

Gene library based Resource Allocation in Time Sensitive Large Scale Networked Control Systems

Preliminary Exam Presentation Unnati Ojha





- Objectives, Motivation
- System Description
- Gene Library
 - Biological Background
 - Formulation
- Adaptive Bandwidth Management
 - Formulation
 - Analytical Solution using Lagrange Multipliers
 - Results
- Case Study Gene Library based Bandwidth Allocation for Intelligent Transportation System
- Conclusion and Future Work



- Objective:
 - To develop a real-time resource allocation algorithm based on a gene library for large scale networked control system such as the intelligent transportation system
 - To introduce Artificial Immune System based update algorithms in order to tune the gene library
- Motivation
 - In large scale network control systems with hard real-time constraints, such as the intelligent transportation system, bandwidth is a limited resource that should be allocated efficiently according to the need of the vehicles, thus it is necessary to develop a real time bandwidth allocation algorithm
 - Study on extraction of relevant features that indicate the risk/abnormal behavior in large scale systems can reduce the dimensionality of the problem





- Local Agents
 Environment Sensor Agents
- Environment Sensor Agents
 Supervisory Agent with Bondwidth C
- Supervisory Agent with Bandwidth Constraint



■ Local Agents $\dot{\mathbf{x}}_i = f(\mathbf{x}_i, \mathbf{u}_i, t) + \mathbf{f}_i^d(\cdot) = \text{Dynamics for of } i^{\text{th}} \text{ agent}$ $\mathbf{x}_i = \begin{bmatrix} x_{i,1} & x_{i,2} & \cdots & x_{i,n} \end{bmatrix}^{\text{T}} = \text{State variables of } i^{\text{th}} \text{ agent}$ $\mathbf{u}_i = \begin{bmatrix} u_{i,1} & u_{i,2} & \cdots & u_{i,m} \end{bmatrix}^{\text{T}} = \text{Input variables for } i^{\text{th}} \text{ agent}$ $\mathbf{f}_i^d(\cdot) = \text{Disturbance on } i^{\text{th}} \text{ agent}$ $\mathbf{x} = \begin{bmatrix} \mathbf{x}_1^T & \mathbf{x}_2^T & \cdots & \mathbf{x}_N^T \end{bmatrix}^{\text{T}} = \text{State variables from every agent}$ $\mathbf{y}_i = h_x(\mathbf{x}_i, \mathbf{u}_i) = \text{Measurement vector from } i^{\text{th}} \text{ agent}$ $\mathcal{U}^l: \mathcal{U}_1(\mathbf{y}_i, \mathbf{y}_{ref,i}) \rightarrow \mathbf{u}_i^L = \text{Local controller for } i^{\text{th}} \text{ agent}$

Environmental Sensor Agents

 $E_{j} = \begin{bmatrix} E_{j,1}, E_{j,2} \dots, E_{j,L_{j}} \end{bmatrix}^{T} = \text{State variables of } j^{\text{th}} \text{ environmental agent}$ $E = \begin{bmatrix} E_{1}^{T}, E_{2}^{T} \dots, E_{N_{E}}^{T} \end{bmatrix}^{T} = \text{State variables from all environmental agents}$ $\mathbf{q}_{j} = h_{E}(E_{j}) = \text{Measurements from } j^{\text{th}} \text{ environmental agent}$



 Bandwidth constraint expressed as a sampling rate assignment problem

> $F_{\max}(t)(samples / sec) = \varsigma \cdot B_{\max}(t)(bits / sec),$ $\varsigma = \frac{D(samples / packet)}{Q_{total}(bits / packet)}$

- Supervisory Agent
 - supervisory agent will use a multi-rate sampling technique to perform smart sampling in order to conserve bandwidth

 $\mathbf{Y}_{k} = \begin{bmatrix} \mathbf{y}_{1,k}^{T}, \mathbf{y}_{2,k}^{T}, ..., \mathbf{y}_{N,k}^{T}, \mathbf{q}_{1,k}^{T}, \mathbf{q}_{2,k}^{T}, ..., \mathbf{q}_{N_{E},k}^{T} \end{bmatrix}^{\mathrm{T}} = \mathrm{Data from local agents}$ $\mathbf{Z}_{k+1} = f(\mathbf{\tau}_{k}, \mathbf{Y}_{k}) = \mathrm{Selective sampling of available data}$ $\mathbf{\tau}_{k} = \begin{bmatrix} \tau_{1,k}, \tau_{2,k}, ..., \tau_{N+N_{E},k} \end{bmatrix}^{\mathrm{T}} = \mathrm{Sampling rates for each agent}$



Relevant measurement for each agent

 $\mathbf{Z}_{i,k} = f(\mathcal{N}_{i,k}, \mathbf{Z}_k) =$ Measurement vector associated with i^{th} agent $\mathcal{N}_{i,k} =$ Neighborhood of i^{th} agent

Decisions from supervisory agent

 $G: \psi_{\tau} (\mathbf{Z}_{k}, \mathcal{L}) \to \mathbf{\tau}_{k} = \text{sampling rate assignment}$ $\mathcal{L} = \text{Gene Library}$





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Gene – a locatable region of genomic sequence, corresponding to a unit of inheritance, which is associated with regulatory regions, transcribed regions, and or other functional sequence regions



- Phenotype: The set of observable characteristics of an individual resulting from the interaction of its genotype with environment.
 E.g. eye color, blood type, hair type,
- Genotype: The genetic code carried by all living organisms, that holds the critical instructions that are used and interpreted by the cellular machinery to produce the or Phenotype of the individual.



- For every phenotypic trait, there is a specific genotype that encodes it.
- A genotype may contain the transcribed region from one or more genes



Genotypes	Protein Phenotypes		
FfBb	Dark Blue		
Ffbb	Dark Blue		
ffBB	Light Blue		
ffBb	Light Blue		
ffbb	Pale blue		
FFBb	Brown		
FFbb	Brown		
FfBB	Brown		
FFBB	Dark brown		

Sturm, R.A. & Frudakis, T.N. Eye colour: portals into pigmentation genes and ancestry. Trends in Genet. 20, 327-332 (2004)

Biological Background



Allele: An allele is a viable DNA (deoxyribonucleic acid) coding that occupies a given position (gene) on a chromosome. It is one of two or more versions of a gene(s)



*Image from www.wikipedia.org



Gene Expression: process by which information from a gene is used in the synthesis of a functional gene product which results in some phenotypic trait.



- Transcription: Process of activation of a gene and creation a complimentary copy of a the DNA sequence in the transcribed portion of the gene.
- Translation: Process of decoding the transcribed genetic code to create proteins

What is a gene library?



Database, mapping

Input(s)

- Set that contains the genotypes that map the relevant variations in a phenotypic trait
- Phenotypic trait
 - system behavior of interest (e.g. facial expression)
- Genotypes
 - Genes: lip shape, eyebrow shape
 - 9 genotypes to represent 9 different scenarios
- Relevant variations
 - Happy, sad, angry, others





■ **Input Space** (Y): Data available to the system

• $Y = \{y_1, y_2, y_3, \dots, y_N\} = Gene Pool$

- Allele (λ_i) : The value of a *i*th gene in the Gene Pool for an agent
- **Genome of an individual** (Λ): The values of all genes for an individual = $[\lambda_1, \lambda_2 \dots \lambda_N]^T$
- **Dominant genes** (G_d)
 - For specific phenotypic trait, Φ
 - $\bullet G_d = \{g_{d,1}, g_{d,2}, \dots g_{d,Nd}\} G_d \subset \mathbf{Y}$
 - Selection of features using PCA, kernel-PCA, expert system etc
- Genotype (for $\boldsymbol{\Phi}$)
 - Vector of actual values for dominant genes of $\Phi = [\lambda_{d,1}, \lambda_{d,2} \dots \lambda_{d,Nd}]^T$





Genotype – Phenotype Map (GP-Map): A 2-tuple that contains activator proteins to express the genotype and maps the genotype to the phenotypic trait associated with it

 $\zeta = (\pi, \mathcal{M}),$

 π = Activator/Supressor proteins

 $= [\pi_1, \pi_2, \pi_3, ..., \pi_N]^T, \pi_i \in \{0, 1\}$

 \mathcal{M} = mapping from transcribed genes

to simple proteins

$$= (\mathcal{M}_1, \mathcal{M}_2, ..., \mathcal{M}_{N_d}), \quad \mathcal{M}_j : f_j(\lambda_{d,j}) \to \rho_j$$

 $\lambda_{d,j}$ = An Allele of j^{th} dominant gene

 ρ_j = Simple protein produced by the mapping

 Output of the GP-Map is a complex protein that partly/fully expresses the phenotypic trait

 Υ = complex protein produced by the mapping = $\prod \rho_j$

Formation of Gene Library





If a phenotype needs to be expressed using m proteins

$$\Phi = w_1 \Upsilon_1 + w_2 \Upsilon_2 + \ldots + w_m \Upsilon_m,$$

 w_i = normalization weight for each protein

• Gene Library: Collection of GP-Maps $\mathcal{L} = \{\zeta_1, \zeta_2, ..., \zeta_{S_L}\}$









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Optimal Adaptive Sampling



Ν	Total number of vehicles
$ au_i$	Sampling time for vehicle <i>i</i> , $\tau_{min} \le \tau_i \le \tau_{max}$
$ au_{min}$	Minimum allowable sampling time.
$ au_{max}$	Maximum allowable sampling time. Data from each vehicle should be sampled at least once
	within τ_{max}
$lpha_i$	The actual risk measure for vehicle <i>i</i>
L	Length of the data packet sent from the vehicle to the supervisor
BW_i	Bandwidth allocated for vehicle <i>i</i>
BW_T	Total bandwidth available for the network
$ au_w$	Sampling window: The sampling rates are updated every seconds
$\overline{\alpha_{i}^{n}}_{i}$	The number of samples of vehicle <i>i</i> in the update interval
	The average risk of vehicle <i>i</i> over sampling window







 To selectively sample data from the vehicles under the bandwidth constraint such that the changes in the risk is accurately captured in order to reconstruct the risk signal



Objective



Mathematically,



Select the sampling times τ_i to minimize the cost J



Simplification by using Taylor Series Expansion

$$J = \sum_{i=1}^{N} \overline{\alpha_{i}} \sum_{k=1}^{n_{i}} \int_{k\tau_{i}}^{(k+1)\tau_{i}} \|\alpha(k\tau_{i}) + \dot{\alpha}(k\tau_{i})(t - k\tau_{i}) + H.O.T - \alpha(k\tau_{i})\| dt$$
$$J \approx \sum_{i=1}^{N} \overline{\alpha_{i}} \sum_{k=1}^{n_{i}} \int_{k\tau_{i}}^{(k+1)\tau_{i}} \|\dot{\alpha}(k\tau_{i})(t - k\tau_{i})\| dt = \sum_{i=1}^{N} \overline{\alpha_{i}} \sum_{k=1}^{n_{i}} \|\dot{\alpha}(k\tau_{i})\| \int_{k\tau_{i}}^{(k+1)\tau_{i}} \|(t - k\tau_{i})\| dt$$
$$J \approx \sum_{i=1}^{N} \overline{\alpha_{i}} \sum_{k=1}^{n_{i}} (\dot{\alpha}(k\tau_{i}))^{2} \int_{k\tau_{i}}^{(k+1)\tau_{i}} (t - k\tau_{i})^{2} dt = \sum_{i=1}^{N} \overline{\alpha_{i}} \sum_{k=1}^{n_{i}} (\dot{\alpha}(k\tau_{i}))^{2} \frac{\tau_{i}^{3}}{3}$$
$$J \approx \frac{1}{3} \sum_{i=1}^{N} \overline{\alpha_{i}} \tau_{i}^{3} \sum_{k=1}^{n_{i}} (\dot{\alpha}(k\tau_{i}))^{2} = J_{approx}$$



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Solving Optimization using Lagrange Multipliers



By replacing $\sum_{k=1}^{n_i} (\dot{\alpha}(k\tau_i))^2$ with $n_i \frac{1}{n_i} \sum_{k=1}^{n_i} (\dot{\alpha}(k\tau_i))^2$ and noticing that $\frac{1}{n_i} \sum_{k=1}^{n_i} (\dot{\alpha}(k\tau_i))^2$ is the average of $\dot{\alpha}(t)^2$ over τ_w :

$$J_{approx} = \frac{1}{3} \sum_{i=1}^{N} \overline{\alpha_i} \tau_i^3 n_i \overline{\dot{\alpha_i}^2}$$

- Considering $n_i \approx \frac{\tau_w}{\tau_i}$, $J_{approx} = \frac{1}{3} \tau_w \sum_{i=1}^N \overline{\alpha_i} \tau_i^2 \overline{\dot{\alpha}_i^2}$
- Thus we can represent our optimization problem as:

$$min \ J_2 = \sum_{i=1}^{N} \frac{L^2 w_i}{B W_i^2}$$

s.t.
$$BW_i \ge BW_{\min}, \ \sum_{i=1}^{N} BW_i = BW_T$$

where,

$$BW_i = \frac{L}{\tau_i}, \ w_i = \overline{\alpha_i} \overline{\dot{\alpha_i}^2}$$



• Changing inequalities to equalities $\min J_3 = \sum_{i=1}^{N} \frac{L^2 w_i}{(BW_i^{'})^2}$, s.t. $\sum_{i=1}^{N} BW_i^{'} = BW_T - N \times BW_{\min}$

where,

$$BW_i = BW_{\min} + BW_i$$

The lagrangian thus becomes

$$L = \sum_{i=1}^{N} \frac{L^2 w_i}{(BW_i^{'})^2} + \lambda \left(\sum_{i=1}^{N} BW_i^{'} - (BW_T - N \times BW_{\min}) \right)^2$$

To find the optimal point, we have



where

 $w_i = \overline{\alpha_i} \overline{\dot{\alpha}_i}^2$

Simple Case Study: Results





Connecting the Dots









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 - Resource Allocation
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Gene Library in ITS







$$RI = \frac{2h_R a_y \cos \varphi + 2h_R \sin \varphi}{L_w g \cos \varphi}$$

$$a_{y} = \frac{0.3739 \times v^{2} \times \sin\left(\frac{\theta}{n}\right)}{\pi^{2} \left(4L_{w}\right)}$$

$$(I_{xx} + mh_R^2)\ddot{\varphi} = ma_y h_R \cos\varphi + mgh_R \sin\varphi$$
$$-\frac{1}{2}kl_s^2 \cos\varphi \sin\varphi - \frac{1}{2}cl_s^2 (\cos^2\varphi)\dot{\varphi}$$

<i>m</i> , mass (kg)	2205		
I_{xx} (kg m ²)	5512		
h_{R} , Height of c.g. (m)	0.7		
L_w , Wheel base (m)	1.75		
k, Spring Stiffness (N/m)	20000		
<i>c</i> , Damping coefficient (Ns/m)	3900		
<i>l</i> _s (m)	1.5		

- R. Rajamani, *et al.*, "Real-time estimation of roll angle and CG height for active rollover prevention applications," in *American Control Conference*, 2009. ACC '09., 2009, pp. 433-438.
- Y. Jangyeol and Y. Kyongsu, "A rollover mitigation control scheme based on rollover index," in *American Control Conference*, 2006, 2006, p. 6 pp.



- **Phenotype,** Φ = Rollover Probability
- Rollover Index (RI) can be expressed as

$$RI = a + b, \ a = \frac{2h_R a_y}{L_w g}, \ b = \frac{2h_R \sin\varphi}{L_w g\cos\varphi}$$

• Candidate **Complex proteins**, $\Upsilon_1 = a$, $\Upsilon_2 = b$, such that

$$\bullet \Phi = w_1 \Upsilon_1 + w_2 \Upsilon_2$$



Velocity (m/s)	[0 43] (0 – 100mph)		
Steering Angle (deg)	[-270 270]		



Step 1: Dominant genes





- a has almost linear relationship to Φ
- Error is small at low values of *a*
- If we use a to represent rollover risk, then we can save computation time







• *Case* 1: Step velocity input (from v = 5 m/s to v = 30 m/s)

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• *Case 2:* Step theta input (from $\theta = 0.2$ to $\theta = 5.12$ rad)





• *Case* 3: Ramp Velocity input (10-40m/s in 5 secs)



• *Case* 4: Sine with Dwell



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Improving Performance



• Assigning weight for a

 $\Phi = w_1 \Upsilon_1 + w_2 \Upsilon_2 + \dots + w_m \Upsilon_m,$ $w_i = \text{ normalization weight}$ w = 1.1385 (using linear regression) $\Phi = w \times a$





Improving Performance - Results





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Resource Allocation using Gene Library





• Recall

$$BW_{i}^{*} = BW_{\min} + \left(\frac{\sqrt[3]{w_{i}}}{\sum_{i=1}^{N}\sqrt[3]{w_{i}}}\right) (BW_{T} - N \times BW_{\min}),$$

where,

- $w_i = \overline{\alpha_i} \overline{\dot{\alpha_i}^2}$
- $\alpha = \Phi$ (calculated using Gene Library)

Vehicle 1	v = 22 m/s, Delayed Sine with dwell (1s)
Vehicle 2	v = 22 m/s, Delayed Sine with dwell (2s)



Total Bandwidth (bytes/sec)	100
Data Packet Size (bytes)	5
BW _{max}	90%
BW_{min}	10%
τ_{min} (secs)	0.05
$ au_w$	0.5s





10

10

9



Vehicle 1	v = 22 m/s, Delayed Sine with dwell (1s)
Vehicle 2	v = 22 m/s, Delayed Sine with dwell (2s)





BW_T	Constant I	Bandwidth	Adaptive Bandwidth		Percent Improvement	
(bits/s)	Vehicle 1	Vehicle 2	Vehicle 1	Vehicle 2	Vehicle 1	Vehicle 2
50	3.0e-5	2.56e-5	2.098e-5	2.606e-5	42.99	-1.77
100	1.104e-5	1.276e-5	9.917e-6	9.739e-6	11.32	31.02
200	5.919e-6	6.808e-6	4.998e-6	6.180e-6	18.43	10.16
300	4.012e-6	4.603e-6	3.395e-6	4.578e-6	18.17	0.55
400	3.244e-6	3.709e-6	2.726e-6	3.199e-6	19.00	15.94
500	2.557e-6	2.952e-6	2.137e-6	2.500e-6	19.65	18.08



- A formulation for gene library was introduced. The gene library store the genotype-phenotype maps.
- An optimal adaptive bandwidth scheme was presented that minimized the error in signal reconstruction
- Preliminary results on developing a gene library for intelligent transportation system were shown. The dimensionality and the computation time to calculate the rollover risk was reduced by using Gene Library.
- The Gene Library was used for resource allocation in an intelligent transportation monitoring system. The improvement over the static (equal) bandwidth allocation scheme was as high as 42%

What Next?





- Sensitivity Analysis: Determine performance degradation after introducing delays, packet loss in the communication process of the NCS and introduce methods to alleviate the performance loss
- Adaptive Gene Library: Use Artificial Immune Systems to adaptively update gene library



Thank You

Questions ?

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