



Frequency isolation algorithms for hyperbolic quadratic eigenvalue problems

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Outline

- 1 The frequency isolation problem
- 2 The algorithms
 - The basic isolation algorithm
 - A continuation algorithm
- 3 Numerical results
 - Box vs. basic
 - Box vs. continuation

Hyperbolic QEPs

- Consider **quadratic e-value problem (QEP)**

$$Q(\lambda)u = (\lambda^2 M + \lambda C + K)u = 0.$$

with M, C, K **symmetric, positive definite** $n \times n$.

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- Nice properties of hyperbolic QEPs:
 - $2n$ **real** and semisimple e-values
 - e-values can be obtained by **bisection**

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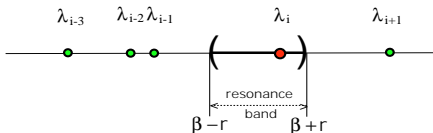
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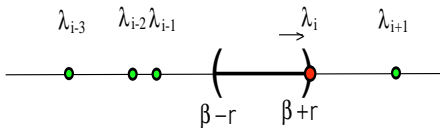
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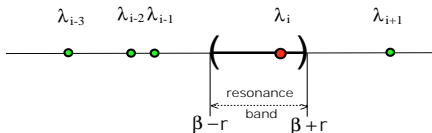
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Frequency isolation problem: Given a resonance band $I_r = (\beta - r, \beta + r)$ and a vibrational system (M, C, K) with some eigenvalue in $(\beta - r, \beta + r)$, **redesign the system** in such a way that the new system (M^*, C^*, K^*)

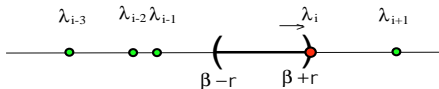
- has **no eigenvalue in the resonance band**, and
- **is close to** (M, C, K) in some sense.

Frequency isolation algorithms: the undamped case

Egaña, Kuhl & Santos '02: Tridiagonal QEP with $C = 0$ (no damping). Given initial, resonant spectrum



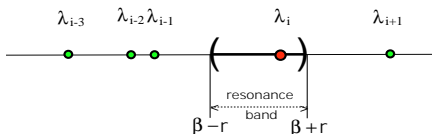
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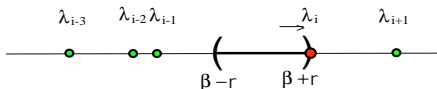
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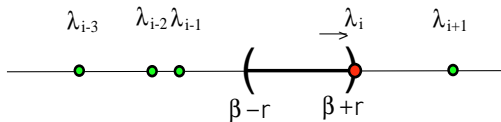


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Very expensive: cost **well over $O(n^4)$** + quite restrictive conditions.

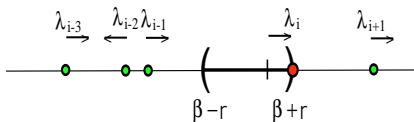
How to improve it?

Fixing a target spectrum is **unnatural**, since “good” eigenvalues are not allowed to change at all



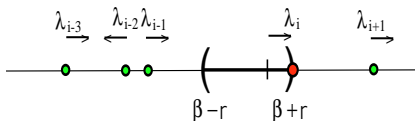
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Idea of new algorithm: Identify a direction in (M, C, K) space along which:

- variation of “bad” eigenvalues is **maximal**, and
- variation of “good” eigenvalues is **minimal**.

Then, modify (M, C, K) along this direction up to isolation.

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A simple situation

As an example, consider hyperbolic QEP

$$Q(\lambda) = \lambda^2 M + \lambda C + K$$

with

$$M = \text{diag}(m) = \text{diag}(m_1, \dots, m_n), \quad m_i > 0,$$

$$C = \text{diag}(c) = \text{diag}(c_1, \dots, c_n), \quad c_i > 0,$$

$$K = \begin{bmatrix} k_1 + k_2 & -k_2 & & & & & \\ -k_2 & k_2 + k_3 & -k_3 & & & & \\ & & \ddots & \ddots & \ddots & & \\ & & & -k_{n-1} & k_{n-1} + k_n & -k_n & \\ & & & & -k_n & k_n & \end{bmatrix}, \quad k_i > 0$$

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$$\lambda_j = \lambda_j(m, c, k) \quad \text{for} \quad (m, c, k) = (m_1, \dots, m_n, c_1, \dots, c_n, k_1, \dots, k_n) \in \mathbb{R}^{3n}.$$

Thus,

Work in parameter space (m, c, k) instead of in matrix space (M, C, K)

How to choose directions in (m, c, k) space?

- Consider initial configuration

$(m, c, k) = (m_1, \dots, m_n, c_1, \dots, c_n, k_1, \dots, k_n) \in \mathbb{R}^{3n}$, and call

good e-values those s.t. $\lambda_j(m, c, k) \notin (\beta - r, \beta + r)$

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- Assume we are **close to isolation**. Let $\Delta = (\delta m, \delta c, \delta k) \in \mathbb{R}^{3n}$, and write perturbed e-values as

$$\lambda_j((m, c, k) + \Delta) = \lambda_j(m, c, k) + \langle \nabla \lambda_j(m, c, k), \Delta \rangle + \dots$$

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 - 2) as small as possible for **good** λ_j

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 - as large as possible for **bad** λ_j
 - as small as possible for **good** $\lambda_j \rightarrow$ **zero** for **good** λ_j i.e.,

$$\Delta \perp \nabla \lambda_j(m, c, k) \quad \text{for all } \text{good } \lambda_j.$$

The basic isolation algorithm

Since

$$\Delta = (\delta m, \delta c, \delta k) \perp \nabla \lambda_j(m, c, k) \quad \text{for all good } \lambda_j,$$

denote

$$V_{\text{good}}^\perp = \{w \in \mathbb{R}^{3n} : \langle \nabla \lambda_j(m, c, k), w \rangle = 0 \text{ for all good } \lambda_j\}.$$

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- 2) Given w_{\max} from **Stage 1**), find smallest $\alpha^* \in \mathbb{R}$ s.t. e-values corresp. to

$$(m^*, c^*, k^*) = (m, c, k) + \alpha^* w_{\max}$$

are all outside the resonance band.

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- $w_{\max} \equiv$ **singular vector** corresp. to σ_{\max} of scalar product matrix

OVERALL COST: $O(n^3)$

Implementation of Stage 2): detecting isolation

Stage 2) Given optimal direction $w_{\max} \in V_{\text{good}}^\perp$, find smallest $\alpha^* \in \mathbb{R}$ such that spectrum of

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All these constraints lead to a maximal range for α

$$-\tau^- \leq \alpha \leq \tau^+$$

for appropriate **thresholds** $\tau^-, \tau^+ > 0$.

Algorithm **only works** if there are **no e-values** in $(\beta - r, \beta + r)$ either for $\alpha = -\tau^-$ or for $\alpha = \tau^+$ \longrightarrow provides **starting interval for bisection**.

The basic isolation algorithm: Shortcomings

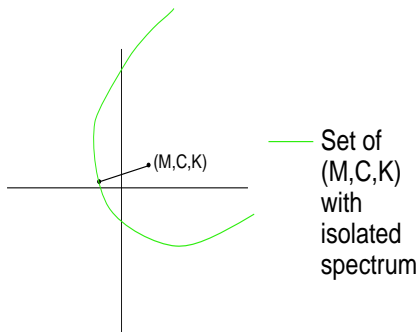
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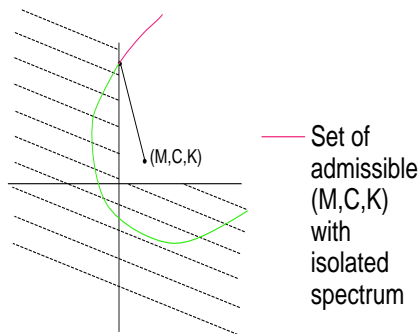
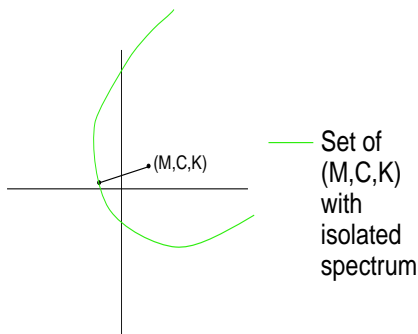
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Both difficulties may be overcome

A continuation algorithm:

Instead of trying to isolate in one single run, **repeat** basic isolation procedure **over and over**, setting $(M_0, C_0, K_0) = (M, C, K)$ and updating

$$(M_{i+1}, C_{i+1}, K_{i+1}) = (M_i, C_i, K_i) + h_i w_{\max}^{(i)},$$

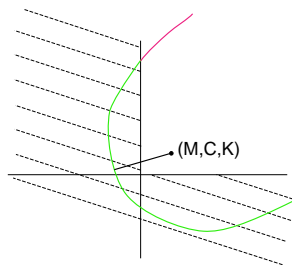
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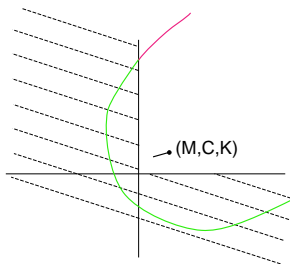
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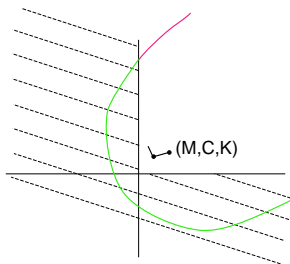
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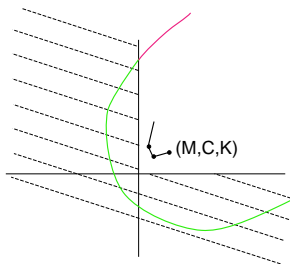
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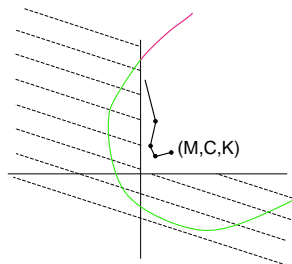
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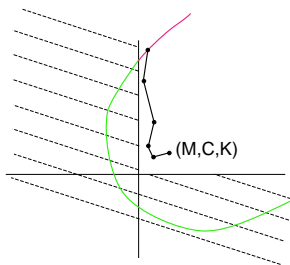
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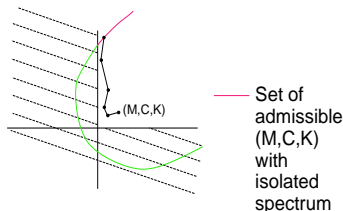
— Set of admissible (M, C, K) with isolated spectrum

A continuation algorithm:

Instead of trying to isolate in one single run, **repeat** basic isolation procedure **over and over**, setting $(M_0, C_0, K_0) = (M, C, K)$ and updating

$$(M_{i+1}, C_{i+1}, K_{i+1}) = (M_i, C_i, K_i) + h_i w_{\max}^{(i)},$$

with some appropriate, small step size h_i , where $w_{\max}^{(i)}$ is the optimal direction at step i . Graphically,



How to choose h_i ?

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Several possible choices for h_i . Best performance so far:

Greedy version: Try to isolate at each step. If not possible, then advance as far as possible in the optimal direction and repeat.

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Several possible choices for h_i . Best performance so far:

Greedy version: Try to isolate at each step. If not possible, then advance as far as possible in the optimal direction and repeat.

Compute thresholds τ_i^+, τ_i^- and optimal direction $w_{\max}^{(i)}$ at step i .

- **If possible**, compute α_i^* isolating the spectrum, take $h_i = \alpha_i^*$ and stop.
- **If not**, take h_i equal either to τ_i^+ or $-\tau_i^-$ and continue.

Outline

- 1 The frequency isolation problem
- 2 The algorithms
 - The basic isolation algorithm
 - A continuation algorithm
- 3 Numerical results
 - Box vs. basic
 - Box vs. continuation

Numerical experiments: comparison with EKS

- Both **basic** and **continuation** algorithm implemented for **tridiagonal undamped case ($C = 0$)** in FORTRAN POWER STATION 4.0 on a PC with IEEE arithmetic
- Generate **1000 random 10×10 QEPs** with one single e-value in the resonance band. **Radius r** of resonance band inversely proportional to **$\delta < 1$** :

the smaller the parameter δ , the smaller the **radius r**

- Compare obtained solutions with solutions provided by '**Box**' algorithm by Egaña, Kuhl & Santos '02 (**EKS**) **whenever possible**:
 - **Box algorithm** works only **for low dimension** (too expensive).
 - **Box algorithm** works only **for uniform distributions** of initial e-values.

Numerical experiments: Box vs. **basic** isolation

Generate 1000 random 10×10 mass-spring systems for each value of δ .

Set

- $m_{box}^*, k_{box}^* \equiv$ solutions computed by the 'Box' algorithm of Egaña, et al.
- m_{β}^*, k_{β}^* : solutions computed by the **basic isolation algorithm**.

$$Dist_{m,k}^{(\square)} = \frac{\|(m, k) - (m^*, k^*)_{\square}\|}{\|(m, k)\|},$$

where \square is either 'box' or ' β '. Define the **quotients**

$$Q_{m,k}^{(\beta)} = \frac{Dist_{m,k}^{(box)}}{Dist_{m,k}^{(\beta)}}, \quad Q_T^{(\beta)} = \frac{\text{CPU time for Box alg.}}{\text{CPU time for basic isolation alg.}}$$

and the **percentage** $p_{m,k}$ of cases with $Q_{m,k}^{(\beta)} < 1$.

Numerical experiments: Box vs. **basic** isolation

Generate 1000 random 10×10 mass-spring systems for each value of δ .

$$\text{Dist}_{m,k}^{(\square)} = \frac{\|(m, k) - (m^*, k^*)_{\square}\|}{\|(m, k)\|},$$

where \square is either 'box' or ' β '. Define the **quotients**

$$Q_{m,k}^{(\beta)} = \frac{\text{Dist}_{m,k}^{(\text{box})}}{\text{Dist}_{m,k}^{(\beta)}}, \quad Q_T^{(\beta)} = \frac{\text{CPU time for Box alg.}}{\text{CPU time for basic isolation alg.}}$$

and the **percentage** $p_{m,k}$ of cases with $Q_{m,k}^{(\beta)} < 1$.

	$Q_{m,k}^{(\beta)}$			$Q_T^{(\beta)}$		
δ	Average	Min	$p_{m,k}$	Average	Min	isolated
0.1	0.74	0.09	53.1%	514	61	97.8%
0.15	0.9	0.1	66.4%	420	53	96.9%
0.2	1.31	0.15	82.2%	359	51	89.1%
0.4	2.38	0.39	97.3%	228	48	59.6%

Numerical experiments: Box vs. continuation

Generate 1000 random 10×10 mass-spring systems for each value of δ .

Set

- $m_{box}^*, k_{box}^* \equiv$ solutions computed by the ‘Box’ algorithm of Egaña, et al.
- m_{cont}^*, k_{cont}^* : solutions computed by the continuation algorithm (greedy version).

$$Dist_{m,k}^{(\square)} = \frac{\|(m, k) - (m^*, k^*)_{\square}\|}{\|(m, k)\|},$$

where \square is either ‘box’ or ‘cont’. Define the quotients

$$Q_{m,k}^{(cont)} = \frac{Dist_{m,k}^{(box)}}{Dist_{m,k}^{(cont)}}, \quad Q_T^{(cont)} = \frac{\text{CPU time for Box alg.}}{\text{CPU time for continuation alg.}}$$

and the percentage $p_{m,k}$ of cases with $Q_{m,k}^{(cont)} < 1$.

Numerical experiments: Box vs. continuation

Generate 1000 random 10×10 mass-spring systems for each value of δ .

$$\text{Dist}_{m,k}^{(\square)} = \frac{\|(m, k) - (m^*, k^*)_{\square}\|}{\|(m, k)\|},$$

where \square is either 'box' or 'cont'. Define the **quotients**

$$Q_{m,k}^{(cont)} = \frac{\text{Dist}_{m,k}^{(box)}}{\text{Dist}_{m,k}^{(cont)}}, \quad Q_T^{(cont)} = \frac{\text{CPU time for Box alg.}}{\text{CPU time for continuation alg.}}$$

and the **percentage** $p_{m,k}$ of cases with $Q_{m,k}^{(cont)} < 1$.

	$Q_{m,k}^{(cont)}$			$Q_T^{(cont)}$	
δ	Average	Min	$p_{m,k}$	Average	Min
0.2	0.66	0.04	61.2%	532	67
0.3	0.67	0.009	65.3%	398	65
0.4	0.83	0.016	69.3%	276	50
0.6	1.06	0.04	77.4%	218	36

Summary:

New, directional algorithm for the frequency isolation problem proposed for **hyperbolic QEPs**.

Tested only for **tridiagonal undamped case**.

- **Basic algorithm**: $O(n^3)$, but isolation guaranteed **only** for systems **close to non-resonance**.
- **Continuation algorithm**:
 - Cost $O(n^3)$ per step.
 - Much **faster** than 'Box' algorithm.
 - Same quality of approximations as Box alg.
 - More **robust**: works irrespective of spectral distribution or distance to non-resonance.