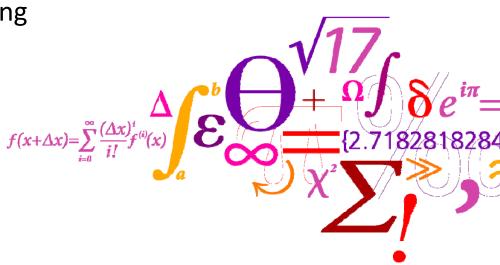


L4_1 Morris Screening for sensitivity analysis

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DTU Kemiteknik
Institut for Kemiteknik



Agenda

9:00-12:00	L4.1 Morris Screening
	Exercises
Lunch break	
1:00-4:00	Catch up with exercises
	Free time with instructors



Objective of this lecture

- At the end of the lecture, you should be able to:
 - Perform sensitivity analysis using Morris Screening on a simple model
 - Apply the method and Interpret the results on a slightly complex model



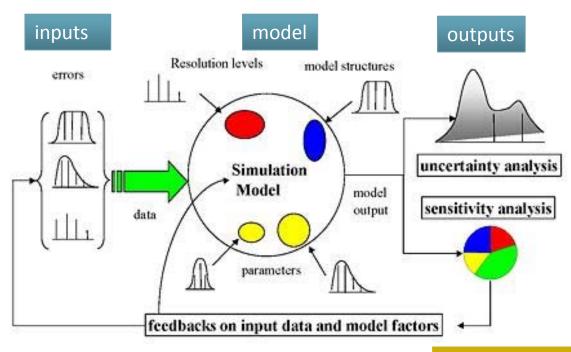
Outline

- On sensitivity analysis (recall)
- Morris method
 - Elementary effects (EE)
 - Morris sampling
- Case study: Morris method in batch fermentation models
- Example: Oxygen Uptake Rate (OUR)
- Exercise: Simple fermentation model



Sensitivity analysis – a definition

Sensitivity analysis "studies how variation (uncertainty) in the outputs of a model can be apportioned to different sources in the input of a model" SA complimentary to uncertainty analysis: "quantifying uncertainty in the outputs of a model from uncertainty in its inputs"





Sensitivity analysis – practices

SA may be used for a number of purposes:

- 1. Identify critical region in the input space of a model
- 2. Establish research priorities (by knowing to which inputs the model response is the most sensitive)
- 3. Debugging model coding errors (detecting a non-important parameter as important)
- 4. Simplify models / test hypothesis
- 5. ..

Sensitivity analysis – Putting Morris method in context



A number of methods available each with its own advantages/drawbacks

- Local methods
 - Derivative based, One-factor-at-A-Time (OAT), ...
 - Local measure: small perturbation around base value
 - Hence the analysis is locally bounding, not extrapolative!
- Global methods
 - Regression, variance-based, ...
 - May be computationally demanding

Morris method (1991):

Combines advantages of the two: Performs local sensitivity
 calculations in a global context (thanks to special sampling method)

Morris method (Morris, 1991) – Elementary effects (EE)



Let us take a model of the form:

$$\frac{d\mathbf{x}}{d\mathbf{t}} = \mathbf{f}(\mathbf{x}, \mathbf{\theta}, \mathbf{u}, t); \quad \mathbf{x}(0) = \mathbf{x}_0$$
$$\mathbf{y} = \mathbf{g}(\mathbf{x}, \mathbf{\theta}, \mathbf{u}, t)$$

The elementary effect of the ith input factor, θ_i , in a point θ^0 (input space):

$$EE_{i}^{0} = \frac{y(\theta_{1}^{0}, \theta_{2}^{0}, \theta_{i}^{0} + \Delta, \dots, \theta_{m}^{0}) - y(\theta^{0})}{\Delta}$$

$$\theta_{2}$$

$$(\theta_{1}^{0}, \theta_{2}^{0}) \quad (\theta_{1}^{0} + \Delta, \theta_{2}^{0})$$

Note: it is hard to visualize mdimensional input space. Take a 2-D input space as an example!





Each input assumed to vary across *p* levels (discretized approach):

For
$$\theta_i \sim U(0,1) \& p = 4 \rightarrow p_1 = 0$$
, $p_2 = 1/3$, $p_3 = 2/3$ and $p_4 = 1$

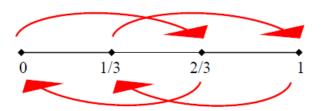
Optimal choice of perturbation coefficient, Δ , depends on the levels:

$$\Delta = p / 2(p-1)$$
 (E.g. for $p = 4$, $\Delta = 2/3$)

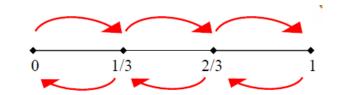
Morris method (Morris, 1991) -am Concept of elementary effects (EE)



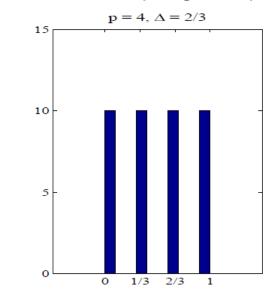
The choice of perturbation factor: Δ is optimal when $\Delta = p / 2(p-1)$

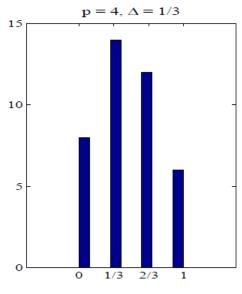


Uniform sampling of input



Not-uniform sampling of input





Histogram



The Morris sampling

EEi is still a local measure, so?

Solution: take the average of several EEi!

Morris suggests calculations of EEi at randomly selected points in the input space (m-dimensional p-level grid) and to approximate the distribution of elementary effects, Fi.

To this end, Morris performs EEi calculations *r* times following an efficient randomized sampling scheme (see Morris Sampling, 1991). *r* is chosen in the range of 5-10.

$$EE_{i}^{r} = \frac{y(\theta_{1}^{r}, \theta_{2}^{r}, \theta_{i}^{r} + \Delta, \dots \theta_{m}^{r}) - y(\mathbf{\theta}^{r})}{\Delta}$$

$$\theta_{2}$$

$$\theta^{1}$$

$$\theta^{2}$$

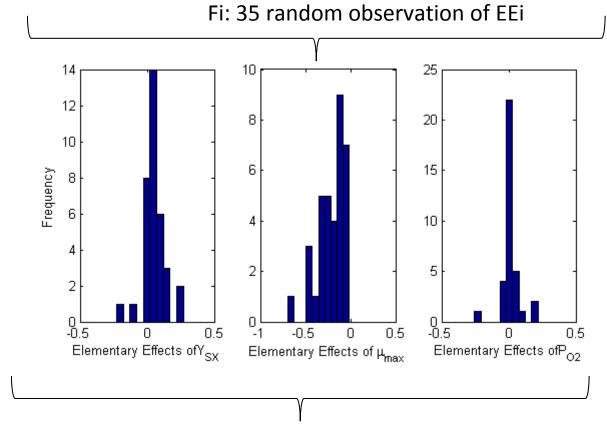
$$\theta^{r}$$

$$\theta^{r}$$



Interpretation of Morris method

The distribution of elementary effects of model inputs on the model outputs,



Analyse & compare the mean and standard deviation of these distributions. Higher mean and higher standard deviation of FEEi indicates strong sensitivity!



The Morris sampling

Low computational cost: *Morris requires only* $r^*(k+1)$ *model evaluations*

Example:

For k = 10 parameters, Fractional factorial design at 2 levels \rightarrow 2¹⁰ = 1024 Morris sampling = 10*(10+1) = 110

For k = 20 parameters, FF design at 2 levels
$$\rightarrow$$
 2²⁰ = 1048576
Morris sampling \rightarrow 10*(20+1) = 210



Morris method – the extended

To enable comparison of the elementary effects on different model outputs, y_j , a relative measure of elementary effects is needed (where j >2)

A possible relative measure is obtained by sigma-scaling:

$$SEEij = EEij \frac{\sigma_{xi}}{\sigma_{yj}}$$



Case study: Application of Morris method to fermentation models

S. COELICOLOR CULTIVATION FOR ANTIBIOTIC PRODUCTION



Morris method: methodology

Morris sampling for EEi

Step 1. Specify range for each input parameter

Step 2. Morris Sampling

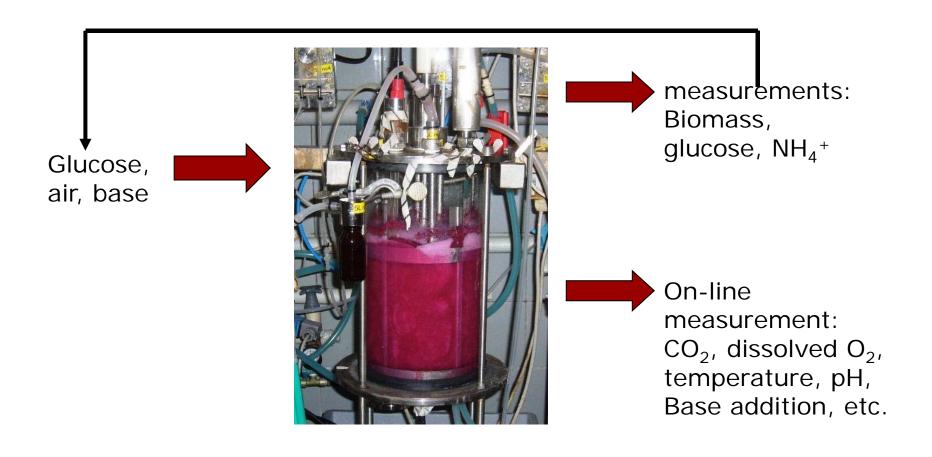
Step 3. Model evaluations of Morris samples

Step 4. Compute and plot elementary effects (EEi)

Step 5. Rank parameters according to μi & σi (Morris) or absolute μi* (Saltelli)

Case study: Batch cultivation of *S. coelicolor* for antibiotic production





Matrix, model of S. coelicolor fermentation

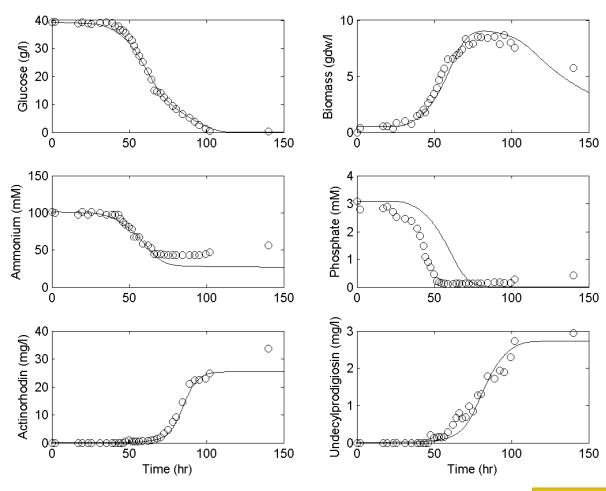


							Liquid phase										Gas phase			
	Components → i	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	
	Name	Glucose	Oxygen	Ammonia	Phosphate	Biomass	Antibiotic 1	Antibiotic 2	Carbon dioxide	Hydrogen ion	Ammonium	Phosphate	Bicarbonate	Hydroxyl ion	Nitrogen	Oxygen	Carbon dioxide	Nitrogen	Ammonia	Rates
	Symbol	Sg	S_0	SNH	S_{PO}	X	S_{P1}	S _{P2}	S ₀₀₂	$S_{\mathbf{H}}$	S _{NH4}	S _{HPO4}	S _{HCO3}	Som	S _{N2}	Go	G ₀₀₂	G _{N2}	G _{NH3}	
	Chemical composition	C ₆ H ₁₂ O ₆	O ₂	NH ₃	H ₂ PO ₄	CH1 xO0 5N0 2P0.015	C32H26O14	C25H35N3O	CO ₂	H*	NH.*	HPO4-2	HCO ₂	OH	N_2	O ₂	CO ₂	N ₂	NH ₃	
j	Processes (Units)	C-mmol/l	O-mmol/I	N-mmol/l	P-mmol/l	C-mmolf	C-mmol/l	C-mmol/l	C-mmol/I	H-mmol/l	N-mmol/l	P-mmol/l	C-mmol/l	H-mmol/l	N-mmol/l	O-mmol/I	C-mmol/l	N-mmol/l	N-mmol/l	mmo/l-d
	Biomass growth																			Lance 1 Sr So Shorts Sro to
1		-1/Y _{SX}	$\gamma_{\rm X}/4.0 - \gamma_{\rm S}/(Y_{\rm SX}*4.0)$	-İve	-İpx	1			1/Y _{SX} - 1	-İpx										$\mu^{\text{mer}} = \frac{1}{1 + \sigma^{2} - r^{2}} \frac{S_{g}}{S_{g} + K_{g}} \frac{S_{O}}{S_{O} + K_{O}} \frac{S_{MIS}}{S_{MIS} + K_{MIS}} \frac{S_{FO}}{S_{FO} + K_{FO}} X$
	Actinorhodin		70 to 00 to 00	140																
2		-1/Yexer	γ _{ACT} /4.0 - γS/(Y _{SACT} *4.0)				1		1/Yever-1											$\alpha_{ACT} \cdot r_X + \beta_{ACT} \cdot \left(1 - \frac{S_{ACT}}{S_{ACT}^{max}}\right) \left(\frac{S_g}{K_g + S_g} \frac{K_B}{K_B + S_{FQ}}\right) X$
	production	- II SACI	ACITIO PORTSACT TO			Equa	_ + : .		IT SALL I		~: a		-							
3	production	1//	γ _{RED} /4.0 = γS/(Y _{SRED} *4.0)	i						НОІ		: 21	Or	OCE	-28	se				$\left(\alpha_{BBD} \cdot r_X + \beta_{BBD} \cdot \left(1 - \frac{S_{BBD}}{S_{BBD}^{max}}\right) \left(\frac{S_g}{K_S + S_g} \frac{K_D}{K_D + S_{FO}}\right) X\right)$
	Undecylprodiziosin	- IT I SKED	7KED/4.0 - 73/(1SKED 4.0)	"INRED					SILD		J.,		Γ.							
4	production	-1	44.0						4											$m_s = \frac{S_s}{S_s + K_s} \frac{S_o}{S_o + K_o} X$
	Biomass maintenance		-y ₅ /1.0																	
-	Biomass margenance		-nd4	W-000	Acres	4			4											$k_d \frac{S_0}{S_0 + K_0} \frac{K_5}{S_5 + K_5} X$
			- _{7X} ,14	INDIC	I _{PX}	61.1.			131	1pX										20 T 20 25 T 25
	Ammonium dissociation																			$k_{x,yy}S_{yyy} - \frac{k_{x,yy}}{2}S_{yyy}S_{yy}$
- 6				1						. 1	-1									Katt
	Dibydrogen phosphate																			$k_{f,H2F0i}S_{H3F0i} = \frac{k_{f,H3F0i}}{K_{H1AF0i}}S_{H00i} \cdot S_{H}$
7	dissociation				-1					-										Kinton arton Kinton
	Carbon dioxide															161				$k_{f,cos}S_{cos} - \frac{k_{f,cos}}{K_{Mos}}S_{Mos}S_{H}$
8	directation								-1	1			1							VACOTORS RESERVE
	Water dissociation																			A A A A A A A A A A A A A A A A A A A
9														4						$1 - \frac{E_{f,\Psi}}{K_{\Psi}}S_{H} \cdot S_{OH}$
	Aeration (Ozygen)																			$K_1 a_{02} \cdot (S_0^* - S_0)$
10			4													-1				C-11 - C-17
10	CO ₂ stripping															227				$K_{A}a_{CM} \cdot (S_{CM}^{*} - S_{CM})$
11							: .		-		4	0.10	-5-				2.4			-1-04 -05 -05
1.1	Nitrogen stripping					Equa				35		din	516	÷ [-1	*		$K_L a_{H_2} \cdot (S_{H_2}^* - S_{H_2})$
40	ron-Sear surphast														-					Wind war war
12	Ammonia stripping														1			-1		$K_{1}a_{son} \cdot (S_{son}^{*} - S_{son})$
680	Ammonia stripping			2.0															-	K_121013 (S1013 = S1013)
13			-		_													_		
in the state of th	tion matrix Units																			
Elements				-	_					_								_	_	
MW	g/C-mmol; g/N-mmol;	30.00	32.00	14.00	21.00	25.07	10.01	15.70	12.00	1.00	14.00	21.00	1.4	- v	14	32.00	12.00	14.00	14.00	
C	g/P-mmol C-mmol/mmol	1.00	0.00	14.00	31.00	25.07	19.81	15.72	12.00	1.00	14.00	31.00	14	0.00	0.00	32.00 0.00	12.00	0.00	14.00	
N	N-mmol/N-mmol	0.00	0.00	1.00	0.00		100°	Val	0.30-	6.0				S 0.00	1.00	0.00	0.00	1.00	1.00	
P	P-mmol/P-mmol	0.00	0.00	0.00	1.00	0.02	0.00	0.00	0.00	0.00	0.0	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
Y	mmol e/ C-mmol	4.00	-4.00	0.00	0.00	4.13	3.94	4.96	0.00	0.00	0.00	0.00	0	0.00	0	0.00	0.00	0.00	0.00	
Charge	mmol /mmol	0.00	0.00	0.00	-1.00	0.00	0.00	0.00	0.00	1.00	1.00	-2.00	-1.00	-1.00	0	0.00	0.00	0.00	0.00	

Many outputs (around 20) Many parameters (around 60) Sin et al. (2008). Biotechnol. Bioeng., 101:153-171



Model fits to measurements



Morris method for sensitivity analysis

Sin et al. (2008), Biotechnol. Bioeng., 101:153-171 19

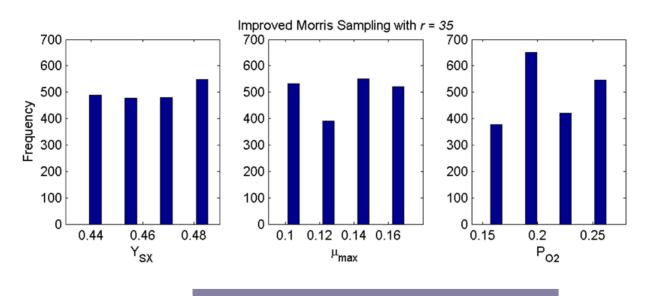


Morris method – sampling specifications

Morris method specifications:

$$p = 4$$
, $\Delta = 2/3$, $r = 35$, $k = 60$ (# number of parameters)

Total model evaluations = $r^*(k+1)$ = 2135

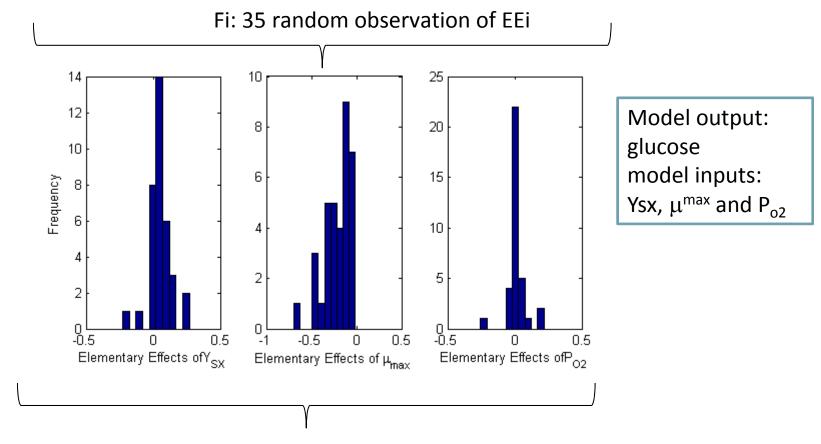


Morris sampling of 3 model parameters



Results – Typical outcome of Morris method

The distribution of elementary effects of model inputs on the model outputs,

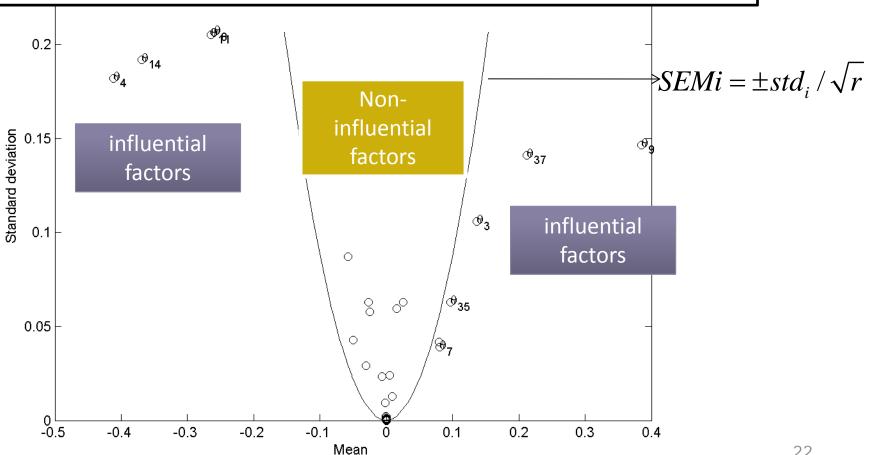


Analyse & compare the mean and standard deviation of these distributions

Results – typical results of Morris method

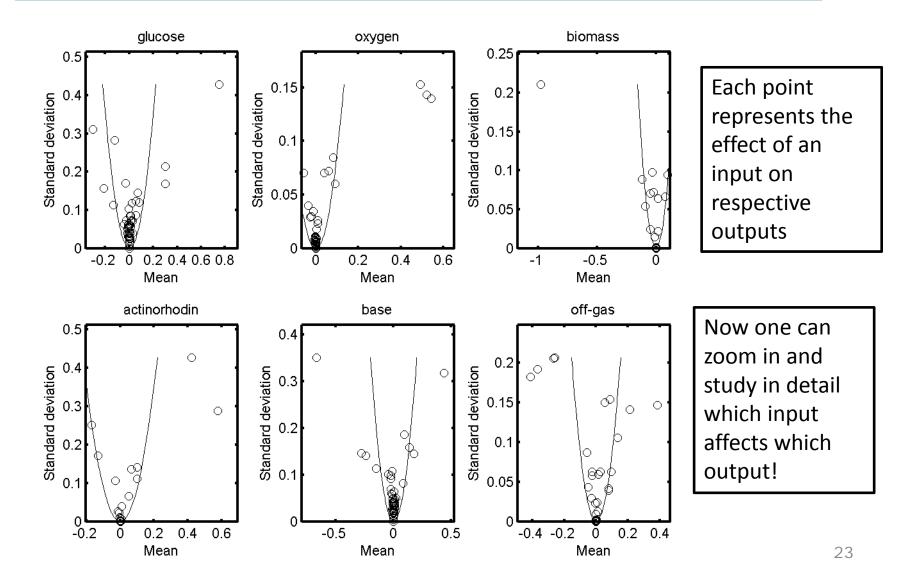


Example: Glucose as model output versus a total of 56 input factors Conclusion: 8 influential factors, the rest of the factors have insignificant contribution to the variation in glucose





Elementary effects of different model outputs





Comparison of extended Morris with Monte Carlo based regression method (SRC)

Table. Method comparison for screening influential factors: Model output glucose

	Morris Met	hod	Monte-Carlo based regression					
Rank	Input symbol	μ^*	Input symbol	SRC*				
1	i_{PX}	0.75	K_{P}	0.74				
2	$m_{\rm S}$	-0.30	$\mu_{ ext{max}}$	-0.65				
3	K_{P}	0.30	i_{PX}	0.61				
4	K_{S}	0.30	K_{S}	0.50				
5	$\mu_{ ext{max}}$	-0.21	m_S	-0.47				

Bottom line: Morris method agreed mostly (6/8) with the well established regression based method



Morris method for sensitivity analysis

EXAMPLE: AEROBIC GROWTH OF MICROORGANISMS



Morris method: methodology

Monte Carlo simulations + linear regression for sensitivity analysis

Step 1. Specify range for each input parameter

Step 2. Morris Sampling

Step 3. Model evaluations of Morris samples

Step 4. Compute and plot elementary effects (EEi)

Step 5. Rank parameters according to μi & σi (Morris) or absolute μi* (Saltelli)



step 1 to 2: Morris sampling results

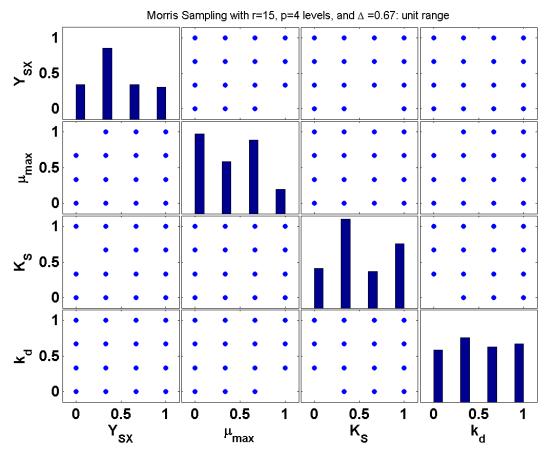
Matlab code (Morrissampling.m)

```
ourinit
pmor=par(1:4); % get the reference parameter values /we assume we dont
have any data for PE. otherwise we dont use Monte Carlo
lp = \{ 'Y_{SX} ', 'mu_{max} ', 'K_S', 'k_d' \};
inputunc=[0.05 0.10 0.25 0.25]; % expert input uncertainty indicates
degree of uncertainty [0: Low , 1: High]
k=length(pmor); % number of parameters
xl= pmor .* (ones(1,k)-inputunc);
xu= pmor .* (ones(1,k)+inputunc);
%% Morris sampling parameters
k = k; % no of parameters or factors
p = 4; % number of levels \{4,6,8\}
dt = p/(2*(p-1)); % perturbation factor.
r = 15; % number of repetion for calculating the EEi, e.g. 4 - 15
%% Morris sampling will produce discrete uniform probabilities for each
%% factor.
X = morris(p, dt, k, r);
Xmean = mean(X);
```



step 1 to 2: Morris sampling results

k=4 (parameters), p = 4 (levels), r = 15 (repetition), Δ =2/3, n= 75 (r*(k+1)



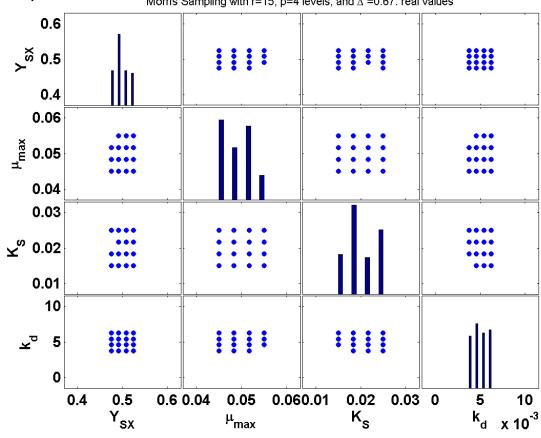
Morris method for sensitivity analysis



step 1 to 2: Morris sampling results

m=4 (parameters), p = 4 (levels), r = 15 (repetition), Δ =2/3, n = 75 (15*4+1) (# simulations)

Morris Sampling with r=15, p=4 levels, and Δ =0.67: real values





step 3: Model evaluations of Morris samples (raw data)

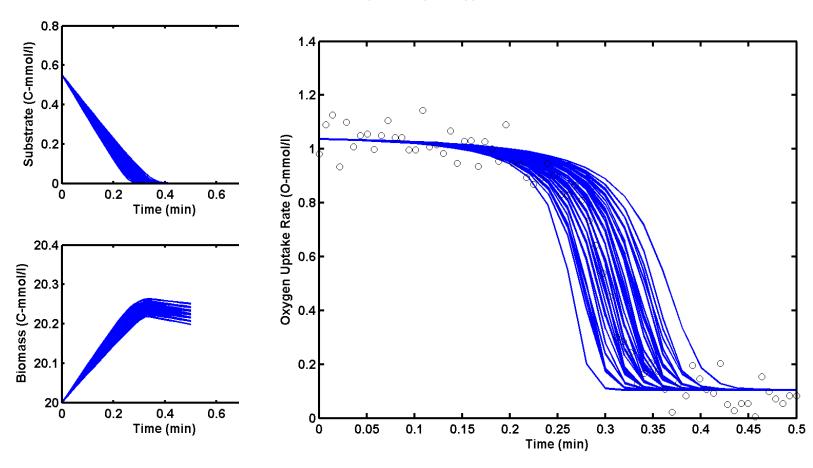
Matlab code (morrissim.m)

```
% load sampling matrix
load MorrisSampling r15 p4
[n m] = size(Xval);
% specify time (in hr) % initialize:
time = [0:(1/50):0.5];
ourinit
% run Morris simulations
for i=1:n
% update the uncertain parameters
par(1:4)=Xval(i,:);
%% Solution of the model
options=odeset('RelTol',1e-7,'AbsTol',1e-8);
[t,y] = ode45(@ourmod,time,x0,options,par);
%% calculate oyxgen uptake rate (0-mmol/l-min)
y1(:,i) = y(:,1);
y2(:,i) = y(:,2);
y3(:,i) = y(:,3);
end
```



step 3: Model evaluations of Morris samples (raw data)

Total number of simulations, n = 75 (=15*(4+1))



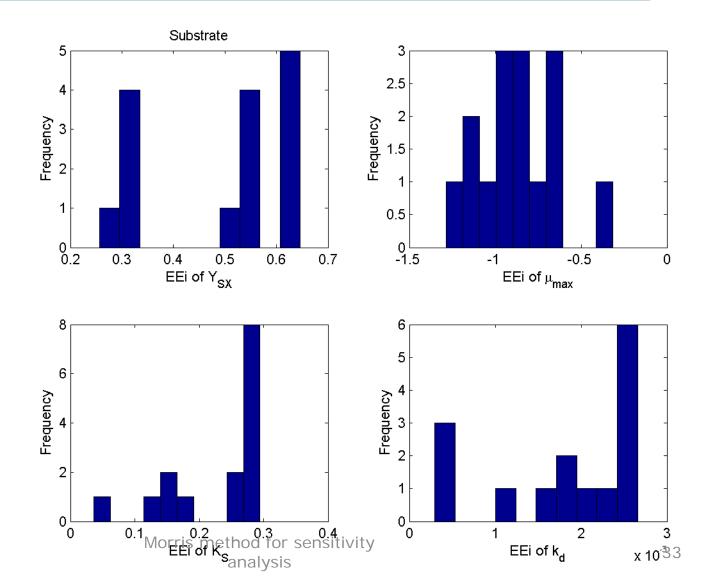


Matlab code: computeEEi.m

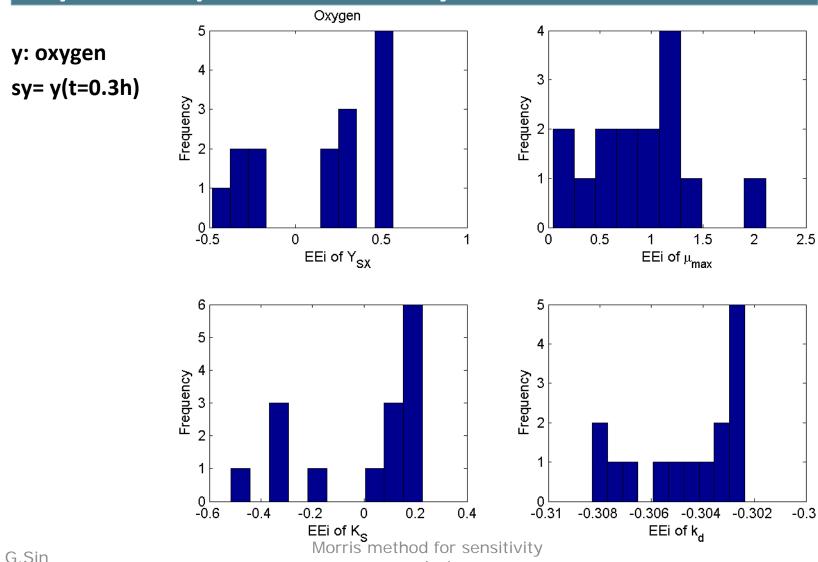
```
load MorrisSims r15 p4.mat
%% this method requires scalar outputs, y:
% hence one needs to specify a meaningful property of time-series data: Let us
focus on time=0.3 hr
ii = find(time == 0.3);
y1s = y1(ii,:); y2s = y2(ii,:); y3s = y3(ii,:); ours = our(ii,:);
%% compile an model output matrix
Sim = [y1s' y2s' y3s' ours']; [n k] = size(X); n = n / (k+1);
[mm ll] = size(Sim);
%% below info needed for sigma-scaling of EEi
siq_y = std(Sim);
siq x = std(Xval);
%% compute the corresponding Eei
for i=1:n
    for j=1:k
        m1 = (k+1)*(i-1);
        r1 = m1 + j;
        ix = find (X(r1,:) - X(r1+1,:)) ; % find the non-zero value
        if length(ix) > 1
            warning('there is more than one factor changed')
            return
        end
```



y: Substrate sy= y(t=0.3h)



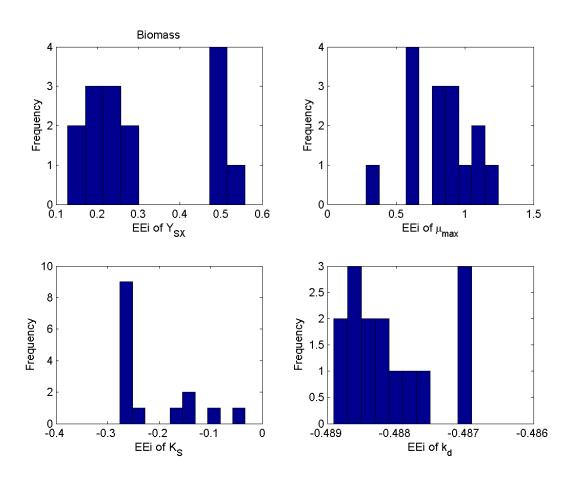




analysis



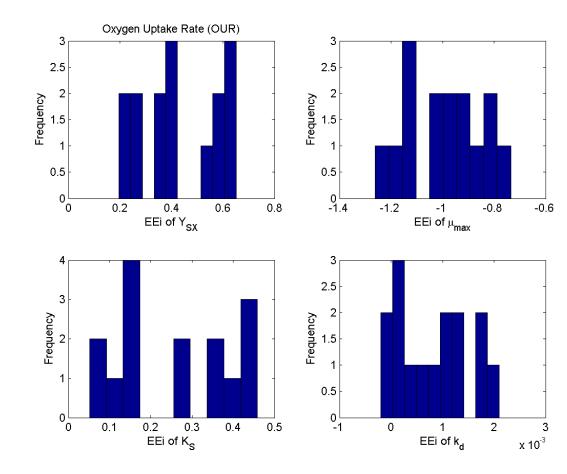
Y: biomass sy= y(t=0.3h)





y: our

sy = y(t=0.3h)



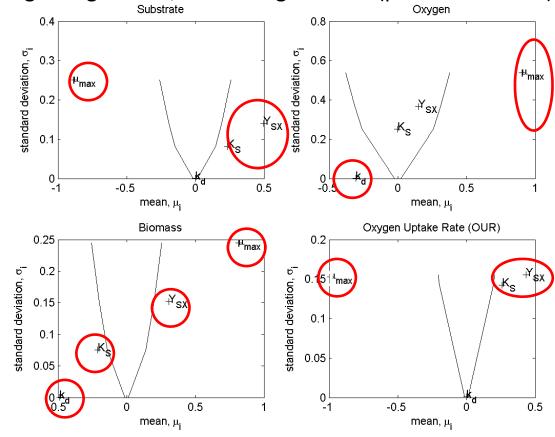


step 5: Rank parameter significance

Morris: consider standard error on the mean of EEi(sem). Use this to form a wedge! Parameters inside the wedge insignificant, outside significant. (plotmorrissim.m)

Positive:

- Visually appealing!
- consider the quality of estimating mean Eei
- •Combines info of mean and sigma of Eei Negative
- •Becomes cumbersome for models with many parameters!



Morris method for sensitivity analysis



step 5: Rank parameter significance

Saltelli: Focus on the absolute measure of the mean of EEi and rank them!

	Substrate	Rank*	Oxygen	Rank	Biomass	Rank	OUR	Rank
Y_{SX}	0.50	2	0.15	3	0.31	3	0.43	2
μ_{max}	-0.89	1	0.90	1	0.81	1	-0.99	1
K_{S}	0.23	3	0.00	4	-0.21	4	0.26	3
k_d	0.00	4	-0.30	2	-0.49	2	0.00	4

Positive:

• Helps ranking parameter importance with single measure!

Drawback:

•Ignores information in standard deviation



Quality check: compare the results of Morris with SRC or other SA methods

$$sy = y(t=0.3h)$$

	substrate		oxygen		biomass		our		
	Morris, μ_i	SRC	Morris, μ_i SRC		Morris, μ	SRC	Morris, μ_i SRC		
Y_{SX}	0.50	0.38	0.15	-0.14	0.31	0.47	0.43	0.36	
μ_{max}	-0.89	-0.85	0.90	0.85	0.81	0.79	-0.99	-0.89	
K_S	0.23	0.22	0.00	-0.03	-0.21	-0.21	0.26	0.16	
k_{d}	0.00	0.01	-0.30	-0.09	-0.49	-0.20	0.00	0.04	

Bottom line: The results of Morris and SRC agree well with each other with one exception (Ysx on Oxygen)! Empirical evidence that senstivity analysis results are reliable!



To sum up

Morris method allows screening of the importance of model parameters (inputs) on the outputs

It is robust wrt type II error (identifying a non-important parameter as important)

The original method considers one type of model output. The extended method is applicable to a model with many outputs (thanks to sigmascaling of EEi)

Recommended as efficient screening method prior to more detailed and computationally exhaustive methods, such as Sobol's variance decomposition.



Exercise 1: Repeat Morris method of sensitivity analysis

AEROBIC GROWTH OF MICROORGANISM



Exercise details

- Do the exercise individually
- Use the matlab scripts introduced earlier using the OUR example
- Follow the steps outlined above in the example (slide # 23)
- and learn by doing! For example to learn Morris sampling theory in detail, first read the accompanying paper and then check the morris code. you may do the following:
 - Open the morrissampling.m
 - Set r equal to 1. investigate the resulting samples (X and Xval)
 - Set r equal to 2. investigate the resulting samples (X and Xval)
 - In the same manner, change the p parameter to 6 and repeat above steps.
 - Write down the results on a paper and compare them with the theory of morris sampling (see the paper).



Exercise 1: Repeat Morris method of sensitivity analysis

SIMPLE FERMENTATION MODEL



Exercise details

- Do the exercise individually
- Use the matlab scripts introduced earlier using the OUR example, BUT this time use the fermentation model!
- Adopt the scripts if necessary for your exercise!
- Follow the steps outlined above in the example (slide # 23)
- and learn by doing!
- We will be around to help you out!....