## Social robotics and membrane computing

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January 30, 2018, 16th BWMC, Seville





## Outline

Social robotics

- FROG project
- TERESA project
- Robot navigation
  - ► The RRT algorithm
- The RENPSM framework
- Conclusions and future work





#### **Social robotics**

- A social robot is an autonomous robot that interacts with humans by following social behaviors.
- From 2014 to 2017 I was working at the Service Robotics Lab at UPO
- I was involved in two FP7 European Projects:
  - FROG: Fun Robotic Outdoor Guide
  - TERESA: Telepresence Reinforcement-learning Social Agent





# FROG

#### Fun Robotic Outdoor Guide (https://www.frogrobot.eu)







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## FROG

Fun Robotic Outdoor Guide (https://www.frogrobot.eu)

In the Alcazar of Seville (2014)

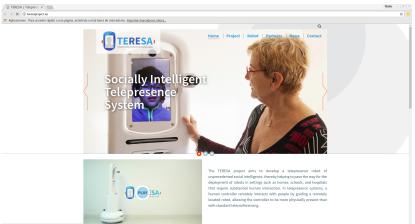






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#### TElepresence REinforcement-learning Social Agent (http://teresaproject.eu/)



Conectando.

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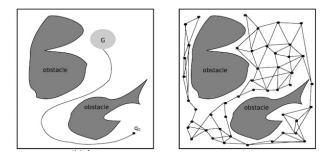






## **Robot navigation**

Particular case of the motion planning problem



Given (1) a start configuration state, (2) a goal configuration state, (3) a geometric description of the robot, and (4) a geometric description of the environment: find a path that moves the robot gradually from start to goal.

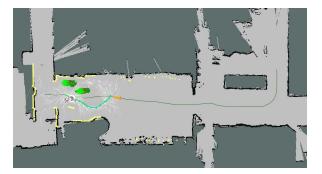




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TElepresence Einforcement-learning Social Agent (http://teresaproject.eu/)

TERESA uses a variant of the RRT algorithm  $^{1}% ^{1}$  for navigation



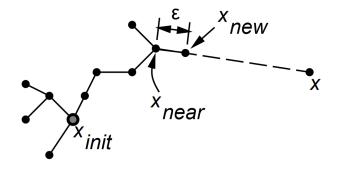
<sup>1</sup>S.M. LaValle. Rapidly-Exploring Random Trees: A New Tool for Path Planning, *Computer Science Dept.*, Iowa State University, October 1998



$$\begin{array}{l} V_{\tau} \leftarrow \{x_{init}\} \\ E_{\tau} \leftarrow \emptyset \\ \text{for } k = 1 \text{ to } K \text{ do} \\ & x_{rand} \leftarrow \text{RANDOM\_STATE}(X); \\ & x_{near} \leftarrow \text{NEAREST\_NEIGHBOR}(x_{rand}, \tau); \\ \text{ if } \text{DISTANCE}(x_{rand}, x_{near}) \geq d_{min} \text{ then} \\ & u \leftarrow \text{SELECT\_INPUT}(x_{rand}, x_{near}); \\ & \text{if } \neg \text{COLLISION}(x_{near}, u, \Delta t, X_{obs}) \text{ then} \\ & x_{new} \leftarrow \text{NEW\_STATE}(x_{near}, u, \Delta t); \\ & V_{\tau} \leftarrow V_{\tau} \cup \{x_{new}\} \\ & E_{\tau} \leftarrow E_{\tau} \cup \{(x_{near}, x_{new})\} \\ & \text{ end if} \\ & \text{end if} \\ & \text{end for} \\ & \text{return } \tau = (V_{\tau}, E_{\tau}) \end{array}$$



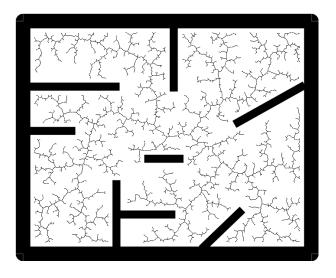








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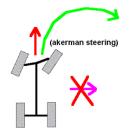






Properties

- It manages nonholonomic, kinodynamic and environment restrictions
- The valid space is explored in an uniform way
- It is computationally tractable
- ► A path can be generated by connecting two RRT: one from the starting state, another from the goal state. *Bidirectional RRT algorithm*<sup>2</sup>



<sup>2</sup>S.M. LaValle, and J.J. Kuffner. Randomized kinodynamic planning. Proceedings IEEE International Conference on Robotics and Automation, 1999 pages 473–479

# The RENPSM framework<sup>3</sup>

A preliminary first approach for the global planner

- We propose an extension of ENPS to solve the global planning by using the RRT algorithm
- New ingredients have been added to ENPS framework to fit the RRT algorithm requirements

<sup>3</sup>I.Pérez-Hurtado, M.J. Pérez-Jiménez. Generation of rapidly-exploring random trees by using a new class of membrane systems. *ACMC17* + (=)



#### The **RENPSM** framework

**RENPSM:** Random Enzymatic Numerical P systems with Proteins and Shared Memory

- Membranes in a cell-like structure represent RRT nodes
- A special membrane called *mem* is used as a shared memory
- Random numbers can be generated in the shared memory
- Proteins are used as regular objects for synchronization





#### The **RENPSM** framework

 $\Pi = (H, \mu, h_0, P, \textit{E}_{mem}, \textit{E}_{mem}(0), \{(\textit{P}_h(0), \textit{Var}_h, \textit{Var}_h(0), \textit{Pr}_h) \mid h \in H\}, \mathcal{R})$ 

1. 
$$H = \{1, \dots, p \cdot q\} \cup \{mem\}, mem \notin \{1, \dots, p \cdot q\}$$
, is the set of labels;

- 2.  $\mu$  is a dynamical membrane structure;
- 3.  $h_0$  is the label of an initial membrane in  $\mu$ ;
- 4. mem is the label of the shared memory;
- 5. P is a set proteins;
- 6.  $E_{mem}$  is a set of enzymes;
- 7.  $Var_h, h \in H$ , is a finite set of variables associated with region h;
- 8.  $Pr_h, h \in H$ , is a set of programs associated with region h:

$$F(x_{1,h},\ldots,x_{k_F,h}) \xrightarrow{e(F);\alpha(F)} C_1|_{V_1},\ldots,C_{n_F}|_{V_{n_F}}$$



#### The **RENPSM** framework

9.  ${\mathcal R}$  is a finite set of rules of the following form:

Protein evolution rules:

$$[\alpha \to \alpha']_h$$

Writing-only communication rules

$$(h, X_h / Y_{h,mem}, mem)^W_{\alpha}$$

Reading-only communication rules:

$$(h, X_h / Y_{mem}, mem)^R_{\alpha}$$

Membrane creation rules:

$$\left[\begin{array}{c}\left[\begin{array}{c}X_{1,h},X_{2,h},\ldots,X_{n,h}\end{array}\right]_{h}\end{array}\right]_{h'};\alpha$$





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For holonomic robots without obstacles

This algorithm will be simulated by a random enzymatic numerical P system with proteins and shared memory of degree (p, q)

$$\mathsf{\Pi}=(\mathsf{H},\mu,\mathsf{P},\mathsf{E}_{\mathit{mem}},\mathsf{E}_{\mathit{mem}}(\mathsf{0}),\{(\mathsf{P}_{\mathit{h}}(\mathsf{0}),\mathsf{Var}_{\mathit{h}},\mathsf{Var}_{\mathit{h}}(\mathsf{0}),\mathsf{Pr}_{\mathit{h}})\mid \mathit{h}\in\mathsf{H}\},\mathcal{R},\mathit{h}_{\mathsf{0}})$$

defined as follows:

$$\begin{aligned} - & H = \{1, \dots, p \cdot q\} \cup \{mem\}, mem \notin \{1, \dots, p \cdot q\}. \\ - & \mu = \{h_0\} \text{ with } h_0 \in \{1, \dots, p \cdot q\}. \\ - & P = \{\alpha_i \mid 1 \le i \le 12\}, \text{ and } P_h(0) = \{\alpha_1\}, \text{ for each } h \in H. \\ - & E_{mem} = \{Flag_{mem}, p \cdot q + 1\} \text{ and } E_{mem}(0) = \{p \cdot q + 1\}. \end{aligned}$$

The set of variables is:

▶ 
$$Var_h = \{X_{1,h}, X_{2,h}, Y_{1,h}, Y_{2,h}, D_h\}$$
, for each  $h, 1 \le h \le p \cdot q$ .  
▶  $Var_{mem} = \{X_{1,mem}, X_{2,mem}, Y_{1,mem}, Y_{2,mem}, Z_{1,mem}, Z_{2,mem}\} \cup \{U_{1,mem}, U_{2,mem}\} \cup \{D_{h,mem}, Y_{h,mem} \mid 1 \le h \le p \cdot q\}$ .

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Two random numbers i, j  $(1 \le i \le p, 1 \le j \le q)$  are generated in the shared memory.

 $\begin{cases} Production function : F(X_{1,mem}) = Random(i, 1 \le i \le p) \\ Repartition protocol : 1|X_{1,mem} \\ Protein : \alpha_1 \end{cases}$ 

 $\begin{cases} Production function : F(X_{2,mem}) = Random(i, 1 \le i \le q) \\ Repartition protocol : 1|X_{2,mem} \\ Protein : \alpha_1 \end{cases}$ 





Each membrane  $h \in \{1, ..., p \cdot q\}$  will read the random numbers previously generated, sharing them with the variables  $X_{1,h}, X_{2,h}$ .

$$\begin{cases} (h, X_{1,h} / X_{1,mem}, mem)_{\alpha_2}^R \\ (h, X_{2,h} / X_{2,mem}, mem)_{\alpha_2}^R \end{cases}$$





For each membrane  $h \in \mu$ , the distance  $D_h$  between its position  $(Y_{1,h}, Y_{2,h})$  and the position given by  $(X_{1,mem}, X_{2,mem})$  is computed.

Production function : 
$$F(X_{1,h}, X_{2,h}, Y_{1,h}, Y_{2,h}) = \begin{cases} \sqrt{\sum_{j=1}^{2} (X_{j,h} - Y_{j,h})^2} & \text{if } h \in \mu \\ p \cdot q + 1 & \text{if } h \notin \mu \end{cases}$$
  
Repartition protocol :  $1|D_h$   
Protein :  $\alpha_3$ 





#### Each membrane h writes its value $D_h$ to the shared memory.

$$(h, D_h / D_{h,mem}, mem)_{\alpha_4}^W$$





The minimum of all distances  $D_h$  is computed in the shared memory.

- ► Production function:  $F(D_{1,mem}, ..., D_{p \cdot q,mem}) = \min\{D_{1,mem}, ..., D_{p \cdot q,mem}\}$
- Repartition protocol: 1|D<sub>min,mem</sub>
- Protein: α<sub>5</sub>





Variable (enzyme)  $Flag_{mem}$  is set to zero if  $D_{min,mem} \leq Threshold$ .

- ► Production function:  $F(D_{1,mem},...,D_{p \cdot q,mem}) =$   $\begin{cases}
  0 & \text{if } D_{min,mem} \leq Threshold \\
  p \cdot q + 1 & \text{otherwise}
  \end{cases}$
- Repartition protocol: 1|Flag<sub>mem</sub>
- Protein:  $\alpha_6$





The label *near*, corresponding to the closer membrane to the randomly generated position, is obtained.

- ▶ Production function:  $F(D_{1,mem},...,D_{p\cdot q,mem}) = \arg-\min\{D_{1,mem},...,D_{p\cdot q,mem}\}$
- Repartition protocol: 1|Y<sub>near,mem</sub>
- Protein: α<sub>7</sub>
- Enzyme: Flag<sub>mem</sub>





The position of membrane *near* is computed.

 $\left\{ \begin{array}{l} \textit{Production function}: F(Y_{\textit{near},\textit{mem}}) = 1 + qt(Y_{\textit{near},\textit{mem}},q) \\ \textit{Repartition protocol}: 1|Y_{1,\textit{mem}} \\ \textit{Protein}: \alpha_8 \\ \textit{Enzyme}: \textit{Flag}_{\textit{mem}} \end{array} \right.$ 

 $\left\{ \begin{array}{l} \textit{Production function}: F(Y_{\textit{near},\textit{mem}}) = \textit{rm}(Y_{\textit{near},\textit{mem}},q) \\ \textit{Repartition protocol}: 1|Y_{2,\textit{mem}} \\ \textit{Protein}: \alpha_8 \\ \textit{Enzyme}: \textit{Flag}_{\textit{mem}} \end{array} \right.$ 





The unitary vector is created in the shared memory.

Production function :  $F(X_{1,mem}, X_{2,mem}, Y_{1,mem}, Y_{2,mem}) = \frac{X_{1,mem} - Y_{1,mem}}{\sqrt{\sum_{j=1}^{2} (X_{j,mem} - Y_{j,mem})^2}}$ Repartition protocol :  $1|U_{1,mem}$ Protein :  $\alpha_9$ Enzyme : Flagmem

Production function :  $F(X_{1,mem}, X_{2,mem}, Y_{1,mem}, Y_{2,mem}) = \frac{X_{2,mem} - Y_{2,mem}}{\sqrt{\sum_{j=1}^{2} (X_{j,mem} - Y_{j,mem})^2}}$ Repartition protocol :  $1|U_{2,mem}$ Protein :  $\alpha_9$ Enzyme : Flagmem





The position of the new membrane is computed in the shared memory.

 $\left\{ \begin{array}{l} \textit{Production function}: F(Y_{1,mem}, U_{1,mem}) = Y_{1,mem} + U_{1,mem} \cdot \Delta t \\ \textit{Repartition protocol}: 1 | Z_{1,mem} \\ \textit{Protein}: \alpha_{10} \\ \textit{Enzyme}: \textit{Flag}_{mem} \end{array} \right.$ 

 $\left\{ \begin{array}{l} \textit{Production function}: F(Y_{2,mem}, U_{2,mem}) = Y_{2,mem} + U_{2,mem} \cdot \Delta t \\ \textit{Repartition protocol}: 1 | Z_{2,mem} \\ \textit{Protein}: \alpha_{10} \\ \textit{Enzyme}: \textit{Flag}_{mem} \end{array} \right.$ 





The membrane labelled by  $Y_{near,mem}$  will read the position  $(Z_1, Z_2)$  corresponding to the new membrane from the shared memory.

$$\begin{cases} (Y_{near,mem}, Z_{1,Y_{near,mem}} / Z_{1,mem}, mem)_{\alpha_{11}}^{R} \\ (Y_{near,mem}, Z_{2,Y_{near,mem}} / Z_{2,mem}, mem)_{\alpha_{11}}^{R} \end{cases}$$





A child membrane with position  $(Z_1, Z_2)$  is created in  $Y_{near}$ , that is, a new state is added to the tree.

$$\left[\begin{array}{ccc} \left[\begin{array}{cc} X_{1,h} & X_{2,h} \\ Y_{1,h} & Y_{2,h} \\ Z_{1,h} & Z_{2,h} \\ D_h \end{array}\right]_{h} \right]_{Y_{near,mem}}$$

Being  $h = (Z_{1,Y_{near,mem}} - 1) \cdot q + Z_{2,Y_{near,mem}}$ . This rule is mediated by protein  $\alpha_{12}$ .





#### **Conclusions and Future work**

- There are robots controllers based on MC
- We could use fast hardware in order to obtain advantage of the current state of the art of simulators and implementations in MC
- We are working in a variant of ENPS in order to simulate RRT algorithms
- There is a preliminary first approach presented in the last ACMC.
- We are currently adapting the RRT\* algorithm: optimal path planning.
- We would like to mix our solution with current robotic controllers based on MC



• We would like to improve our simulator



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# Thanks for your attention!



