

# Mechanism Reduction via Adjacency Matrix Power

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Mechanisms that matter are too large to simulate

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**We must reduce!**

# The Direct Relationship Graph Approach

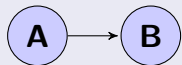
- Build graph from mechanism
- Reduce the graph (prune edges and vertexes)
- Simulate the corresponding reduced mechanism

# How do we build the graph?

Species A



$B + \_ \Rightarrow A + \_$



# How do we build the graph?

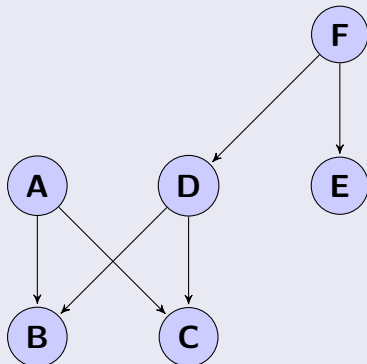
## Mechanism

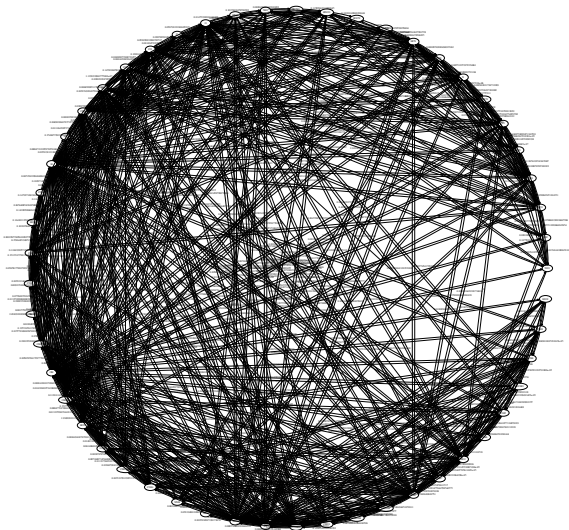
- $B + C \Rightarrow A + D$
- $D + E \Rightarrow F$

## Species

- A
- B
- C
- D
- E
- F

## Graph





- Given a mechanism build corresponding graph
- Reduce the graph (prune edges and vertexes)
- Simulate the corresponding reduced mechanism



# How to reduce?

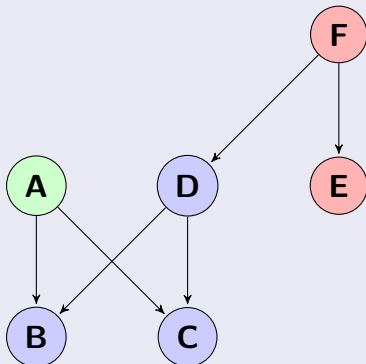
## Mechanism

- $B + C \Rightarrow A + D$
- $D + E \Rightarrow F$

## Species

- A
- B
- C
- D
- E
- F

## Graph



# How to reduce?

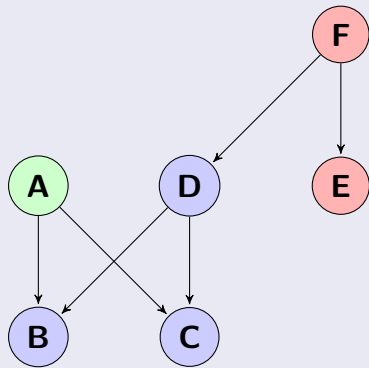
## Mechanism

- $B + C \Rightarrow A + D$
- $D + E \Rightarrow F$

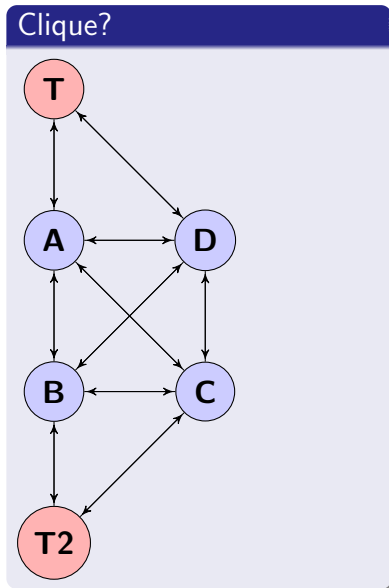
## Species

- A
- B
- C
- D
- E
- F

## Graph

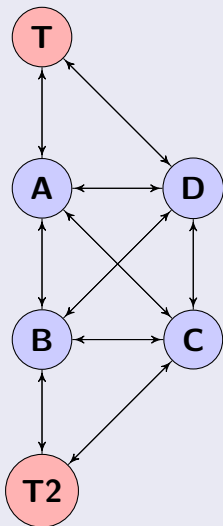


# How to reduce?

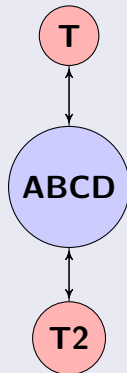


# How to reduce?

Clique?



Lump it!



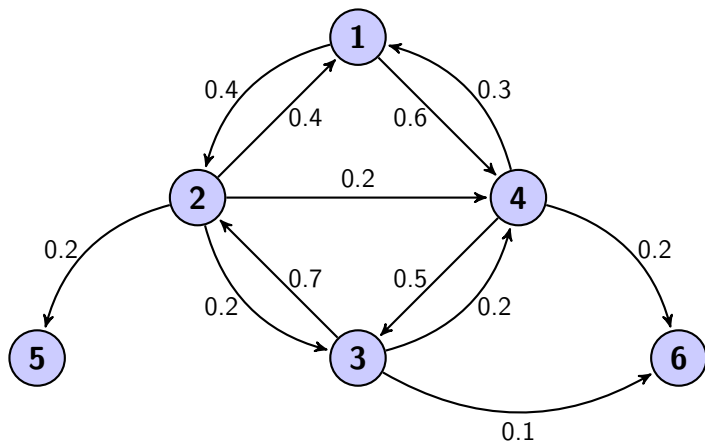
# How much effect on each other?

[Nyemeyer 2013, P. Pepiot-Desjardins and H. Pitsch, 2008]

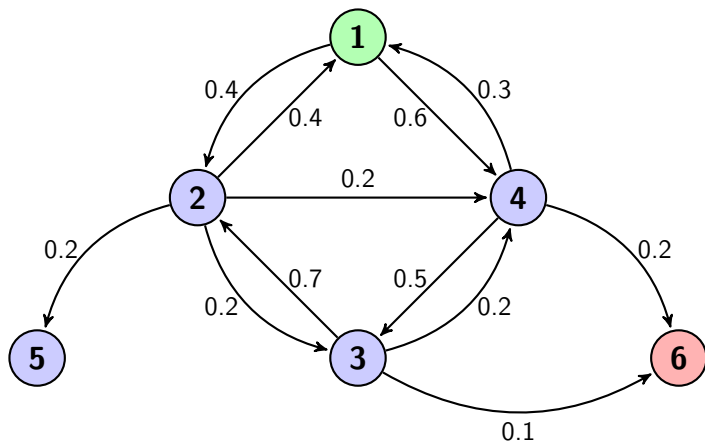
Production of A dependency on B?  $r_{AB} = \frac{|\sum_{i=1}^{N_R} V_{A,i} \omega_i \delta_B^i|}{\max(P_A, C_A)}$

- $N_R$  – # reactions
- $V_{A,i} = V''_{A,i} - V'_{A,i}$
- $V''$  – production stoichiometric coefficient
- $V'$  – consumption stoichiometric coefficient
- $\omega_i$  –  $i$ -esim reaction rate
- $\delta_B^i = 1$  if reaction  $i$  involves  $B$  and 0 otherwise
- $P_A = \sum_{i=1}^{N_R} \max(0, V_{A,i} \omega_i)$  – Production term
- $P_C = \sum_{i=1}^{N_R} \max(0, -V_{A,i} \omega_i)$  – Consumption term

# How much effect on each other?



# How much effect on each other?

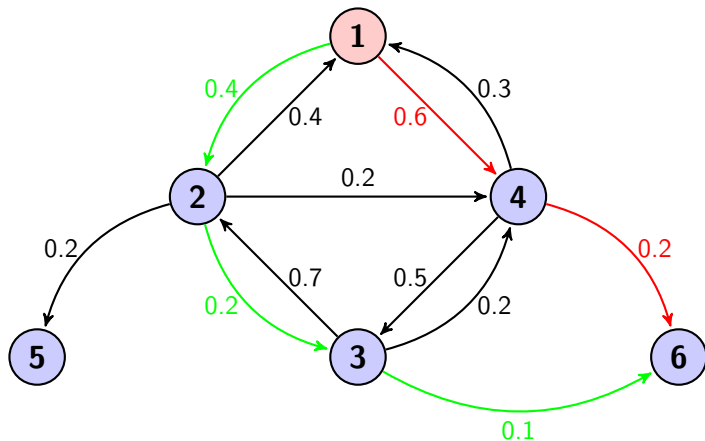


# How much effect on each other?

Use paths in the graph to find out!



# How much effect on each other?



# How to reduce?

Remove the least important reactions/species!

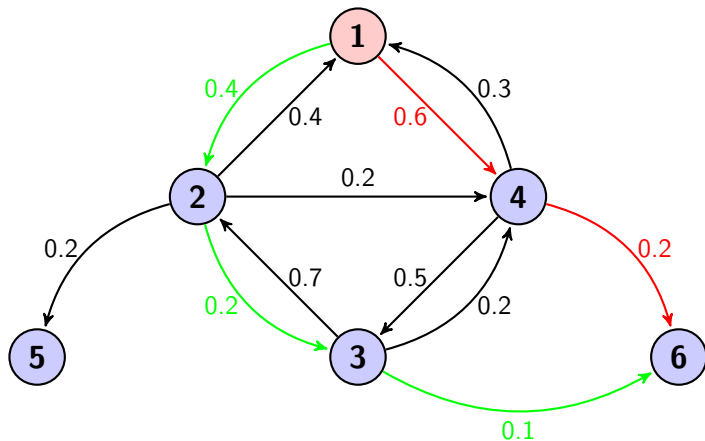
# How to reduce?

Remove the least important reactions/species!  
But which ones are less important?

- Most important path?
  - Biggest throughput?  
Throughput is smaller edge value
  - Longest path?  
Length is sum)  
DRG with Depth First Search
  - Biggest conditional dependency?  
Dependency is product  
DRG-EP with Dijkstra's shortest path

- Most important path?
  - Biggest throughput?  
Throughput is smaller edge value
  - Longest path?  
Length is sum)  
DRG with Depth First Search
  - Biggest conditional dependency?  
Dependency is product  
DRG-EP with Dijkstra's shortest path
- If not important overall, **prune**

# Problem with that?



- Most important path?
  - Biggest throughput?  
Throughput is smaller edge value
  - Longest path?  
Length is sum)  
DRG with Depth First Search
  - Biggest conditional dependency?  
Dependency is product  
DRG-EP with Dijkstra's shortest path
- Combination of **all** paths?

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  - Biggest throughput?  
Throughput is smaller edge value
  - Longest path?  
Length is sum)  
DRG with Depth First Search
  - Biggest conditional dependency?  
Dependency is product  
DRG-EP with Dijkstra's shortest path
- Combination of **all** paths?  $O(n!)$



Proposal: Use all paths of length  $X$ .  
Adjacency Matrix Power

# Adjacency Matrix Power

- All paths of size  $X$  are considered
- Large paths include small paths
- Weight is the product of edges' weights
- Multiplication is  $O(n^{2.373})$
- $x$ -esim power is  $\log(x) * O(n^{2.373})$

# Adjacency Matrix – M

Spc	1	2	3	4	5	6
1	0	0.4	0	0.6	0	0
2	0.4	0	0.7	0.2	0.2	0
3	0	0	0	0.2	0	0.1
4	0.3	0	0.5	0	0	0.2
5	0	0	0	0	0	0
6	0	0	0	0	0	0

Dependency of  $i$  on  $j$

- $M[i, j]$  – directly
- $M[i, k] * M[k, j]$  – via size 2 chain reactions, using  $k$
- $\sum_{k=1}^N M[i, k] * M[k, j] = M^2[i, j]$  – via all size 2 chain reactions
- $M^X[i, j]$  – via all size X chain reactions

# Now we prune!

Dependency factor (DF): how much target(s) depend(s) on species?

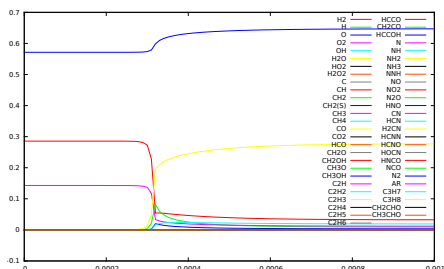
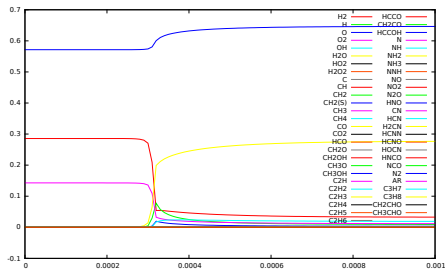
- Cut X% species with the smallest DF
- Cut species with DF smaller than given threshold
- **Sum DFs of reactants; cut X% reactions with smallest sums**
- Cut reactions with sum smaller than given threshold

# Implementation

- Cantera 2.7
- Boost Graph Library (BGL)
- Dijkstra (from BGL)
- Matrix Power (+ BLAS)
- Full
- Mostly qualitative results so far

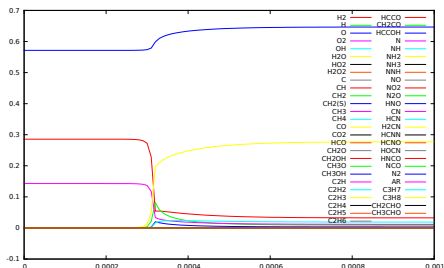
- GRI-MECH 3.0 (53 espécies e 325 reações)
- Initial concentrations: H<sub>2</sub>:2 O<sub>2</sub>:1 N<sub>2</sub>:4
- 1atm
- 1000K
- Prune 25% and 65% less important reactions
- Cut (reactions involving) 25% and 65% less important species

# Cut 25% less important reactions



Dijkstra

Matrix Power



Full Mechanism

# Mean Squared Error – Full

## Dijkstra

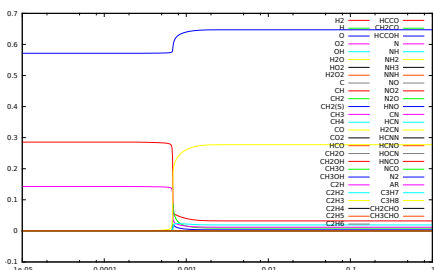
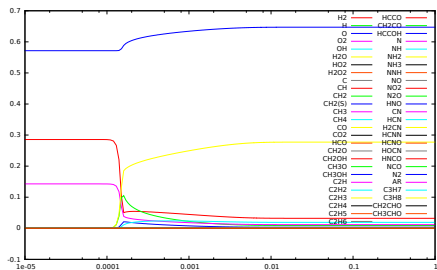
Temperature (K) Density (kg/m3) Pressure (Pa) H2 H O O2 OH H2O HO2 H2O2 C CH CH2 CH2(S) CH3 CH4 CO CO2 HCO  
CH2O CH2OH CH3O CH3OH C2H C2H2 C2H3 C2H4 C2H5 C2H6 HCCO CH2CO HCCOH N NH NH2 NH3 NNH NO NO2  
N2O HNO CN HCN H2CN HCNN HCNO HOCN HNCO NCO N2 AR C3H7 C3H8 CH2CHO CH3CHO  
20.802958 0.001068 0.000000 0.002150 0.001403 0.000382 0.000963 0.000452 0.002752 0.000001 0.000001 0.000000 0.000000  
0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000024  
0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.001077 0.000000  
0.000000 0.000000 0.000000 0.000000

## Matrix

Temperature (K) Density (kg/m3) Pressure (Pa) H2 H O O2 OH H2O HO2 H2O2 C CH CH2 CH2(S) CH3 CH4 CO CO2 HCO  
CH2O CH2OH CH3O CH3OH C2H C2H2 C2H3 C2H4 C2H5 C2H6 HCCO CH2CO HCCOH N NH NH2 NH3 NNH NO NO2  
N2O HNO CN HCN H2CN HCNN HCNO HOCN HNCO NCO N2 AR C3H7 C3H8 CH2CHO CH3CHO  
16.840980 0.000608 0.000000 0.000807 0.000971 0.000334 0.000518 0.000412 0.001916 0.000001 0.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000  
0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000465  
0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000000 0.000820 0.000000  
0.000000 0.000000 0.000000 0.000000

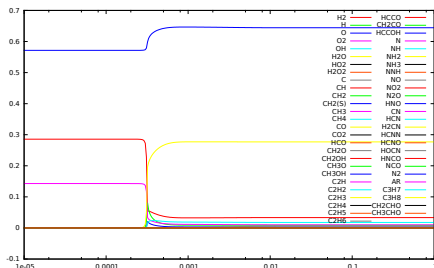


# Cut 65% less important reactions



Dijkstra

Matrix



Full Mechanism

# Mean Squared Error – Full

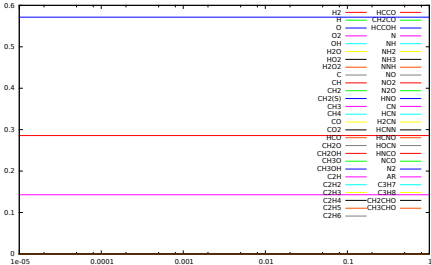
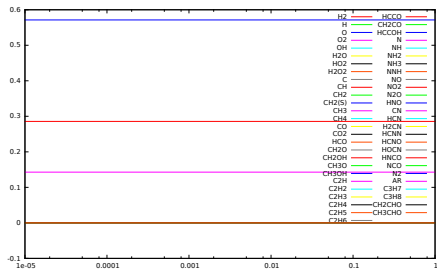
## Dijkstra

Temperature (K)	Density (kg/m3)	Pressure (Pa)	H2	H	O	O2	OH	H2O	HO2	H2O2	C	CH	CH2	CH2(S)	CH3	CH4	CO	CO2	HCO
CH2O	CH2OH	CH3O	CH3OH	C2H	C2H2	C2H3	C2H4	C2H5	C2H6	HCCO	CH2CO	HCCOH	N	NH	NH2	NH3	NNH	NO	NO2
N2O	HNO	CN	HCN	H2CN	HCNN	HCNO	HOCN	HNCO	NCO	N2	AR	C3H7	C3H8	CH2CHO	CH3CHO	18.404417	0.001498	0.000000	0.000000
0.000000	0.003218	0.001081	0.000509	0.002351	0.001373	0.002879	0.000001	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000001	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.005882	0.000001	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.002958	0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000

## Matriz

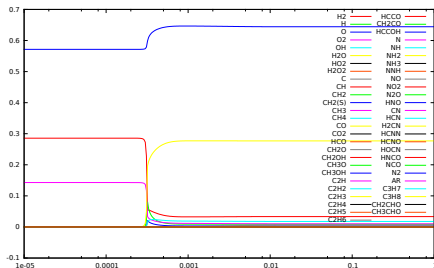
Temperature (K)	Density (kg/m3)	Pressure (Pa)	H2	H	O	O2	OH	H2O	HO2	H2O2	C	CH	CH2	CH2(S)	CH3	CH4	CO	CO2	HCO
CH2O	CH2OH	CH3O	CH3OH	C2H	C2H2	C2H3	C2H4	C2H5	C2H6	HCCO	CH2CO	HCCOH	N	NH	NH2	NH3	NNH	NO	NO2
N2O	HNO	CN	HCN	H2CN	HCNN	HCNO	HOCN	HNCO	NCO	N2	AR	C3H7	C3H8	CH2CHO	CH3CHO	31.011686	0.002647	0.000000	0.000000
0.000000	0.004804	0.000706	0.000461	0.003023	0.001396	0.004960	0.000004	0.000003	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000001	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.005882	0.000001	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.003170	0.000000	0.000000	0.000000	0.000000	0.000000
0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000

# Cut 90% less important reactions



Dijkstra

Matriz



Full Mechanism

# Next steps

## Real Benchmark

Iso-octane? Ethanol? Others?

## Should?

Scaling [Pietot e DesJardins]?

# Questions?

Remember: I am a computer scientist! :)

