

An improved test generation approach from extended finite state machines using genetic algorithms

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Outline

- Problem formulation: EFSM test generation
- Motivation: why **metaheuristics** in **EFSM testing**?
- Previous approaches
- Proposed strategy: decomposing long paths into independent subpaths
- Fitness functions: ***al+nbl*** versus ***ICF***
- Empirical evaluation
- Conclusions and future work

Test Data Generation for State-based Testing

Problem Formulation

Given: some **paths** in the state machine (obtained according to a certain coverage criteria).

Find: input parameter values to trigger the given paths.

Approach: Use metaheuristic search techniques (such as **genetic algorithms**) to find for each path (sequence of methods) the input values for the parameters, which satisfy the corresponding guards (pre-conditions)

Questions:

Encoding: $x = (x_1, x_2, \dots, x_n)$

Fitness function: $f(x) = ?$

Search technique: which one, tunings?

Motivation

- State-based testing
 - test selection methods for FSMs: W, Wp methods etc.
 - **coverage criteria** for state machines diagrams
- Automatic generation of test cases from EFSMs, state machines diagrams, X-machines etc. is not straightforward!
- Dranidis, Bratanis, Ipate . *JSXM: A Tool for Automated Test Generation*. SEFM 2012. <http://www.jsxm.org/>
- Constraints (guards) on transitions → **NP-complete problem!**
- **Idea:** Why not to use the power of **evolutionary algorithms** or other **metaheuristics** to solve state-based testing problems?
- This answer is given by new field of **Search-based Software Engineering**

Search-Based Software Engineering (SBSE)

- Software engineering problems → *optimization problems* + *metaheuristic search techniques* (**GAs**, PSO, SA).
- Term of **SBSE**: first coined by *Harman* and *Jones* (2001).
- Applications: **software testing**, requirements engineering, automated maintenance, service-oriented SE, compiler optimization, quality assessment, project planning and cost estimation.



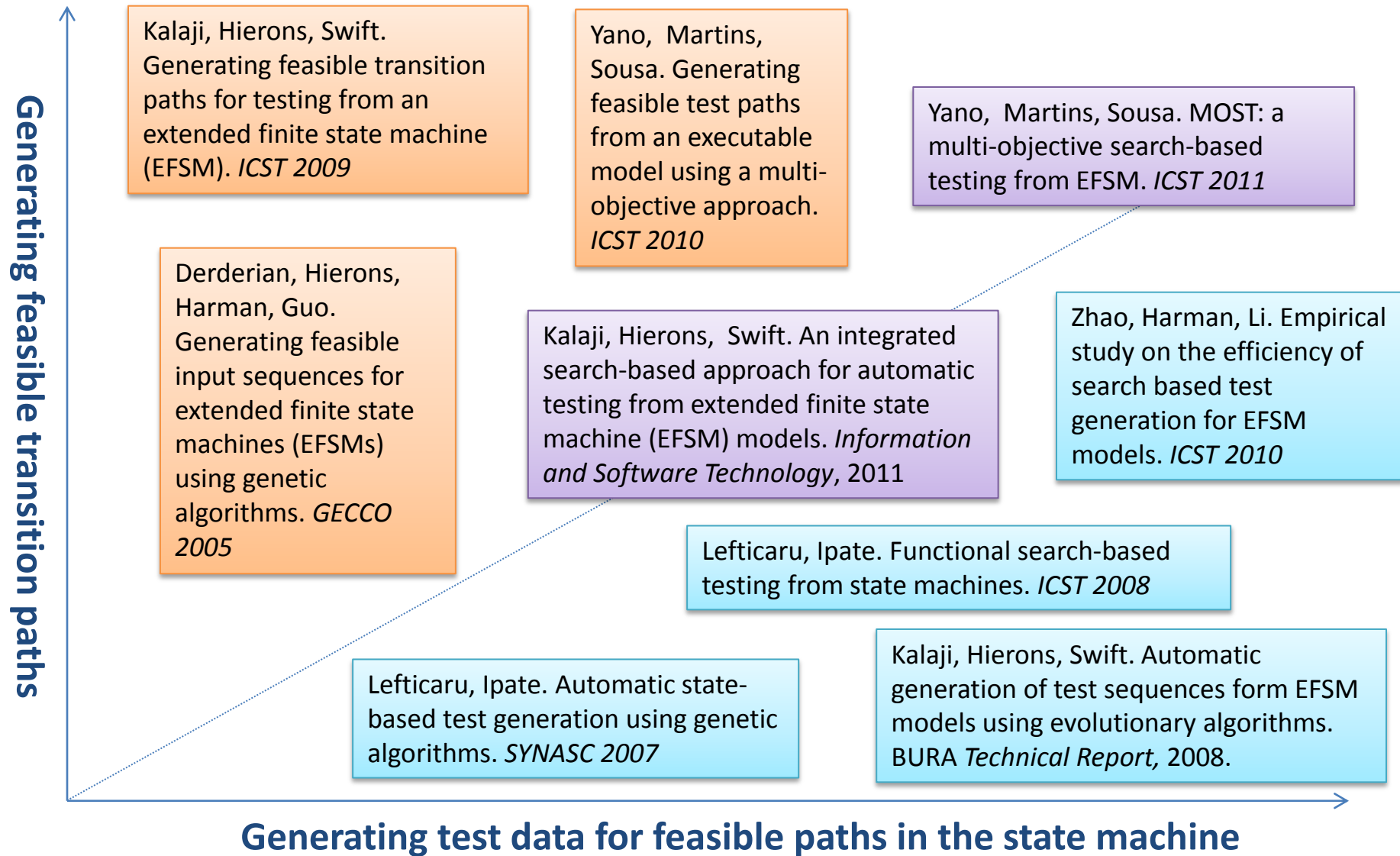
Repository of publications on SBSE:

http://crestweb.cs.ucl.ac.uk/resources/sbse_repository/

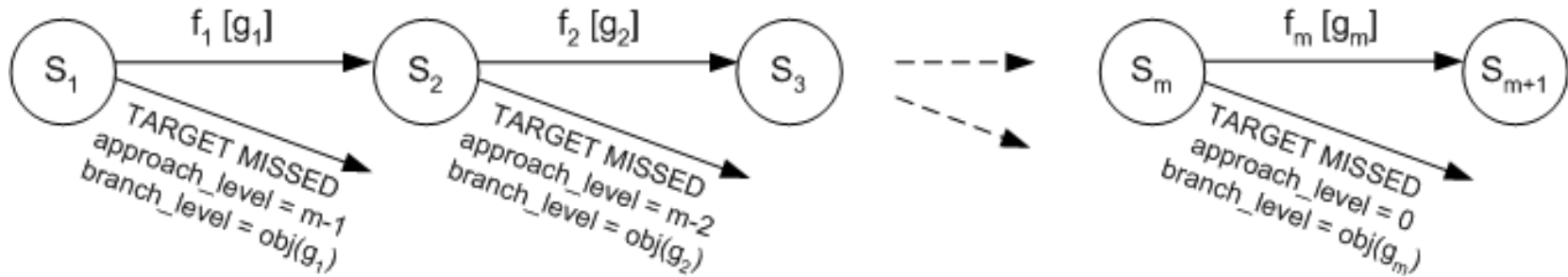


M. Harman, B.F. Jones. **Search-based software engineering**. *Information and Software Technology*, 2001.

Search-based testing from state-based specifications



Fitness Function Calculation: $al+nbl$



Fitness Calculation: $al + nbl$

$fitness = approach_level + normalized_branch_level$

$approach_level \in \{0, 1, \dots, m-1\}$

$normalized_branch_level \in [0, 1]$



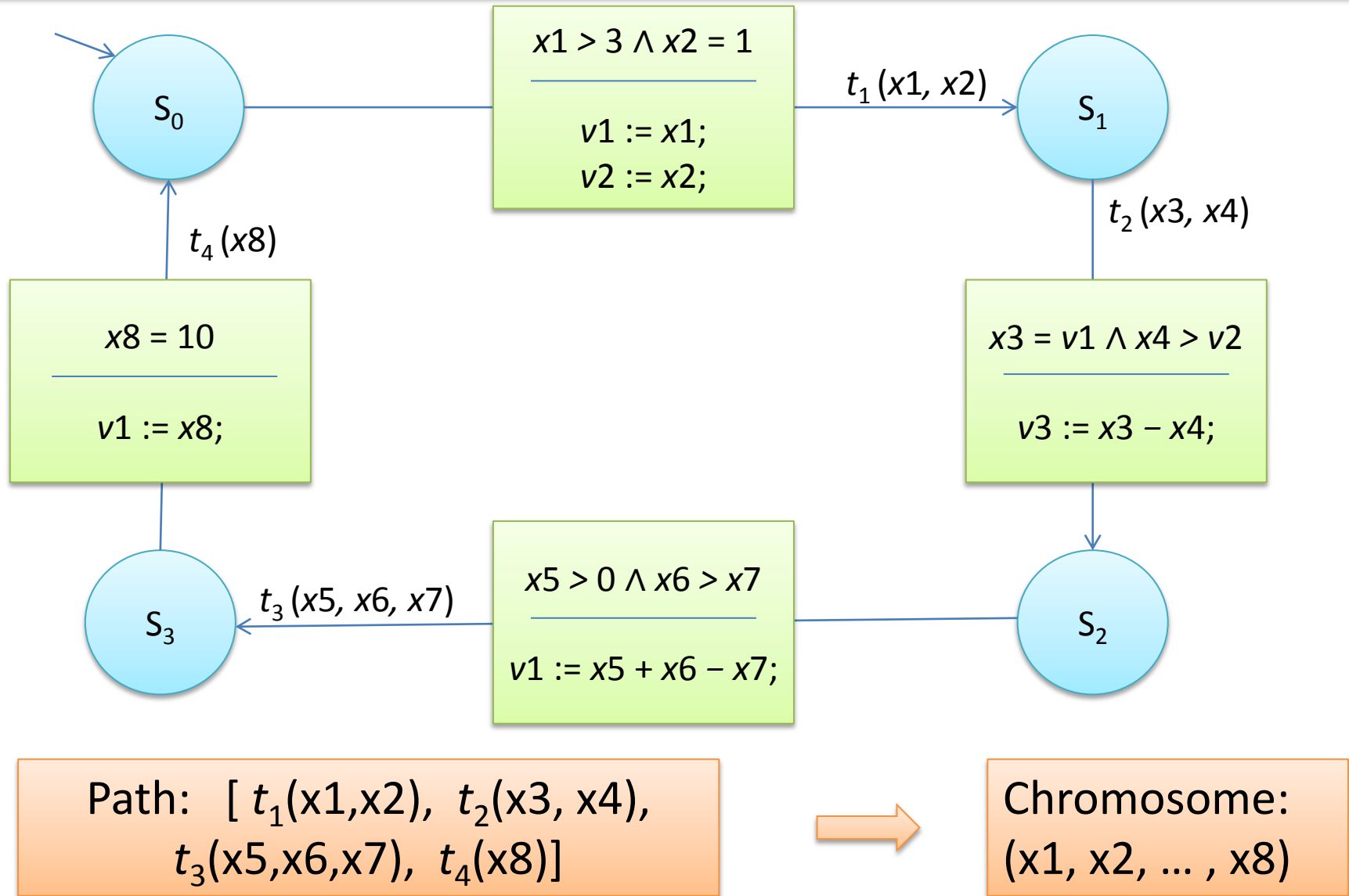
R. Lefticaru, F. Ipate. Automatic state-based test generation using genetic algorithms. In *SYNASC 2007*

Objective Functions used for Branch Level

Classical Tracey's objective functions

Relational predicate or logical connective	Objective function obj
$a = b$	if $abs(a - b) = 0$ then 0 else $abs(a - b) + K$
$a \neq b$	if $abs(a - b) \neq 0$ then 0 else K
$a < b$	if $a - b < 0$ then 0 else $(a - b) + K$
$a \leq b$	if $a - b \leq 0$ then 0 else $(a - b) + K$
$a > b$	if $b - a < 0$ then 0 else $(b - a) + K$
$a \geq b$	if $b - a \leq 0$ then 0 else $(b - a) + K$
Boolean	if $TRUE$ then 0 else K
$a \wedge b$	$obj(a) + obj(b)$
$a \vee b$	$\min(obj(a), obj(b))$
$a \text{ xor } b$	$obj((a \wedge \neg b) \vee (\neg a \wedge b))$
$\neg a$	Negation is moved inwards and propagated over a

EFSM Example



Fitness Function Evaluation: $al + nbl$

Require: Target path p , containing the transitions t_1, t_2, \dots, t_m , corresponding guards

g_1, g_2, \dots, g_m , chromosome $x = (x_1, \dots, x_n)$

Ensure: The fitness value of the chromosome $x = (x_1, \dots, x_n)$ for the given path.

Create an instance of the EFSM in the initial configuration.

$approach_level \leftarrow m - 1$

for $i = 1 \rightarrow m$ do

 {for every transition t_i in the sequence p }

 if not g_i then

 Calculate $obj(g_i)$

 return $approach_level + norm(obj(g_i))$

 else

$approach_level \leftarrow approach_level - 1$

 Apply transition t_i with the corresponding values from (x_1, \dots, x_n)

 end if

end for

return 0

Stopping at the **first unsatisfied guard!**

Give a chance to other blocks to be evaluated, too!

Who's better?

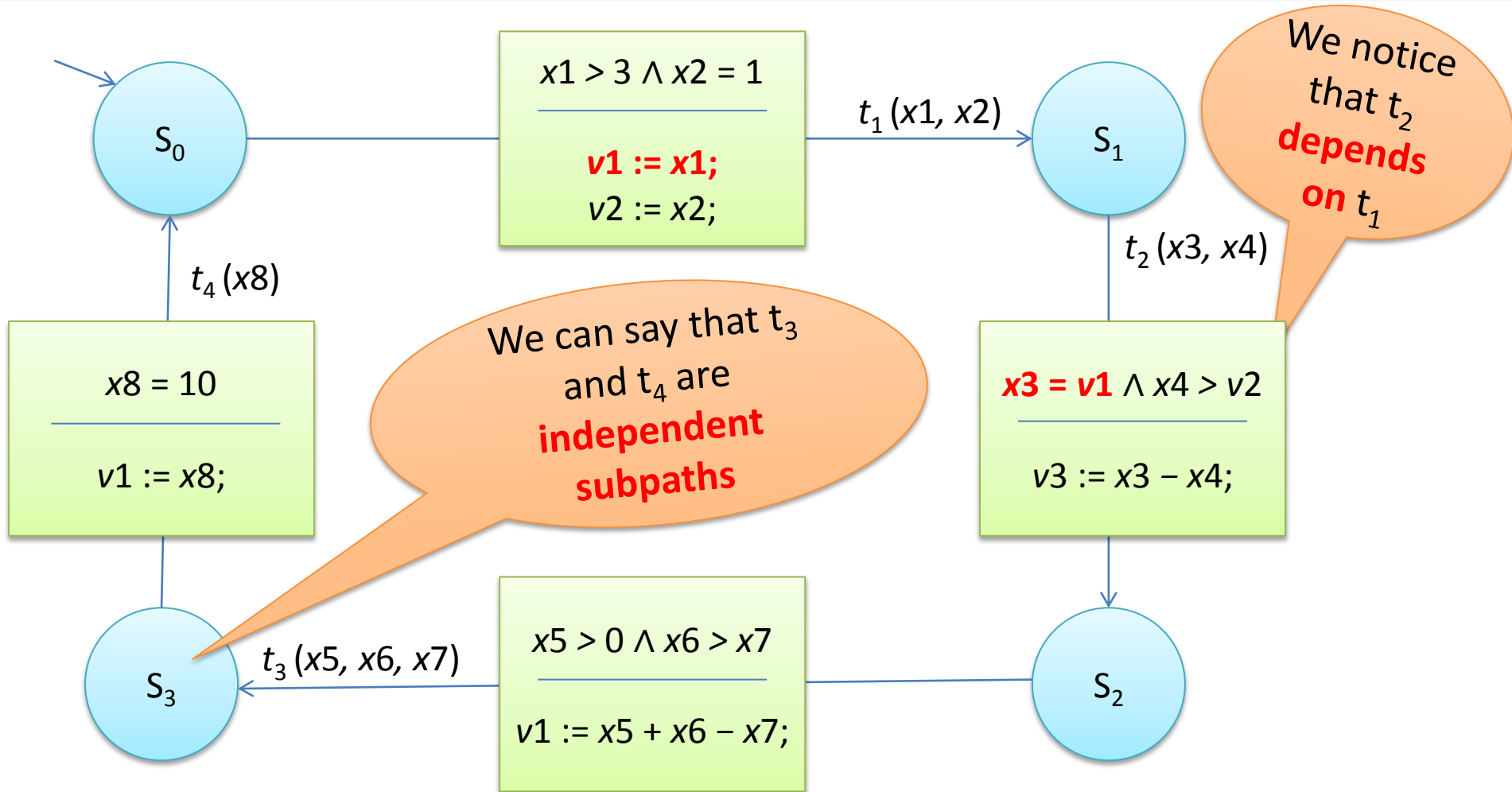
Chromosome1:

(x1, x2, x3, x4, x5, x6, x7, x8)

Chromosome2:

(y1, y2, y3, y4, y5, y6, y7, y8)

Establishing Dependencies in EFSM



Independent sub-paths: $[[t_1(x_1, x_2), t_2(x_3, x_4)] , [t_3(x_5, x_6, x_7)] , [t_4(x_8)]]$

An Improved Fitness Function for EFSM Testing

- **Main idea:** defining **dependency relations** between transitions, decomposing long paths into **independent sub-paths**
- For given paths, that can be logically decomposed into independent sub-paths, a new function, **ICF**, was designed, which takes into account the independent components:

$$fitness(x) = \sum_{i=1}^{subpaths_no} fitness(subpath_i)$$

- **Why?** The **fitness function** that guides the search is **crucial** for the success of a genetic algorithm! An improvement in the fitness function will reduce the duration of the generation process and increase the success chances of the search algorithm.

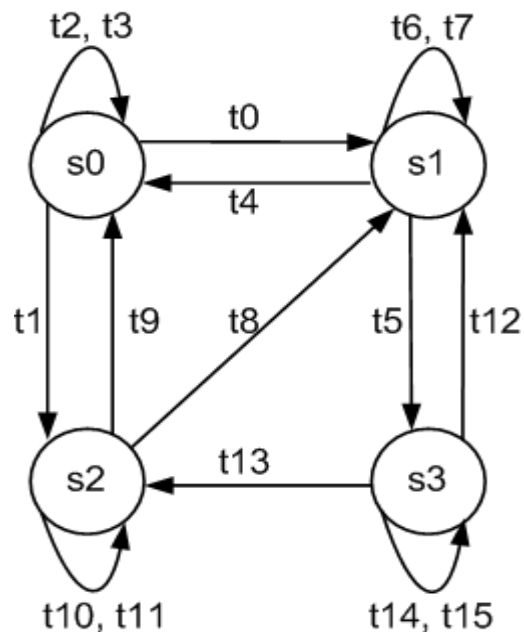
Extended Finite State Machines (EFSM)

- An **Extended Finite State Machine (EFSM)** is a 6-tuple (S, s_0, V, I, O, T) where:
 - S is a non empty *set of logical states*;
 - $s_0 \in S$ is the *initial state*;
 - V is the finite set of *internal variables*;
 - I and O are the set of *input and output interactions*, respectively;
 - T is the *finite set of transitions*.
- A **transition** $t \in T$ has *start* and *end states*, may have associated input parameters, a *guard* and a *computational block* which consists of assignments and output statements.

Dependency Relations on EFSMs

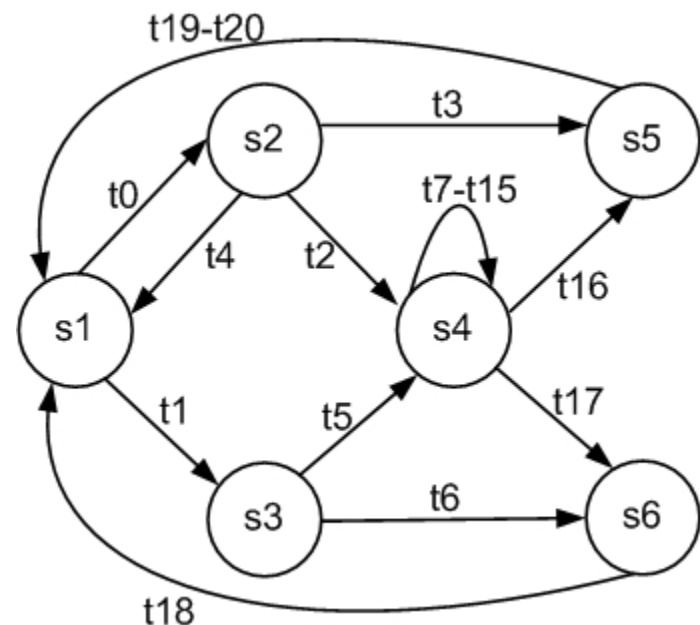
- A transition t **depends on the internal variable** $v_i \in V$ if the value of v_i is evaluated by its guard.
- A transition t **modifies the internal variable** $v_i \in V$ if v_i appears on the left hand side of an assignment operation of its sequence of atomic operations.
- Let $[t_1, t_2, \dots, t_i, \dots, t_j, \dots, t_p]$ be a **path** in the EFSM. The transition t_j **directly depends on the transition** t_i if there exists an internal variable $v_k \in V$ such as t_i modifies the internal variable v_k , t_j depends on v_k and there is no other transition t_r , $i < r < j$ that modifies the internal variable v_k .
- Result: a **dependency graph** between transitions.
- Compute the **independent subpaths** (connected components in the dependency graph).
- **ICF fitness function**: takes into account the fitness of the independent components

Empirical Evaluation



(a) Book

4 states
2 internal variables
16 transitions



(b) Class 2 transport protocol

6 states
5 internal variables
20 transitions

Excerpt from Protocol EFSM

t	$s_s \rightarrow s_e$	Input declaration	Guards	Operations
t_0	$s_1 \rightarrow s_2$	$t1(dst_add, prop_opt)$	Nil	$opt := prop_opt; R_credit := 0;$
t_1	$s_1 \rightarrow s_3$	$t2(peer_add, opt_ind, cr)$	Nil	$opt := opt_ind; S_credit := cr;$ $R_credit := 0;$
t_2	$s_2 \rightarrow s_4$	$t2(opt_ind, cr)$	$opt_ind < opt$	$TRsq := 0; TSsq := 0;$ $opt := opt_ind; S_credit := cr;$
t_3	$s_2 \rightarrow s_5$	$t3(opt_ind, cr)$	$opt_ind > opt$	Nil
t_5	$s_3 \rightarrow s_4$	$t5(accpt_opt)$	$accpt_opt < opt$	$opt := accpt_opt; TRsq := 0;$ $TSsq := 0;$
t_7	$s_4 \rightarrow s_4$	$t7(Udata, E0SDU)$	$S_credit > 0$	$S_credit := S_credit - 1;$ $TSsq := (TSsq + 1) \bmod 128;$ $TRsq := (TRsq + 1) \bmod 128;$ $R_credit := R_credit - 1;$
t_8	$s_4 \rightarrow s_4$	$t8(Send_sq,$ $Ndata, E0TSDU)$	$R_credit \neq 0$ AND $Send_sq = TRsq$	Nil
t_9	$s_4 \rightarrow s_4$	$t9(Send_sq,$ $Ndata, E0TSDU)$	$R_credit = 0 \vee$ $Send_sq \neq TRsq$	Nil
t_{10}	$s_4 \rightarrow s_4$	$t10(cr)$	Nil	$R_credit := R_credit + cr;$
t_{11}	$s_4 \rightarrow s_4$	$t11(XpSsq, cr)$	$TSsq \geq XpSsq \wedge$ $cr + XpSsq - TSsq \geq 0 \wedge$ $cr + XpSsq - TSsq \leq 15$	$S_credit := cr + XpSsq - TSsq;$

Infeasible path example: $[t_1, t_5, t_8, \dots]$ because of R_credit internal variable modification

Experiment Settings and Results: *al+nbl* vs. *ICF*

- EFSM models: Book, Protocol
- Large pool of **randomly generated paths**, for each model, having different lengths (from 6 to 35 transitions)
- GA applied for each path 100 times with *al+nbl*, 100 times with *ICF*
- GA settings: population size 20, *BestChromosomesSelector* 0.8, single point crossover, mutation rate 1/12
- H_0 : *There is no difference in efficiency (number of generations needed by the GA to find a solution) between the two fitness functions, al + nbl and ICF.*
- Statistical tests: *t-test* with significance level $\alpha = 0.05$, *p-values* were also recorded to decide if tests were significant (confidence 95%) and very significant (confidence 99%).

Summary of Experimental Results

EFSM Model	Path Set	No. of Paths	Path Lengths	Stat. Signif.	ICF +	Alnbl +	Very Signif.	ICF +	Alnbl +
Book	T1	20	6 – 15	14	14	0	13	13	0
Book	T2	20	20	16	15	1	15	14	1
Book	T3	20	25	18	18	0	17	17	0
Book	T1–T3	60	6 – 25	48	47	1	45	44	1
Protocol	P1	20	6 – 15	0	0	0	0	0	0
Protocol	P2	20	20	6	6	0	3	3	0
Protocol	P3	20	25	4	4	0	2	2	0
Protocol	P4	20	30	6	6	0	4	4	0
Protocol	P5	20	35	7	7	0	4	4	0
Protocol	P1–P5	100	6 – 35	23	23	0	13	13	0
Book, Protocol	All	160	6 – 35	71	70	1	58	57	1

Conclusions and Future Work

- *ICF* obtains better results than *al + nbl* for the majority of the paths: it improves the success rate of the GA, especially for complex paths
- Easy to trigger paths: similar behaviour
- Complex paths: the differences are very significant (confidence 99%)

Future Work

- Analysing how often independent sub-paths occur in real world EFSMs
- Comparing the results obtained by GA with other metaheuristic search techniques.
- Adapt and integrate this search-based approach into existing tools, such as JSXM

Questions?

