

In silico, in vitro, in vivo as alternatives to
the carcinogenicity bioassay for genotoxic
chemicals

Romualdo Benigni

Istituto Superiore di Sanita'
Rome Italy

rbenigni@iss.it

Chemical Risk Assessment into the new century

- **Traditional toxicology** has been the major source of information
- **Rodent bioassay**: consistent and reliable indicator and predictor of human cancer risk
- **New regulatory policies** (e.g., REACH) tend to drastically reduce the number of new cancer bioassays
- Opportunities to accept “**alternative**” approaches, including (Q)SARs, Read-Across and Chemical Category

Testing strategy for carcinogenicity pre-screening in REACH

- Pivotal role of genotoxicity short-term tests
- Bioassay may be required in the case of high exposure plus genotoxicity evidence

Evolution of theories on the early stages of carcinogenesis:

- **Somatic mutation and its variations** (epigenetic, chromosomal, stem-cell):

Cancer originates at the cellular level of biological organization

Carcinogens alter DNA structure or function in cells in tissues from which cancer arises

- **Tissue organization field:**

Cancer arises from disruption of tissue microarchitecture

Mutations and genetic instability as consequence of disruption of the morphostat gradient

Baker et al., 2010, J.Clin.Oncol., 28: 3215-3218

Prevailing model: somatic mutation theory of cancer

Implementing the somatic mutation theory

- After the success of the **Millers'** electrophilic (DNA-) reactivity theory and of **Ames test**, development of **> 100 Short-Term Tests (STT)**
- Hypothesis on **complementarity of STTs**
to cover the spectrum of cancer-relevant factors:
different genetic endpoints (gene mutation, chromosomal damage)
different cells (bacterial, mammalian)
animals (ADME)
- Implemented into regulations: **Tiered Approach**
In vitro {bacteria + mammalian cells} {gene mutations + chrom. damage}
In vivo {filter *in vitro* false positives}

STTs to predict carcinogenicity: what the data say ?

- **Mutagenicity = Carcinogenicity ?**
Only within a limited area of the chemical space, i.e., **DNA-reactive** chemicals
- **DNA-reactive** chemicals induce **cancer**, and a wide spectrum of mutations
- **Ames test**: most predictive mutagenicity-based assay (80% positive predictivity)

Benigni R. Exp.Opinion Drug Metab.Toxicol., 2012, 8: 1-11.

Zeiger E. Regulat.Pharmacol.Toxicol. 1998;28:85-95.

STTs to predict carcinogenicity: what the data say ?

- **Mutagenicity = Carcinogenicity ?**
Only within a limited area of the chemical space, i.e., **DNA-reactive** chemicals
- **Mammalian *in vitro* STTs** when Ames-negative :
no correlation with carcinogenicity *(too many false positives)*
- No reliable ***in vivo* STTs** (e.g., micronucleus) *(too many false negatives)*
- Present tiered strategy: **genotoxic carcinogens** may go undetected

Benigni R. *Exp.Opinion Drug Metab.Toxicol.*, 2012, 8: 1-11.

Zeiger E. *Regulat.Pharmacol.Toxicol.* 1998;28:85-95.

Ames test *versus* rodent carcinogenicity

		Ames test	
		neg	pos
Carcinogenicity			
Non carcinogens		233	76
Carcinogens {	Non DNA-reactive	136	34
	DNA-reactive	79	277

Ames identifies DNA-reactive carcinogens

Results from 835 chemicals in ISSCAN v3a

<http://www.iss.it/ampp/dati/cont.php?id=233&lang=1&tipo=7>

Ames test *versus* rodent carcinogenicity

		Ames test	
		neg	pos
Carcinogenicity			
Non carcinogens		233	76
Carcinogens {	Non DNA-reactive	136	34
	DNA-reactive	79	277

Ames mutagen: 80% probability of being a carcinogen

Results from 835 chemicals in ISSCAN v3a

<http://www.iss.it/ampp/dati/cont.php?id=233&lang=1&tipo=7>

Backing up the STTs with **Structure-Activity** concepts

Structure-activity relationship concepts:

application to different issues, through different approaches

Coarse-grain

Structural Alerts

(mechanistic classes, category formation, priorities)

Fine-tuned

Quantitative Structure-Activity Relationships (**QSAR**)
of congeneric classes

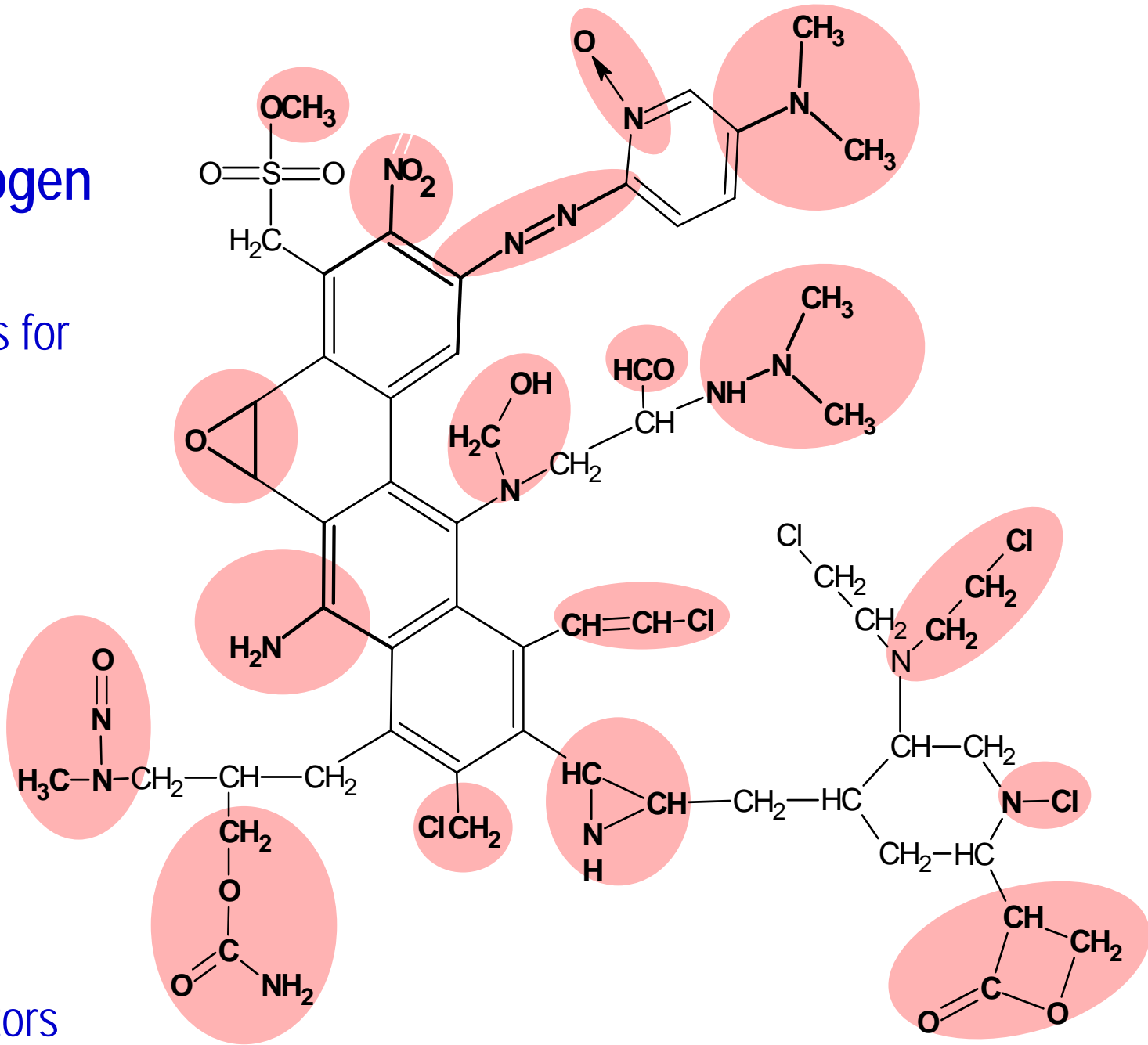
Hybrid (??)

non-local, or global QSARs

Ashby's Poly-carcinogen

- Structural alerts for carcinogenicity;
- DNA-reactive functionalities

Some alerts accompanied by detoxifying (modulating) factors





JOINT RESEARCH CENTRE

Institute for Health and Consumer Protection (IHCP)

European Commission > JRC > IHCP > Our Laboratories > Computational Toxicology and Modelling > QSAR Tools > Toxtree

Computational Toxicology and Modelling

Background

Information Sources

Publications

QSAR Tools

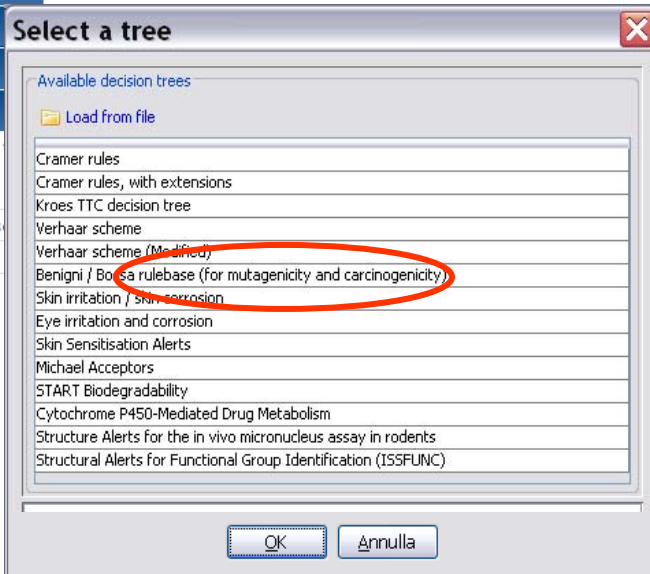
Stat4tox - Software for Statistical Evaluation of In Vitro Assays

Danish (Q)SAR Databases

Toxtree

Toxtree

Toxtree is a flexible and user-friendly open-source application that places chemicals into categories and predicts various kinds of toxic effect by applying decision tree approaches implemented:



- the [Cramer classification scheme](#)
- an [Extended Cramer scheme](#)
- the Kroes TTC decision tree
- the Verhaar scheme for aquatic modes of action
- rulebases for skin and eye irritation and corrosion
- the [Benigni-Bossa rulebase](#) for mutagenicity and carcinogenicity
- the [ToxMic rulebase](#) for the in vivo micronucleus assay
- structural alerts for identification of Michael Acceptors
- the [START rulebase](#) for persistence / biodegradation potential
- structural alerts for the identification of organic functional groups (ISSFUNC rulebase)

Toxtree (Estimation of Toxic Hazard - A Decision Tree Approach) v1.20

File Edit Chemical Compounds Toxic Hazard Method Help

File: C:\Ideacon\A\Toxtree-v1.20\Toxtree\food61.sdf*

Available structure attributes	Toxic Hazard	by Cramer rules
		Estimate
CAS		
FORMULA		
NAME		
SMILES		
Toxtree tree:cramer.Gam...	Intermediate (Class II)	
Toxtree tree:cramer.Gam...	Intermediate (Class II)	

Structure diagram

Verbose explanation

Cramer rules

Rule	Yes	No	Class
Q1: Normal constituent of the body		No	
Q2: Contains functional groups associated with c...		No	
Q3: Contains elements other than C, H, O, N, divalen...		No	
Q4: Simply branched aliphatic hydrocarbon or a c...		No	
Q5: Benzene derivative with certain substituents		No	
Q7: Heterocyclic Yes		No	
Q8: Lactone or cyclic diester		No	
Q10: 3-membered heterocycle		No	
Q11: Has a heterocyclic ring with complex substi...		No	
Q12: Heteroaromatic		No	
Q22: Common component of food	Yes		Class

First Prev 99 / 110 Next Last

Toxtree was developed by Ideacon Ltd (Sofia, Bulgaria) under the terms of a JRC contract. The software is made freely available as a service to scientific researchers and anyone interested in applying decision tree based estimation methods in the assessment of chemical toxicity.

Toxtree (Version 2.5.0) (August 2011)

Toxtree 2.5.0 is a standalone software application that can be run on the Microsoft Windows operating system as well as other platforms with the Java 2 Runtime Environment (Sta...

Many Toxtree rulebases included in the OECD (Q)SAR Toolbox

The QSAR Toolbox

- Facilitates the practical application of grouping of chemicals and read-across approaches for data gap filling.
- Serves as a platform that incorporates various modules and databases from other sources.
- Is applicable to discrete organic chemicals.
- Is available free of charge. Download instructions and free training material are available online at: www.qsartoolbox.org

In cooperation:



© European Chemicals Agency, 2011
Reproduction is authorised provided the source is acknowledged.

ECHA-11-L-08-EN

QSAR TOOLBOX

The OECD QSAR Toolbox
for Grouping Chemicals
into Categories



<http://www.qsartoolbox.org>

Toxtree: Rulebase for mutagens / carcinogens

Structure-based approach consisting of:

- Compilation of *Structural Alerts* (genotox and non-genotox)
- Three mechanistically-based *QSARs* for congeneric classes (aromatic amines, aldehydes)

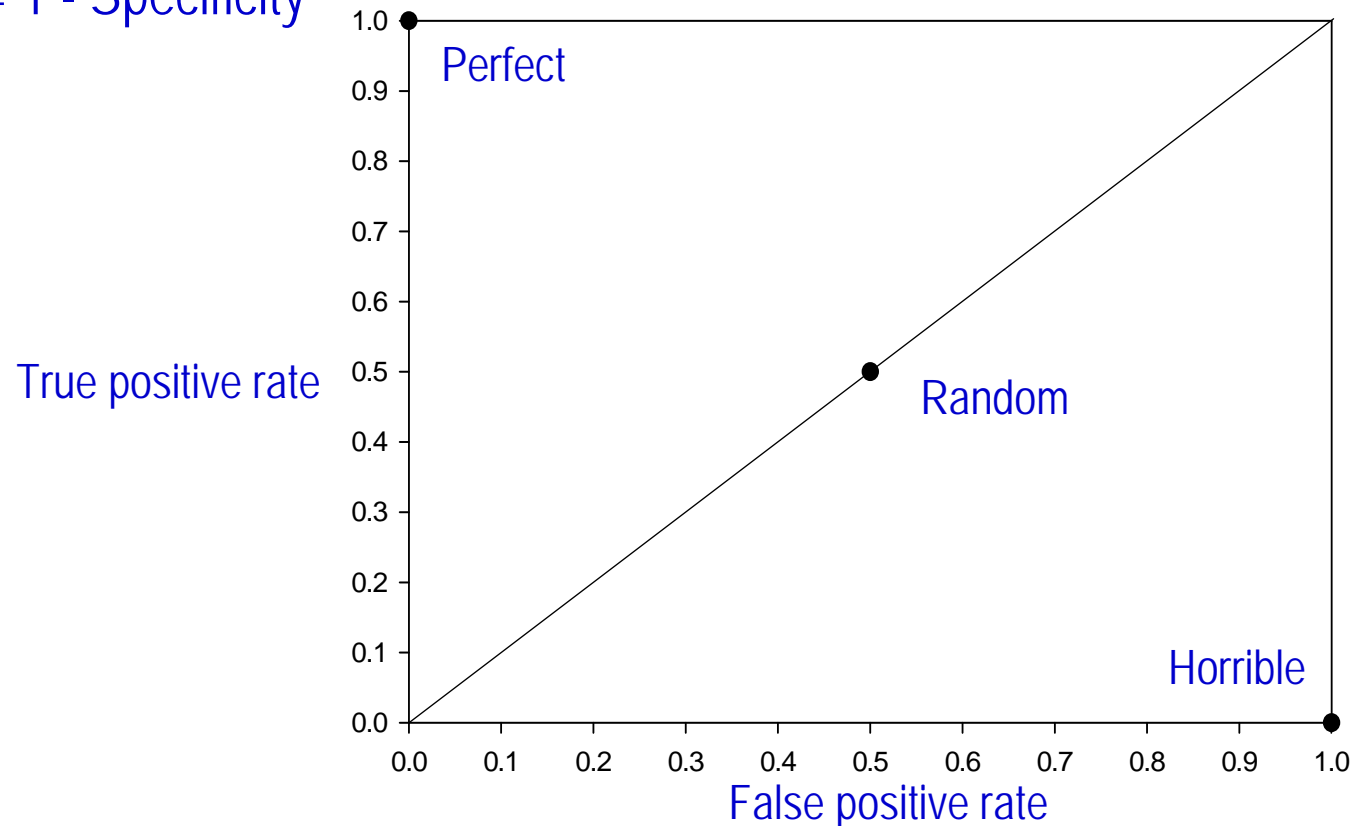
Toxtree (version 2.5)

Open-source, freely available: <http://ecb.jrc.it/qsar/qsar-tools/index.php?c=TOXTREE>

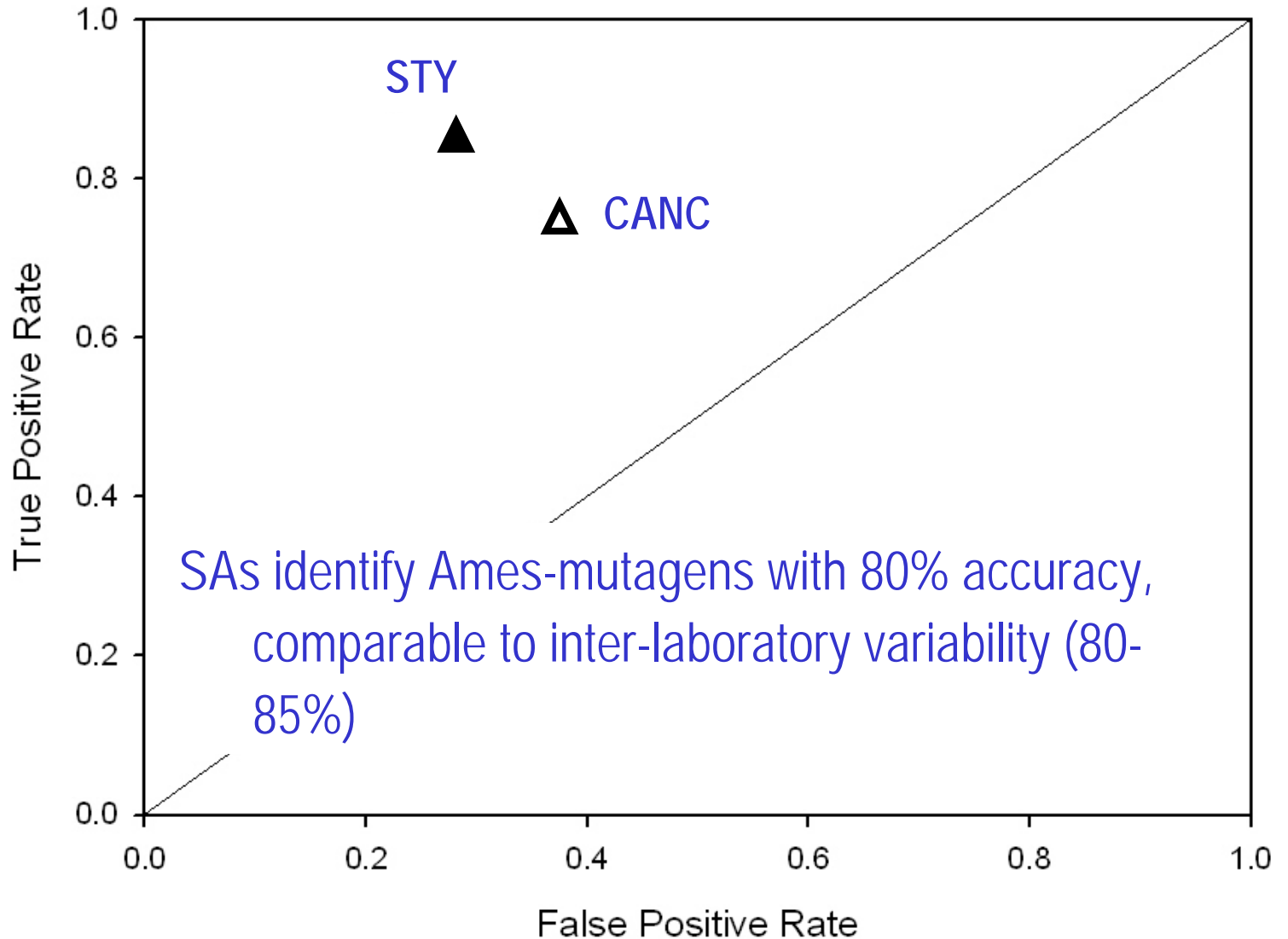
ROC graph: A simple, graphical way of comparing predictions with results

True positive rate = (Positives predicted as positive) / (Real positives)
= Sensitivity

False Positive Rate = (Negatives predicted as positive) / (Real negatives)
= 1 - Specificity



Toxtree SAs: agreement with Carcinogenicity and *Salmonella* (Ames)



Positive Predictivity: Which reliability for toxicity estimates?

Mechanism	Number of substances	SA→Canc	SA→STY	STY→Canc
Acylating	6	0.67	1.0	0.80
Alkylating (direct)	199	0.73	0.60	0.83
Alkylating (indirect)	234	0.86	0.76	0.92
Intercalating	36	0.83	0.86	0.88
Amino-arylated	223	0.75	0.78	0.81
Overall (ISSCAN)	1141	0.77	0.67	0.80

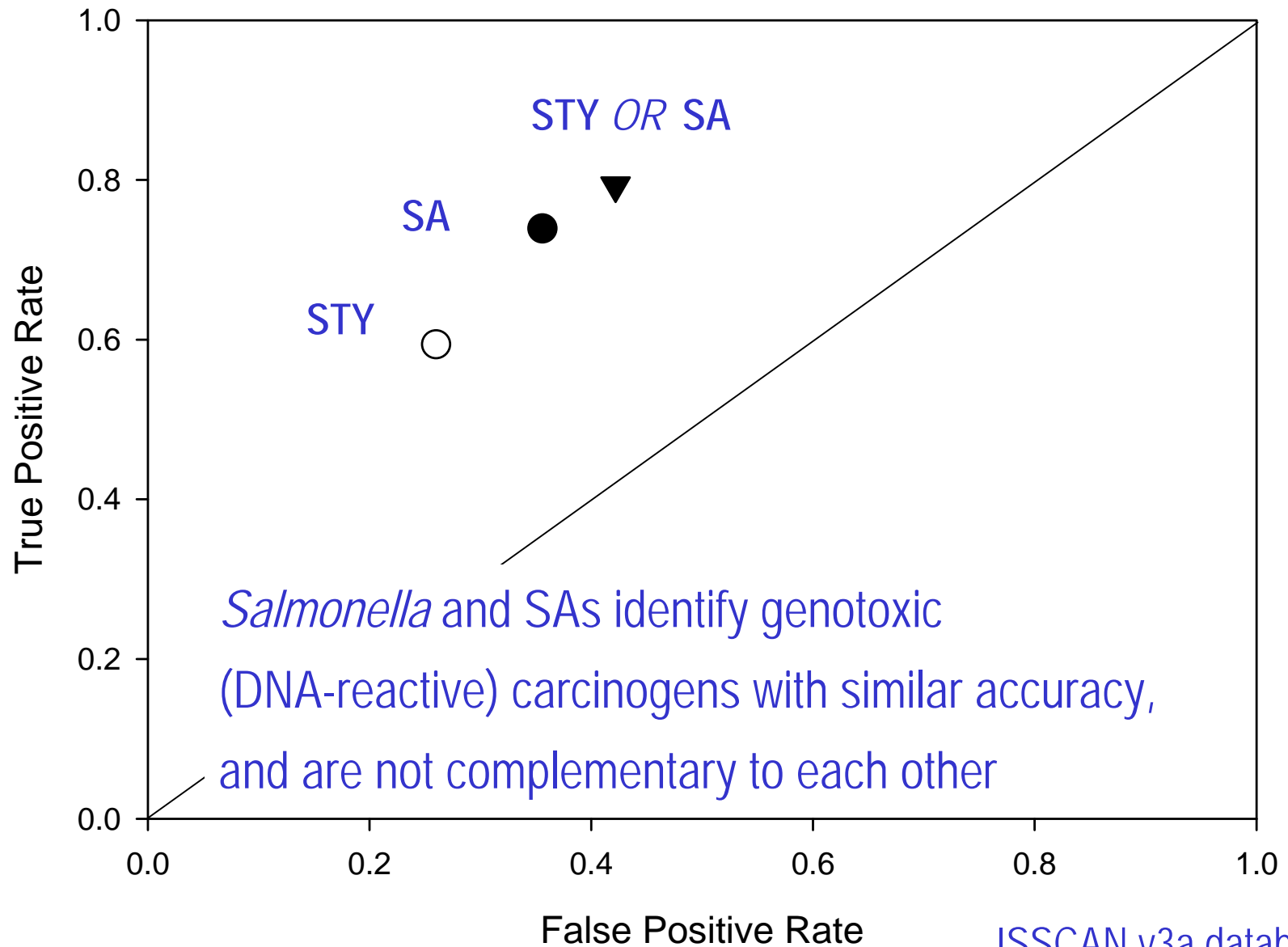
Knowledge on DNA-reactivity (as coded by SAs):

- Reliable enough to predict *Salmonella* results, and identify many carcinogens
- Identify human carcinogens
- Basis for successful priority setting in NTP bioassays (70% carcinogens among structurally suspect chemicals, only 10% among high exposure chemicals)
- Contribution to reduce DNA-reactive carcinogens among synthetic chemicals (pesticides, pharmaceuticals)

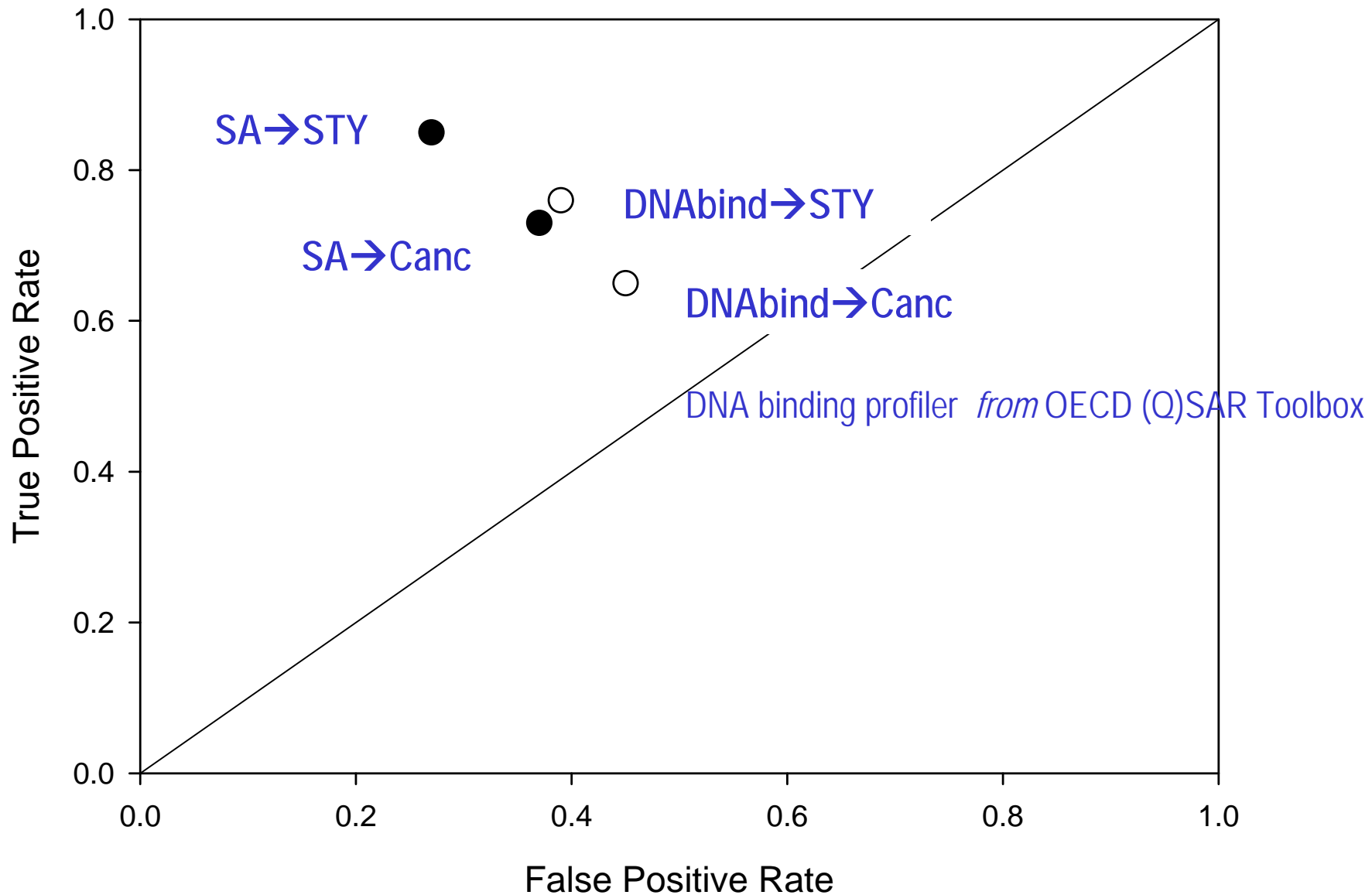
Identifying genotoxic carcinogens through alternative approaches

- *in vitro* assay {*Salmonella*}
- **Structural Alerts** to predict / rationalize experimental results

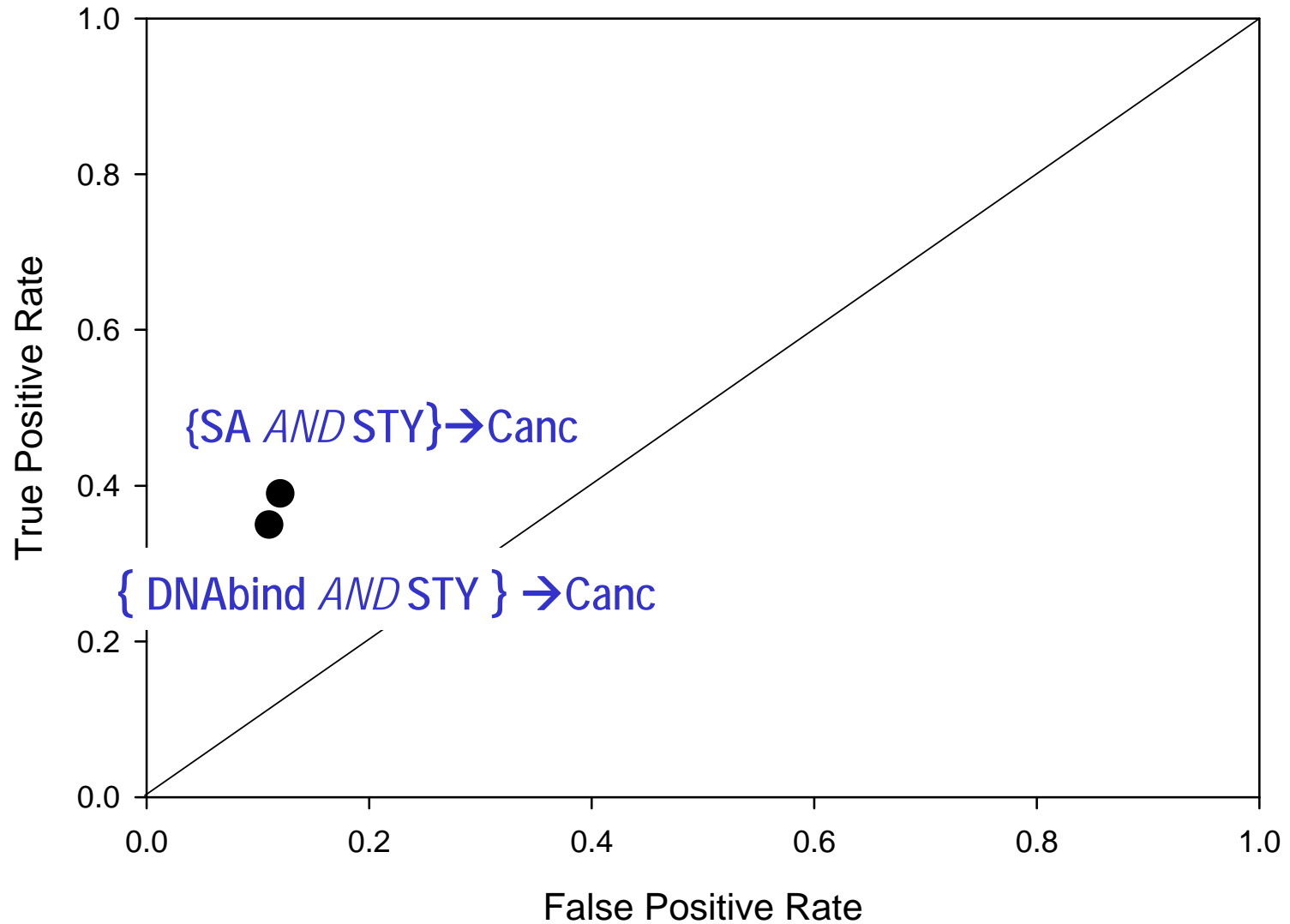
Carcinogenicity prediction: *Salmonella* (Ames) OR SAs



SAs for genotoxic carcinogenicity *versus* DNA-binding potential



Two-tiered approach: Structural considerations *AND* Biological confirmation



Positive predictivity

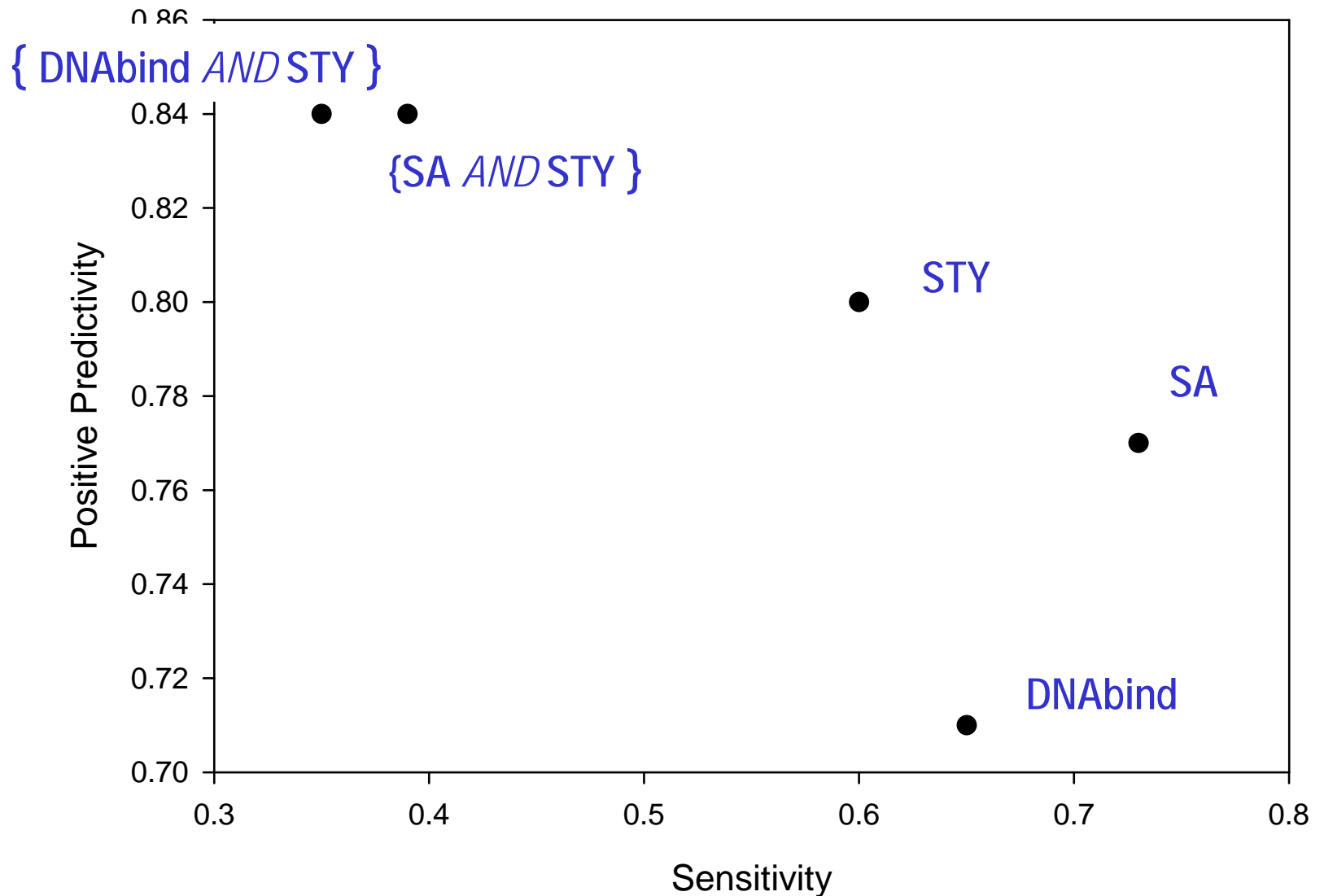
Individual systems

Ames Test	0.80
Structural Alerts	0.77
DNA binding	0.71

Tiered approaches

DNA binding AND Ames Test	0.84
Structural Alerts AND Ames Test	0.84

Positive Predictivity and Sensitivity: inverse functions



Identifying genotoxic carcinogens through alternative approaches:

- *in vitro* assay {*Salmonella*}
- **Structural Alerts** to predict / rationalize experimental results

A flexible process (different estimates can be attached to the chemicals, with different coverage / reliability)

High reliability can be attained

Acknowledgements

- Istituto Superiore di Sanita'

Alessandro Giuliani

Cecilia Bossa

Olga Tcheremenskaia

Chiara Laura Battistelli