LFC_{m,\max}^{Rax} - LFC_{m,RB}\right)}, \frac{\left(LFC_{m,\max}^{Rax} - LFC_{m,RB}\right)}{\left(LFC_{m,\max}^{Rax} - LFC_{m,RB}\right)}, \frac{\left(LFC_{m,RB}^{Rax} - LFC_{m,RB}\right)}{\left(LFC_{m,RB}^{Rax} - LFC_{m,RB}\right)}, \frac{\left(LFC_{m,RB}^{Rax} - LFC_{m,RB}\right)}{\left(LFC_{m,R$$

# Evaluation of Interval Fuzzy Equal Membership Grade for each Mutant to the Template

The interval membership grade for each metabolite of the i<sup>th</sup> mutant is defined as

$$\mathbf{\eta}_{m} ]_{i} = \left[ \max \left\{ \min \left\{ \left( \begin{bmatrix} \mathbf{\eta}_{m}^{L} \end{bmatrix}, \begin{bmatrix} \mathbf{\eta}_{m}^{R} \end{bmatrix}, 1 \right) \right\}, 0 \right\} \right]$$
$$= \left[ \eta_{m,\min}, \eta_{m,\max} \right]$$
$$= \left[ \max \left\{ \min \left( \eta_{m,\min}^{L}, \eta_{m,\min}^{R}, 1 \right), 0 \right\}, \\ \max \left\{ \min \left( \eta_{m,\max}^{L}, \eta_{m,\max}^{R}, 1 \right), 0 \right\} \right]$$

 The interval decision grade for the genome-scale metabolic net of the i<sup>th</sup> mutant is defined as

$$\left[\mathbf{\eta}_{E}\right]_{i} = \left[\eta_{E,\min}, \eta_{E,\max}\right]_{i} = \left[\frac{1}{M}\sum_{m=1}^{M}\eta_{m,\min}, \frac{1}{M}\sum_{m=1}^{M}\eta_{m,\max}\right]_{i}$$

- The interval decision grade can be applied as a quantitative measure to determine how much closeness of each mutant to the template.
- The center and radius of the interval decision grade are defined as

$$Center = \frac{\eta_{E,\min} + \eta_{E,\max}}{2}$$
$$Radius = \frac{\eta_{E,\max} - \eta_{E,\min}}{2}$$

#### Definition of Computation of Interval Numbers

- Suppose that two intervals,  $[C] = [C_{min}, C_{max}]$  and  $[B] = [B_{min}, B_{max}]$
- Subtraction:  $[C] [B] = [C_{\min} B_{\max}, C_{\max} B_{\min}]$
- Addition:  $[C] + [B] = [C_{\min} + B_{\min}, C_{\max} + B_{\max}]$

• Multiplication: 
$$[C]*[B] = \begin{bmatrix} \min\{C_{\min}B_{\min}, C_{\min}B_{\max}, C_{\max}B_{\min}, C_{\max}B_{\min}, C_{\max}B_{\max}\}, \\ \max\{C_{\min}B_{\min}, C_{\min}B_{\max}, C_{\max}B_{\min}, C_{\max}B_{\min}, C_{\max}B_{\max}\} \end{bmatrix}$$

• Division: 
$$[C]/[B] = \begin{bmatrix} \min\{C_{\min} / B_{\min}, C_{\min} / B_{\max}, C_{\max} / B_{\min}, C_{\max} / B_{\max}\}, \\ \max\{C_{\min} / B_{\min}, C_{\min} / B_{\max}, C_{\max} / B_{\min}, C_{\max} / B_{\max}\} \end{bmatrix}, 0 \notin [B]$$

- 1. Arnold Kaufmann and Madan M. Guta, Introduction to Fuzzy Arithmetic: Theory and Application, Van Nostrand Reinhold, 1991
- 2. Eduardo Massad, Laécio Carvalho de Barr, Neli Regina Siqueira Ortega and Claudio José Struchiner, Fuzzy Logic in Action: Applications in Epidemiology and Beyond, Springer, 2008
- 3. Hang Zettervall, Fuzzy set theory applied to make medical prognoses for cancer patients, Doctoral Dissertation, Blekinge Institute of Technology, Sweden, 2014

#### Example: Evaluation of Interval Membership Grades

 Suppose that a toy metabolic network consisted of 7 metabolites, and their synthesis rates for the normal model, cancer model and two mutant models are computed by FSVA

Flux Pattern by FSVA								
	Basal		Cancer		Mutant 1		Mutant 2	
	$BL_{min}$	$BL_{max}$	$CA_{min}$	CA <sub>max</sub>	$\mathrm{MU}_{\mathrm{1,min}}$	$\mathrm{MU}_{\mathrm{1,max}}$	MU <sub>2,min</sub>	MU <sub>2,max</sub>
Metabolite 1	0.5	1	1.5	3	1.2	2.4	1	1.5
Metabolite 2	0.2	1.2	0.5	2	0.4	2.2	0.2	2
Metabolite 3	0.4	0.8	0.4	1.5	0.4	1.2	0.4	1
Metabolite 4	0.5	0.9	0.5	0.8	0.5	0.9	0.4	0.8
Metabolite 5	0.4	0.8	0.2	0.8	0.1	0.8	0.5	1
Metabolite 6	0.2	1.2	0.1	1	0.1	1.1	0.5	1.2
Metabolite 7	1	2	0.2	0.8	0.2	0.8	1	2

• Numerical example for log2 interval fold changes of the template and mutants:

Template:

$$\begin{bmatrix} \mathbf{LFC}_{m}^{CABL} \end{bmatrix} = \begin{bmatrix} LFC_{m,\min}^{CABL}, LFC_{m,\max}^{CABL} \end{bmatrix} = \log 2 \left( \begin{bmatrix} CABL_{m,\min}, CABL_{m,\max} \end{bmatrix} \right) = \begin{bmatrix} \log 2 \left( CABL_{m,\min} \right), \log 2 \left( CABL_{m,\max} \right) \end{bmatrix}$$
  
i<sup>th</sup> mutant:

$$\left[\mathbf{LFC}_{m}^{MUBL}\right]_{i} = \left[LFC_{m,\min}^{MUBL}, LFC_{m,\max}^{MUBL}\right]_{i} = \log 2\left(\left[MUBL_{m,\min}, MUBL_{m,\max}\right]_{i}\right) = \left[\log 2\left(MUBL_{m,\min}\right), \log 2\left(MUBL_{m,\max}\right)\right]_{i}\right]_{i}$$

	Template		Muta	ant 1	Mutant 2	
	$LFC_{m,\min}^{CABL}$	$LFC_{m,\max}^{CABL}$	$LFC_{m,\min}^{MUBL}$	$LFC_{m,\max}^{MUBL}$	$LFC_{m,\min}^{MUBL}$	$LFC_{m,\max}^{MUBL}$
Metabolite 1	0.585	2.585	0.263	2.263	0	1.585
Metabolite 2	-1.263	3.3219	-1.585	3.4594	-2.585	3.3219
Metabolite 3	-1	1.9069	-1	1.585	-1	1.3219
Metabolite 4	-0.848	0.6781	-0.848	0.848	-1.1699	0.6781
Metabolite 5	-2	1	-3	1	-0.6781	1.3219
Metabolite 6	-3.585	2.3219	-3.585	2.4594	-1.263	2.585
Metabolite 7	-3.3219	-0.3219	-3.3219	-0.3219	-1	1

#### The lower and upper bound of membership functions

The user provides the lower and upper bounds of the left and right membership function:

$$LFC_{m,LB} = \begin{cases} LFC_{m,\min}^{CABL} / \delta, LFC_{m,\min}^{CABL} \ge 0\\ \delta LFC_{m,\min}^{CABL}, LFC_{m,\min}^{CABL} < 0 \end{cases}$$
$$LFC_{m,UB} = \begin{cases} LFC_{m,\max}^{CABL} / \delta, LFC_{m,\max}^{CABL} \le 0\\ \delta LFC_{m,\max}^{CABL}, LFC_{m,\max}^{CABL} > 0 \end{cases}$$

where  $\delta = 2$ 

	LFC <sub>m,LB</sub>	$LFC_{m,\min}^{CABL}$	$LFC_{m,\max}^{CABL}$	LFC <sub>m,UB</sub>
Metabolite 1	0.293	0.585	2.585	5.17
Metabolite 2	-2.526	-1.263	3.322	6.644
Metabolite 3	-2	-1	1.907	3.814
Metabolite 4	-1.696	-0.848	0.848	1.696
Metabolite 5	-4	-2	1	2
Metabolite 6	-13.814	-6.907	2.322	4.644
Metabolite 7	-6.644	-3.322	-0.322	-0.161

• Numerical example for interval membership function values of mutants: Interval left membership function,  $[\eta_m^L]_i$ :

$$\begin{bmatrix} \mathbf{\eta}_{m}^{L} \end{bmatrix}_{i} = \begin{bmatrix} \eta_{m,\min}^{L}, \eta_{m,\max}^{L} \end{bmatrix}_{i} = \frac{[\mathbf{LFC}_{m}^{MUBL}]_{i} - LFC_{m,LB}}{[\mathbf{LFC}_{m}^{CABL}] - LFC_{m,LB}}$$
  
Interval right membership function,  $\begin{bmatrix} \mathbf{\eta}_{m}^{R} \end{bmatrix}_{i}$ :
$$\begin{bmatrix} \mathbf{\eta}_{m}^{R} \end{bmatrix}_{i} = \begin{bmatrix} \eta_{m,\min}^{R}, \eta_{m,\max}^{R} \end{bmatrix}_{i} = \frac{LFC_{m,UB} - [\mathbf{LFC}_{m}^{MUBL}]_{i}}{LFC_{m,UB} - [\mathbf{LFC}_{m}^{CABL}]}$$

	Mutant 1			Mutant 2				
	$\eta^{\scriptscriptstyle L}_{\scriptscriptstyle m,\min}$	$\eta^{\scriptscriptstyle L}_{\scriptscriptstyle m,\max}$	$\eta^{\scriptscriptstyle R}_{\scriptscriptstyle m, \min}$	$\eta^{\scriptscriptstyle R}_{\scriptscriptstyle m,\max}$	$\eta^{\scriptscriptstyle L}_{\scriptscriptstyle m,\min}$	$\eta^{\scriptscriptstyle L}_{\scriptscriptstyle m,\max}$	$\eta^{\scriptscriptstyle R}_{\scriptscriptstyle m,\min}$	$\eta^{\scriptscriptstyle R}_{\scriptscriptstyle m,\max}$
Metabolite 1	-0.1007	6.7374	0.634	1.8982	-1	4.419	0.7819	2
Metabolite 2	0.1609	4.739	0.4027	2.4771	-0.0466	4.6301	0.4201	2.7782
Metabolite 3	0.256	3.585	0.463	2.5244	0.256	3.3219	0.5176	2.5244
Metabolite 4	0.3572	3	0.2305	3.2506	0.2216	2.7996	0.3076	3.7254
Metabolite 5	0.2	2.5	0.25	5	0.6644	2.661	0.1695	2.6781
Metabolite 6	0.3777	2.686	0.2655	3.544	0.6223	2.7211	0.2502	2.544
Metabolite 7	0.5255	1.9031	0.0509	19.6377	0.8927	2.301	-7.2126	5.2126

• The interval membership grade for each metabolite

$$\begin{bmatrix} \mathbf{\eta}_{mn} \end{bmatrix}_{i} = \begin{bmatrix} \max\left\{\min\left\{\left(\begin{bmatrix} \mathbf{\eta}_{m}^{L} \end{bmatrix}, \begin{bmatrix} \mathbf{\eta}_{m}^{R} \end{bmatrix}, 1\right)\right\}, 0\right\} \end{bmatrix}$$
$$= \begin{bmatrix} \eta_{m,\min}, \eta_{m,\max} \end{bmatrix}$$
$$= \begin{bmatrix} \max\left\{\min\left(\eta_{m,\min}^{L}, \eta_{m,\min}^{R}, 1\right), 0\right\}, \\ \max\left\{\min\left(\eta_{m,\max}^{L}, \eta_{m,\max}^{R}, 1\right), 0\right\} \end{bmatrix}$$

	Muta	ant 1	Mutant 2		
	$\eta_{m,min}$	$\eta_{m,max}$	$\eta_{m,min}$	$\eta_{m,max}$	
Metabolite 1	0	1	0	1	
Metabolite 2	0.1609	1	0	1	
Metabolite 3	0.256	1	0.256	1	
Metabolite 4	0.2305	1	0.2216	1	
Metabolite 5	0.2	1	0.1695	1	
Metabolite 6	0.2655	1	0.2502	1	
Metabolite 7	0.0509	1	0	1	
[η <sub>ε</sub> ] <sub>i</sub>	0.1663	1	0.1282	1	
Center	0.5	831	0.5	641	
Radius	0.4	169	0.4359		

$$\begin{bmatrix} \mathbf{\eta}_E \end{bmatrix}_i = \begin{bmatrix} \eta_{E,\min}, \eta_{E,\max} \end{bmatrix}_i$$
$$= \begin{bmatrix} \frac{1}{M} \sum_{m=1}^M \eta_{m,\min}, \frac{1}{M} \sum_{m=1}^M \eta_{m,\max} \end{bmatrix}$$
$$Center = \frac{\eta_{E,\min} + \eta_{E,\max}}{2}$$
$$Radius = \frac{\eta_{E,\max} - \eta_{E,\min}}{2}$$