

Interreg
CENTRAL EUROPE



AMIIGA

European Union
European Regional
Development Fund

TAKING
COOPERATION
FORWARD



Milano, 12 giugno 2019



AMIIGA



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Politecnico di Milano - Dipartimento di Ingegneria Civile e Ambientale

INTEGRATED APPROACH TO MANAGEMENT OF GROUNDWATER QUALITY IN FUNCTIONAL URBAN AREAS



AMIIGA

AMIIGA project tackles the issue of complicated groundwater contamination crossing administrative borders.

In 6 Central European countries, representing the typical groundwater contamination problems, AMIIGA project is testing advanced investigation and assessment tools:

- statistical analysis to explore large monitoring datasets
- numerical modelling to spatially delimit the boundary of the plumes
- CSIA (Compound Specific Isotope Analysis) to distinguish between contaminant's sources and demonstrate degradation processes
- BMT (Biological Molecular Tool) to evaluate the capability of indigenous microbial consortia to degrade contaminants in situ.



This transnational cooperation project is funded by **Interreg CENTRAL EUROPE** and aims to improve sustainable use of natural heritage.

12 project partners

8 regions

7 pilot actions

18 outputs

2.9 million EUR Project budget

2.4 million EUR ERDF funding



WORK PACKAGES



WP M	Management [PP1 GIG]	Start: 09.2016 End: 08.2019
WP1	Tools for remediation and pollution management in FUA [PP7 PoliMi]	Start: 10.2016 End: 12.2018
WP2	Groundwater remediation - from conceptual model to realization [PP5 TUL]	Start: 09.2016 End: 08.2019
WP3	Management plan [PP3 Stuttgart]	Start: 10.2016 End: 08.2019
WP C	Communication [PP8 Parma]	Start: 10.2016 End: 08.2019

<http://www.interreg-central.eu/AMIIGA>

This project is supported by the Interreg CENTRAL
EUROPE Programme funded under the European Regional
Development Fund.

€	2.959.471,74	»» Project budget in EUR
€	2.444.589,52	»» ERDF funding in EUR
🕒	01/09/2016 - 31/08/2019	»» Project duration



TAKING COOP

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Grzegorz Gzyl |
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ACTIVITIES



WP1	Tools for groundwater pollution assessment and remediation in Functional Urban Areas (FUAs)	Start date: 10.2016 End date: 12.2018
Activity A.T1.1	FOKS tools amendment and adaptation to FUA scale	Start date: 10.2016 End date: 10.2017
Activity A.T1.2	Innovative CSIA TOOL for pollution and remediation assessment	Start date: 12.2016 End date: 10.2018
Activity A.T1.3	Innovative BMTs TOOL for natural and enhanced bioremediation implementation	Start date: 12.2016 End date: 10.2018
Activity A.T1.4	Harmonizing of innovative tools CSIA with previously amended FOKS tools	Start date: 09.2017 End date: 12.2018
Activity A.T1.5	Trainings and internships for improving technical skills and cooperative development of tools	Start date: 02.2017 End date: 09.2018

Activity
A.T1.1

**FOKS tools amendment and
adaptation to FUA scale**

Start date: 10.2016
End date: 10.2017

The tools developed during the previous FOKS project were designed to be applied at the scale of a single contaminated site

In order to be applied at FUA scale they needed to be adapted considering the existence of 2 kinds of contamination:

Point Sources (PS), responsible of medium-high concentration plumes

Multiple Point Sources (MPS), constituted by multiple small and unidentifiable sources responsible of an anthropogenic diffused contamination

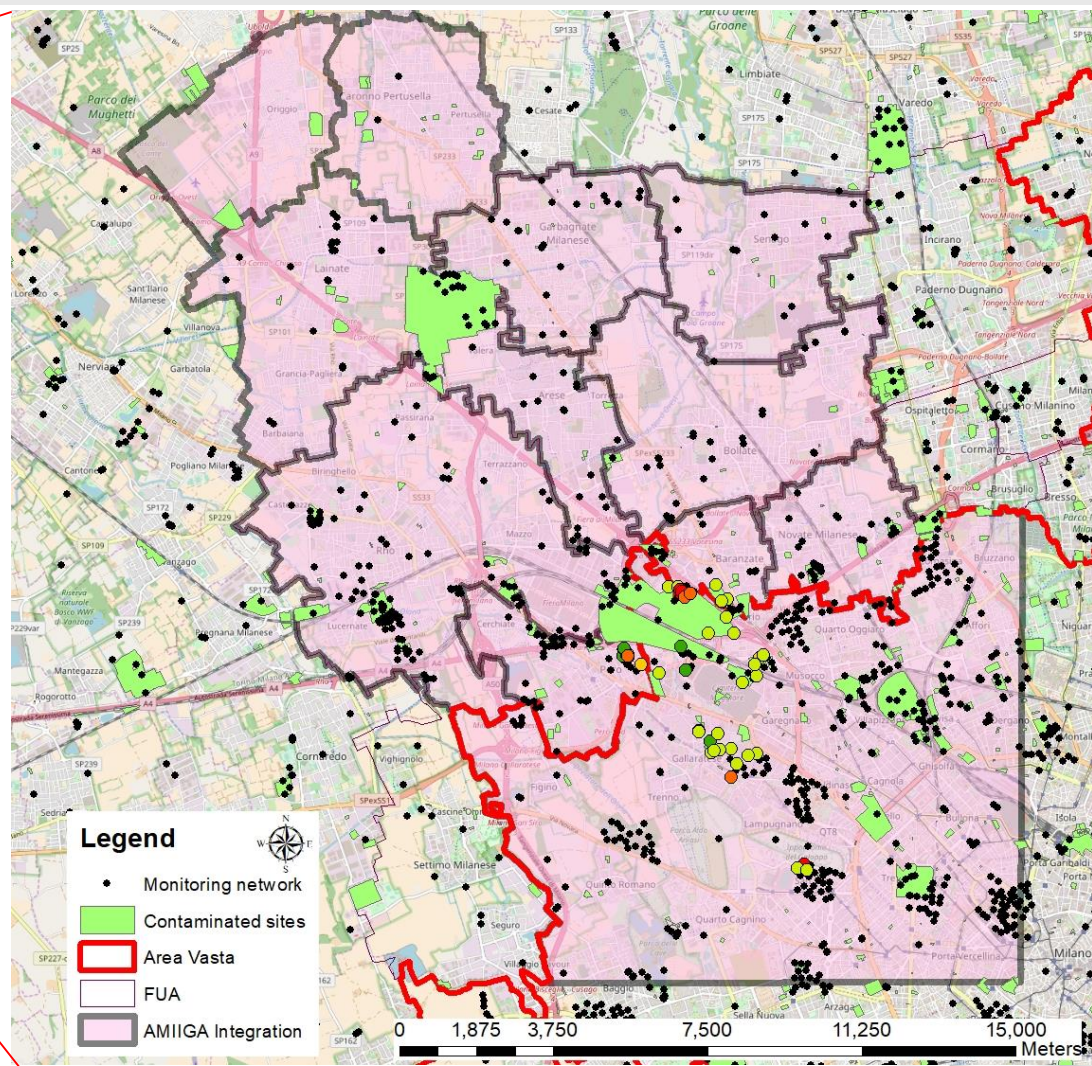
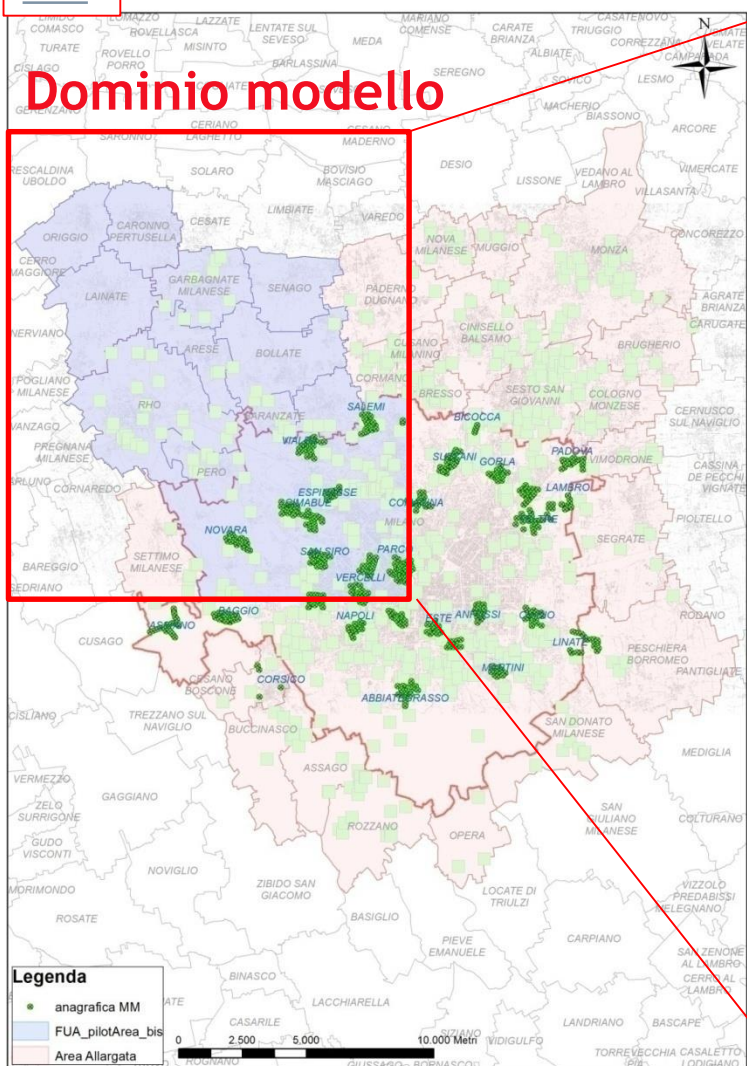


WEBGIS

[link](#)



Dominio modello



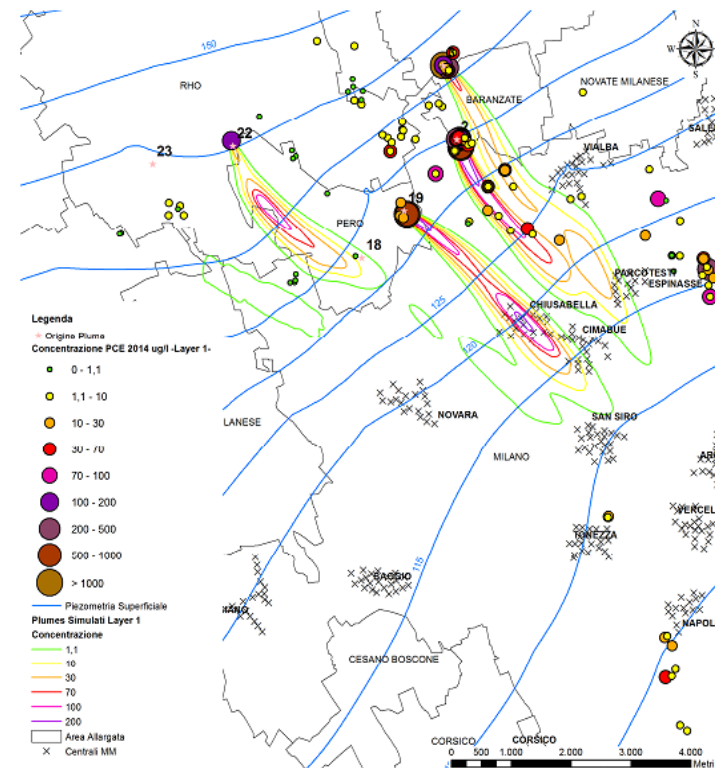
HOW TO LOCATE SUSPECTED SOURCES?



Milano FUA had a long industrial history since the 50^{ies}. Many Chlorinated Hydrocarbons plumes are still present and they hit some public wells. Often, as in many industrial districts, plumes with high concentrations are detected but the contaminant source position (PS) is unknown. As Milano aqueduct is fed only by groundwater the Public Authorities are asking:

HOW CAN WE DISTINGUISH THE DIFFUSE CONTAMINATION FROM THE POINT SOURCES CONTAMINATION?

HOW CAN WE IDENTIFY THE AREA WHERE THE PUNCTUAL SOURCES ARE POSITIONED?



TOOLS DEVELOPMENT



Activity A.T1.1	FOKS tools amendment and adaptation to FUA scale	Start date: 10.2016 End date: 10.2017
Deliverable D.T1.1.1	Web-GIS tool development for groundwater database management and open-access consultation	Delivery date: 10.2017 concluded
Deliverable D.T1.1.2	Guideline for statistical method and geostatistical analysis for GW quality studies at FUA	Delivery date: 03.2017 concluded
Deliverable D.T1.1.3	GW contamination modeling at FUA: “inverse iterative modeling” guideline for implementation and use	Delivery date: 04.2017 concluded
Deliverable D.T1.1.4	Technical protocol for statistical analysis coupled with transport modeling for GW pollution assessment	Delivery date: 05.2017 concluded



STATISTICAL TOOL



In AMIIGA one of the aims of WP1 is to develop and test a methodology to answer these questions

HYDROCHEMICAL DATA SET (2003-2014) AVAILABLE IN MILANO FUA (TCE,PCE,CLF)

Cluster analysis

Hot-spot location

Groundwater
Transport model
(Modflow-MT3D)

PLUME extension
in FUA

GEOSTATISTICAL analysis
(cleaned dataset)

Factor and
Multivariate
analysis

Diffuse contamination MAPS and assessment

Stochastic modelling for
particle backtracking

Probabilistic MAPS of PS position

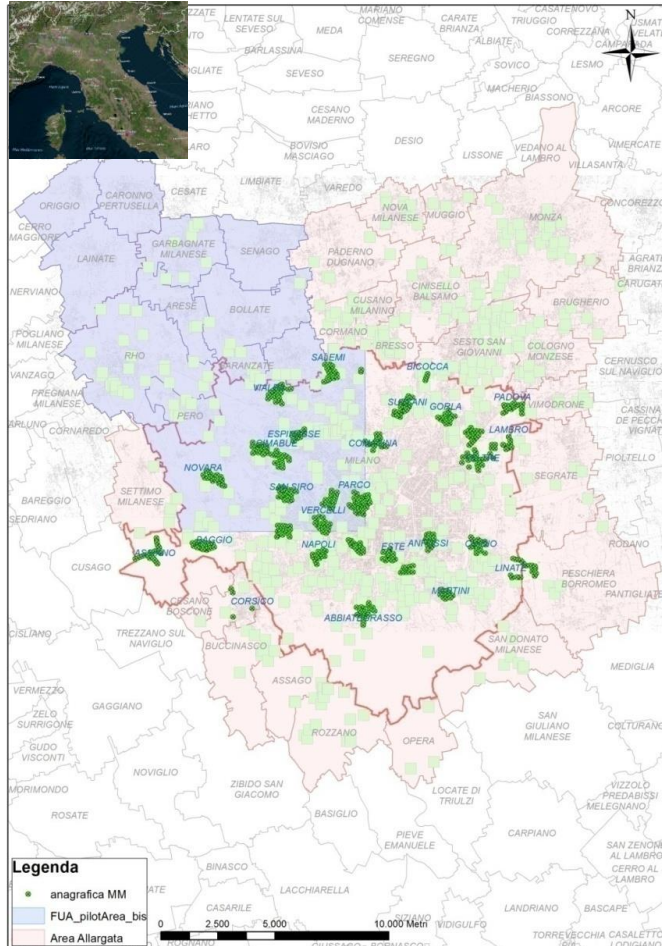
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1st RESULT

METHODOLOGY

2nd RESULT

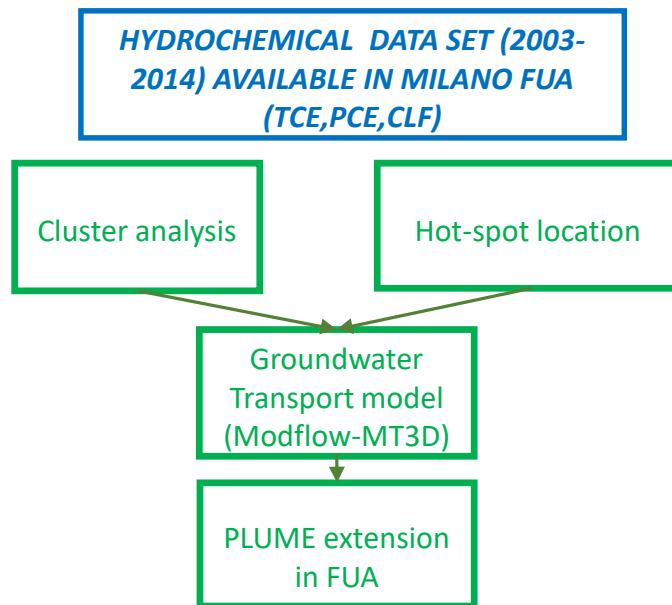
TAKING COOPERATION FORWARD



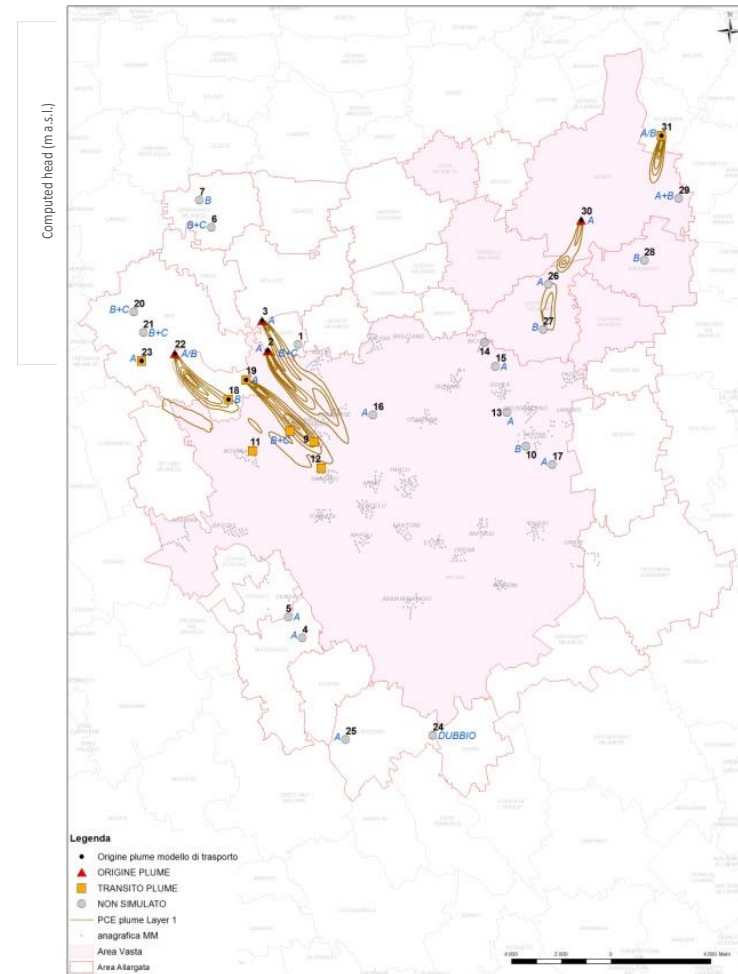
STATISTICAL TOOL



Once hot spots have been identified a groundwater transport model has been applied to assess the PCE plume extension



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STATISTICAL TOOL



Once the plumes extension is simulated the monitoring points hit by them can be canceled from the dataset

HYDROCHEMICAL DATA SET (2003-2014) AVAILABLE IN MILANO FUA (TCE,PCE,CLF)

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Groundwater
Transport model
(Modflow-MT3D)

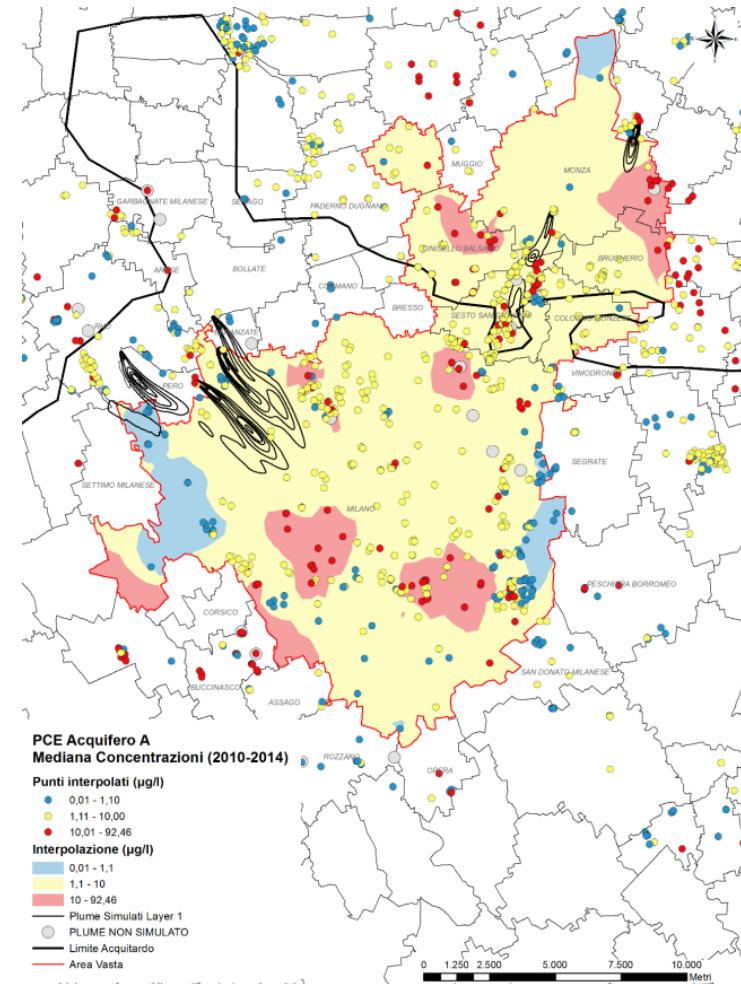
PLUME extension
in FUA

GEOSTATISTICAL analysis
(cleaned dataset)

**Diffuse
contamination
MAP**

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RESULTS



COOPERATION FORWARD

STATISTICAL TOOL



Diffuse contamination map showed that is incorrect to define a single PCE diffuse value for the entire study area. Then Factor and Multivariate analysis have been applied to define the proper value in each of the areas (yellow and read) where concentrations are higher than the Italian threshold limit ($1,1 \mu\text{g/l}$)

HYDROCHEMICAL DATA SET (2003-2014) AVAILABLE IN MILANO FUA (TCE,PCE,CLF)

Cluster analysis

Hot-spot location

Groundwater
Transport model
(Modflow-MT3D)

PLUME extension
in FUA

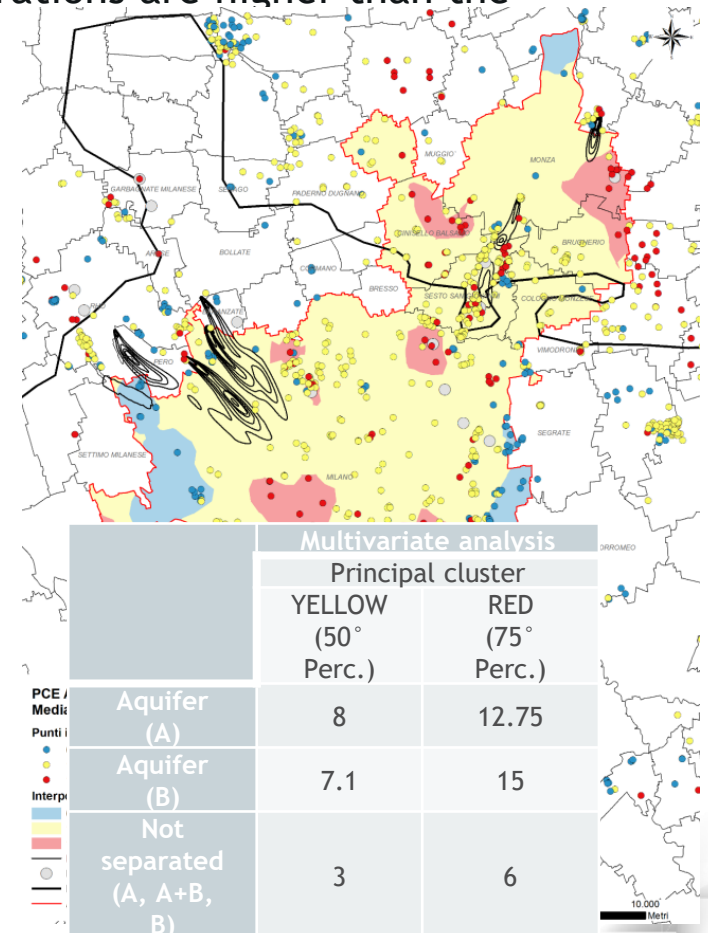
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(cleaned dataset)

Factor and
Multivariate
analysis

Diffuse contamination MAPS and assessment

*M
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RESULTS



COOPERATION FORWARD

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PS POSITIONING

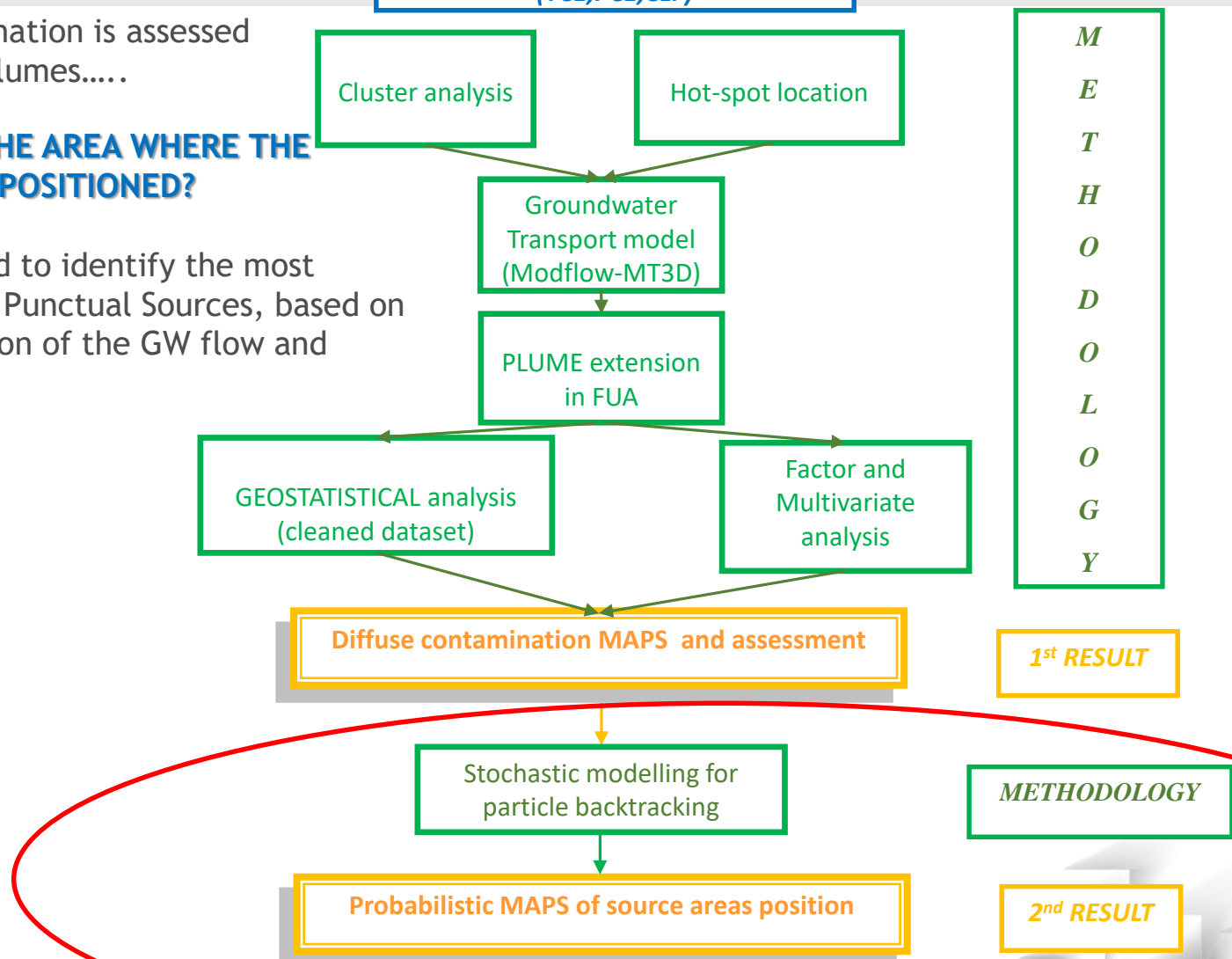


HYDROCHEMICAL DATA SET (2003-2014) AVAILABLE IN MILANO FUA (TCE,PCE,CLF)

Once the diffuse contamination is assessed and separated from the plumes....

HOW CAN WE IDENTIFY THE AREA WHERE THE PUNCTUAL SOURCES ARE POSITIONED?

We are proposing a method to identify the most probable position of these Punctual Sources, based on inverse numerical simulation of the GW flow and advective transport



1- DETERMINISTIC MODEL



First a GW flow model was implemented and calibrated for the Milano Pilot Area

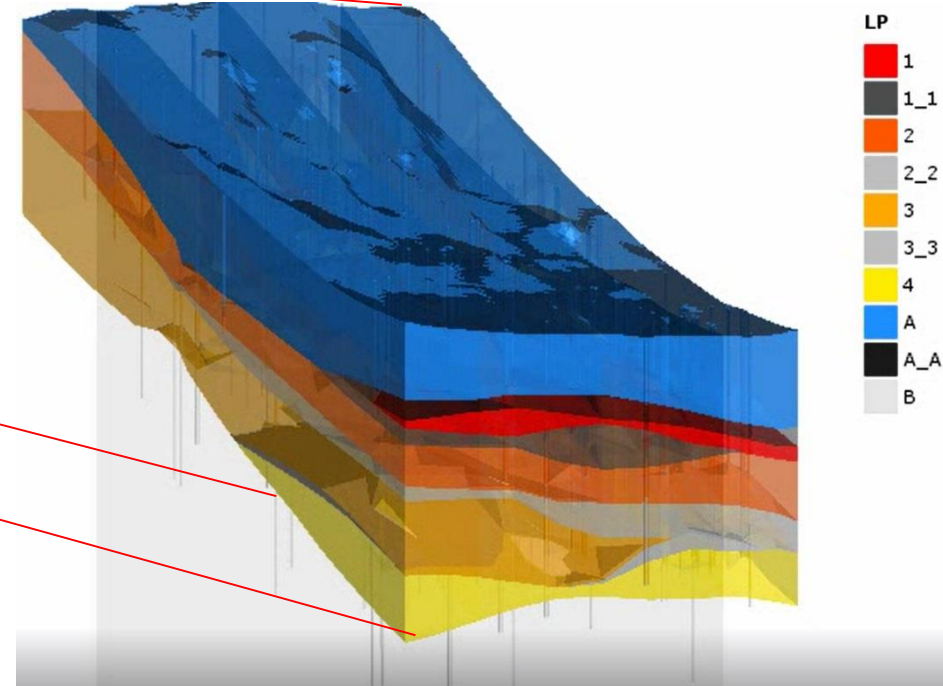
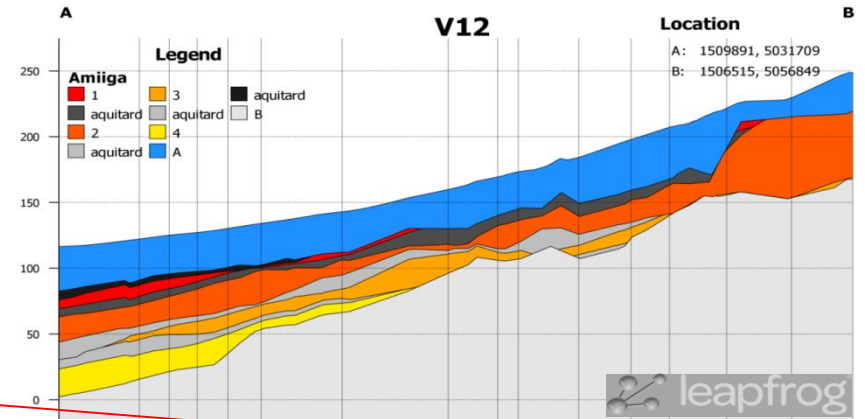
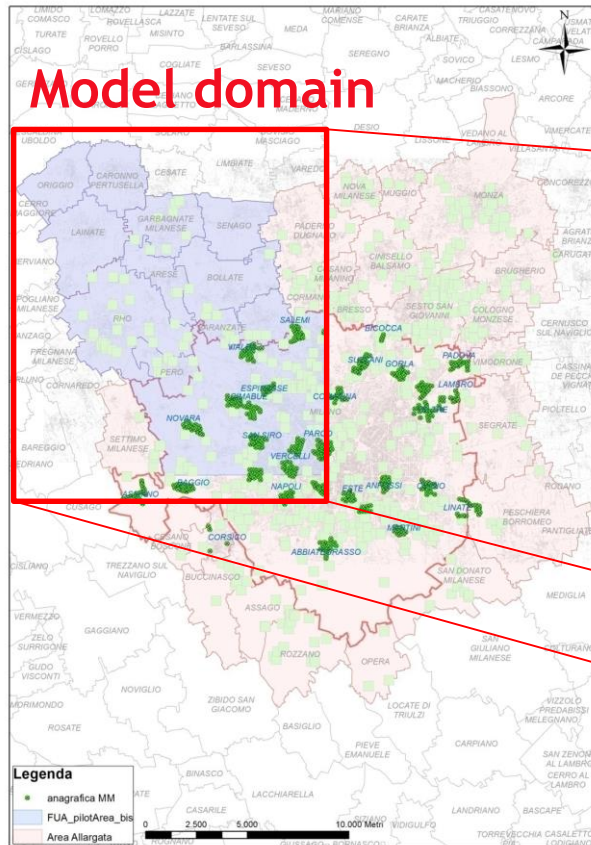
MODFLOW 2005

19x 21 Km

255.320 cells

From 100 m to 50 m

9 layers

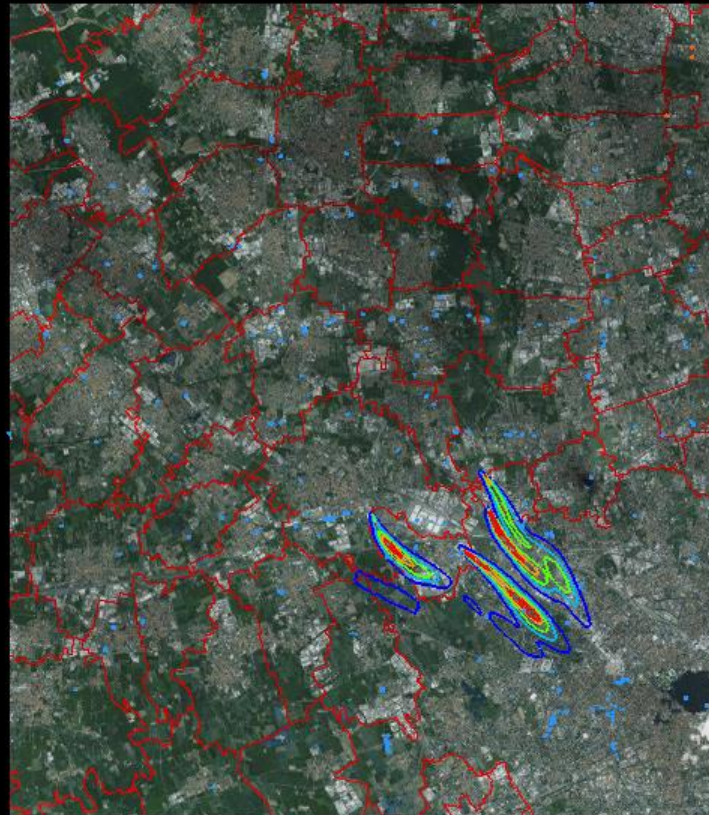


1- DETERMINISTIC MODEL



First a GW flow model was implemented and calibrated for the Milano Pilot Area

MODFLOW 2005
19x 21 Km
255.320 cells
From 100 m to 50 m
9 layers



Aquifer

- Aquifer A
- Aquifer B1
- Aquifer B2
- Aquifer B3
- Aquifer B4
- Aquitard



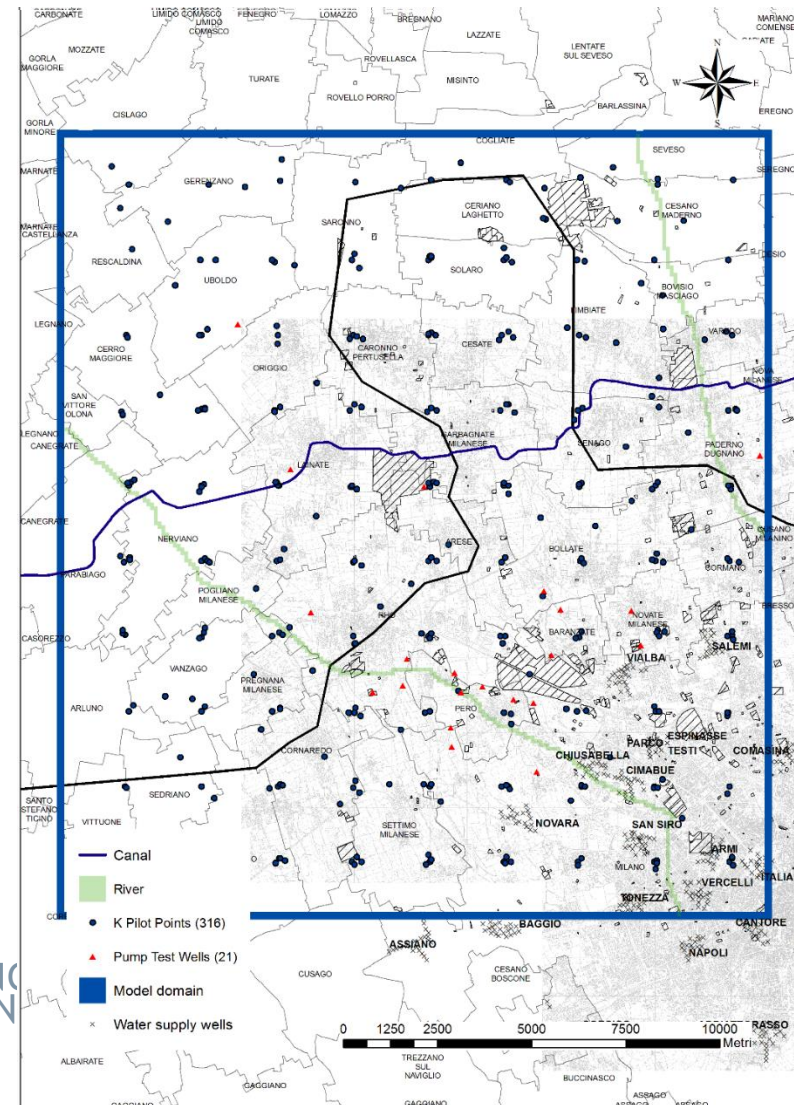
2- STOCHASTIC MODELING



The deterministic model was based in a single distribution of the **hydraulic conductivity (K)**
In order to explore the uncertainty link to the K distribution an inverse calibration through **PEST** was done using the **Pilot Points** technique

- **316 K-pilot points** where regularly placed in the model domain (10^{-5} - 10^{-2} m/s for aquifer layers, 10^{-8} - 10^{-6} m/s for clay lenses)
- **21 aquifer tests** where associated with **Pilot Points**
- **44 observations (head targets)** placed in different layers based on screened levels

Starting from the deterministic calibrated model, we randomly generate 400 different realizations of K-fields. Only them that were able to provide a satisfactory fit to observations were kept for the next step

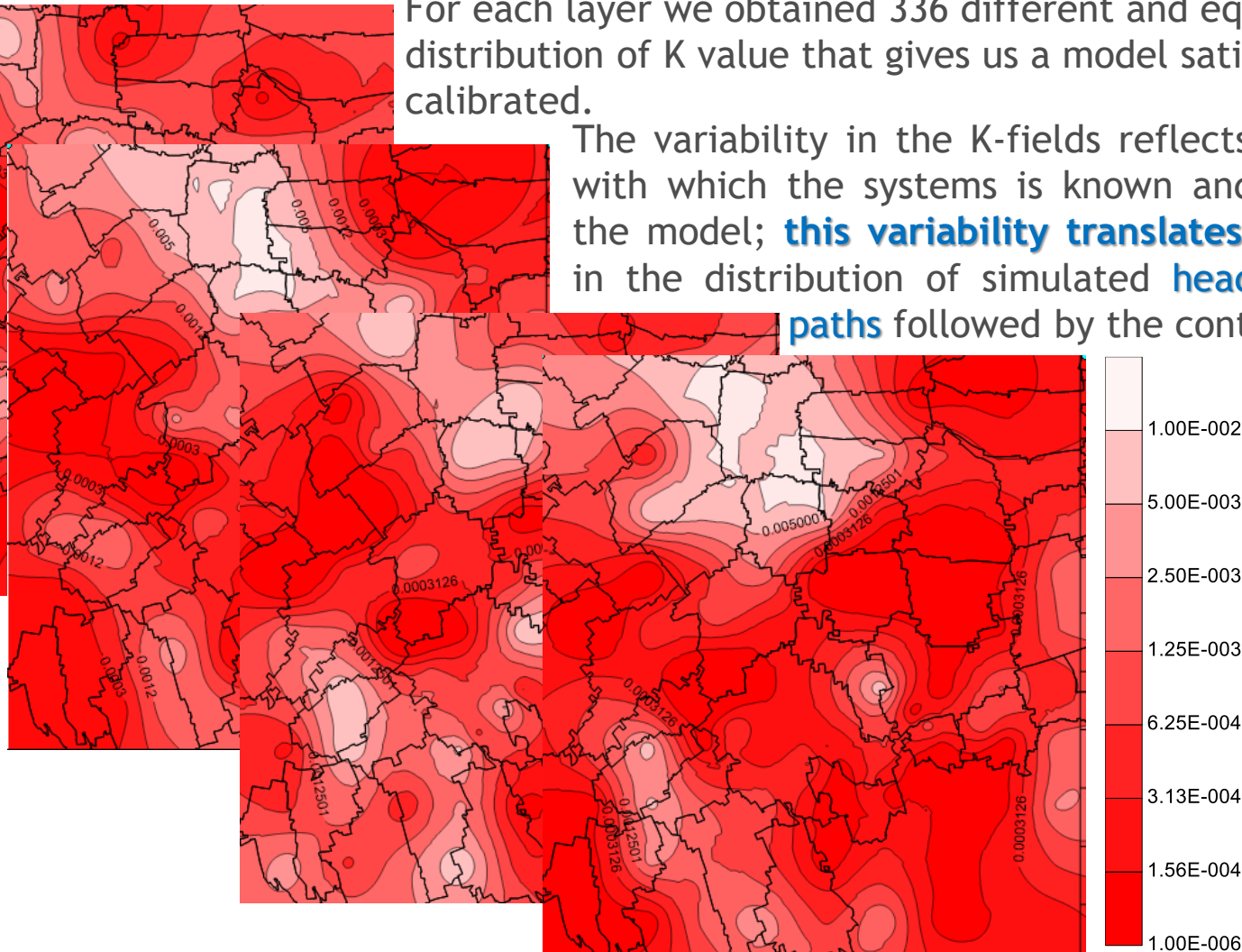


2- STOCHASTIC MODELING



For each layer we obtained 336 different and equally possible distribution of K value that gives us a model satisfactorily calibrated.

The variability in the K-fields reflects the uncertainty with which the systems is known and represented by the model; **this variability translates into** differences in the distribution of simulated **heads**, hence in the **paths** followed by the contaminants.



3- PARTICLE BACK-TRACKING



MONTE CARLO APPROACH

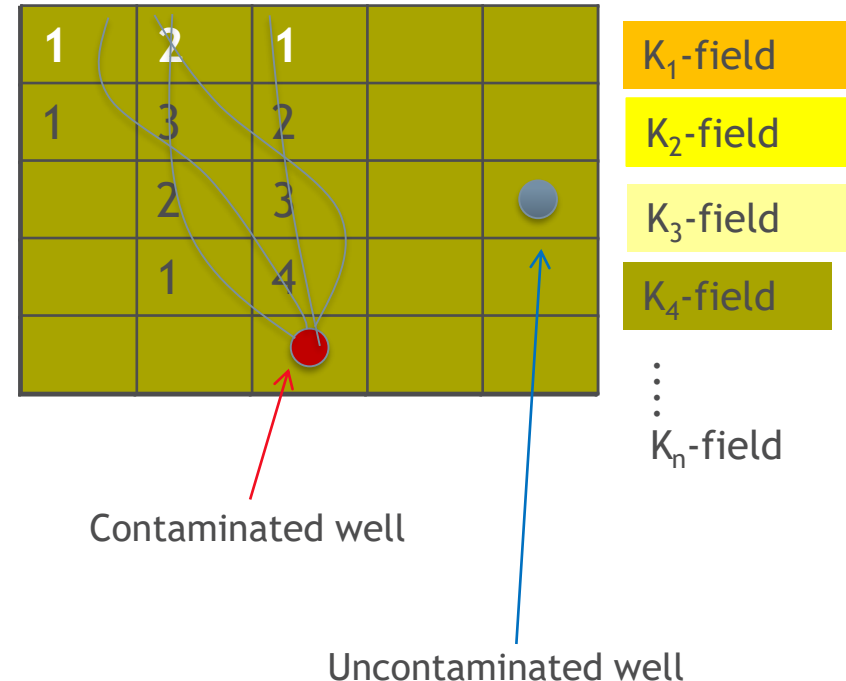
In each well having a concentration $> 10 \mu\text{g/l}$ particles were added

Then particles were traced backward for each of the 336 previously calibrated simulations

Particles follow different paths in each simulation depending on the selected K-field, but some path are followed more frequently

The number of particle passing in each cell is counted for the 336 simulations

Cells with an high number of passages have an high probability to contain the source responsible of the contamination



336 POSSIBLE K-FIELDS

336
BACKWARD PARTICLE
TRACKING (MODPATH)



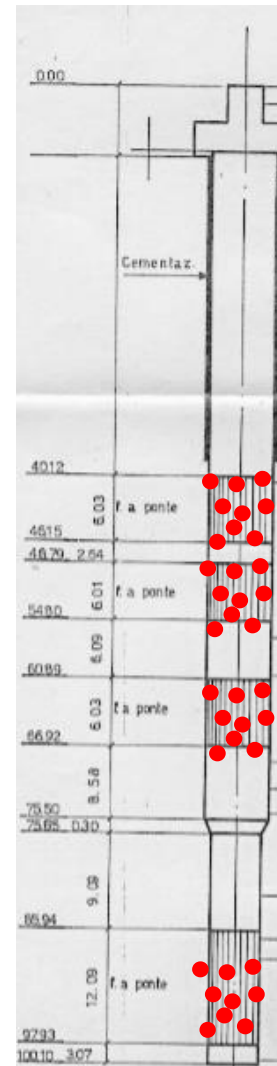
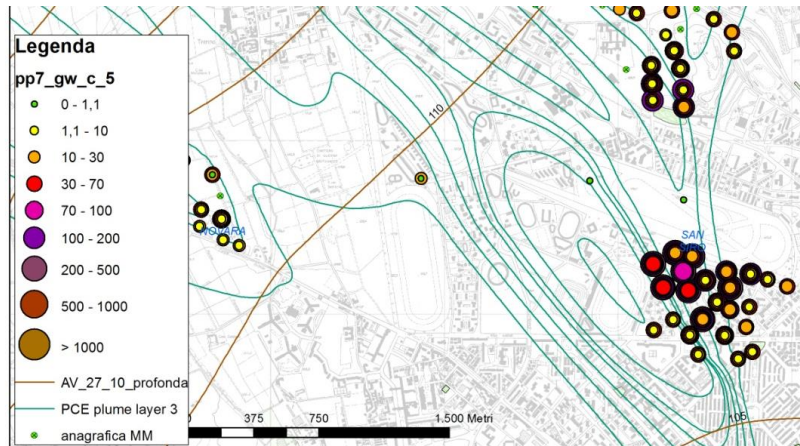
3- PARTICLE BACK-TRACKING



MONTE CARLO APPROACH

San Siro public wells suffer a PCE contamination since at least 30 years. Recently concentration raised till $300 \mu\text{g/l}$. Many industrial sites located up-gradient could be considered responsible of this contamination.

- particles weighted on concentration, (i.e **1 particle every $10 \mu\text{g/l}$**) where added to 6 contaminated wells
- for each well particles are equally distributed in all the layers screened



EXAMPLE San Siro well 3
PCE = $90 \mu\text{g/l}$
Screens in 4 layers
9 particles in each layer

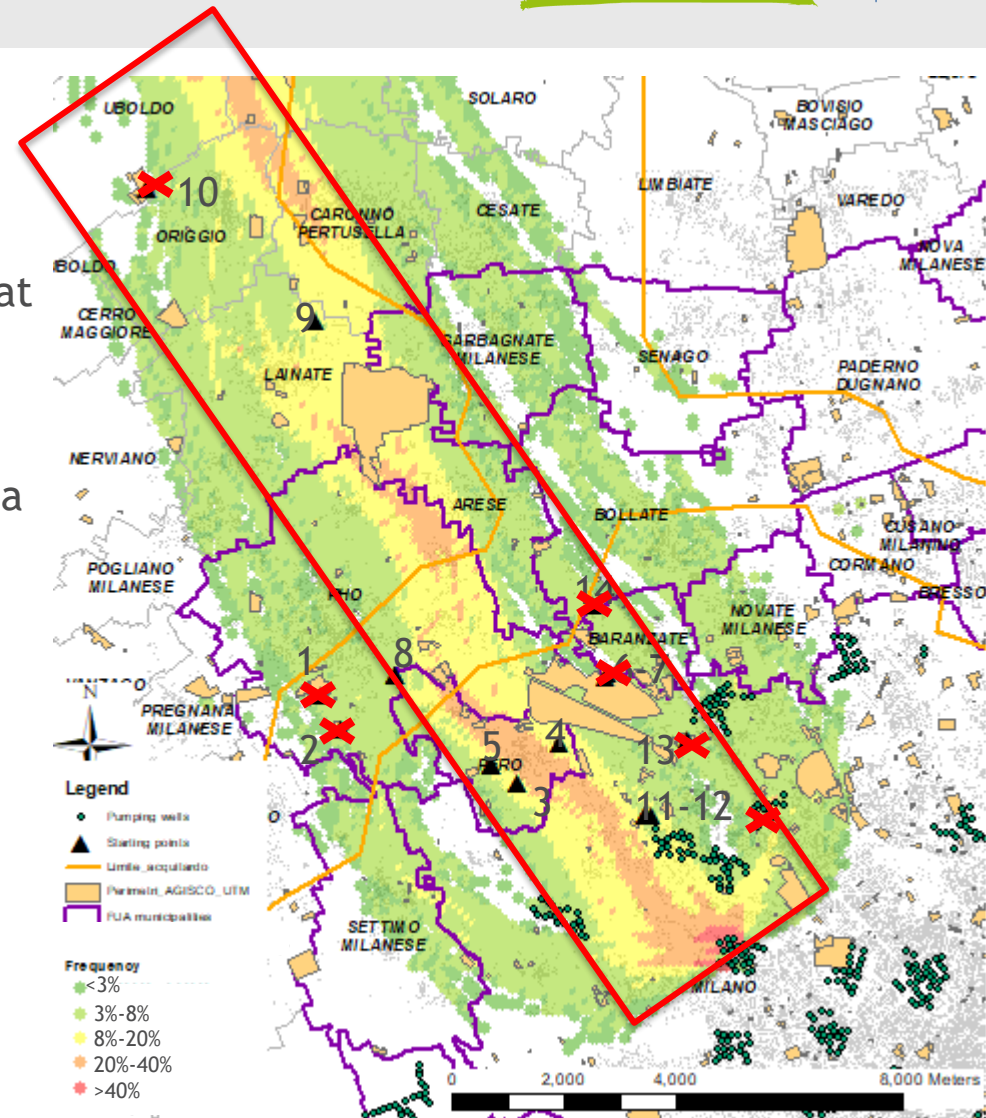
3- PARTICLE BACK-TRACKING



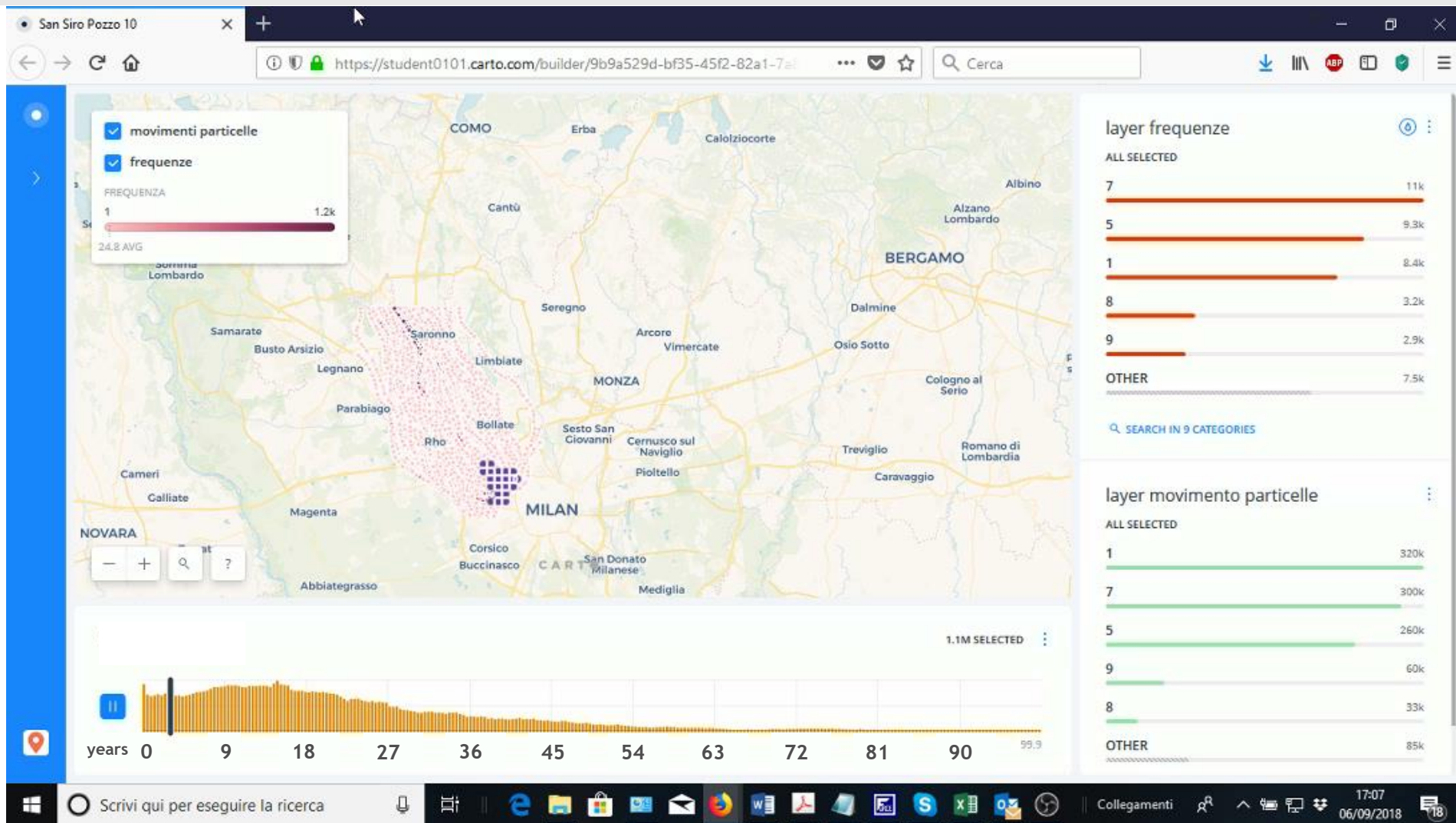
MONTE CARLO APPROACH

We obtained a probabilistic map showing the likelihood of each cell to contain the source that hit the San Siro public wells

Overlapping this map with the layer containing the industries position it is possible to prepare a ranking list of the areas that need to be deeply investigate



RESULTS ANALYSIS



ACTIVITIES



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Activity A.T1.1	FOKS tools amendment and adaptation to FUA scale	Start date: 10.2016 End date: 10.2017
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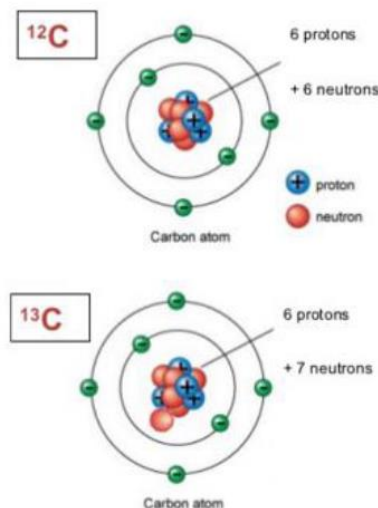
ISOTOPE FINGERPRINTING



Another activity developed in the AMIIGA project is the application of **Isotope Fingerprinting techniques (CSIA)**

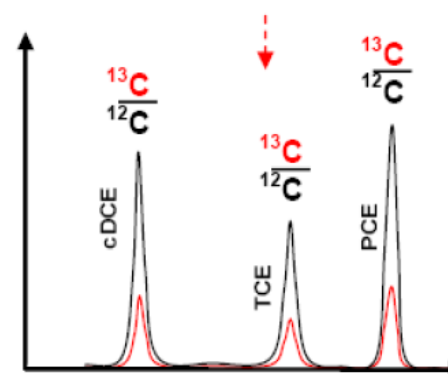
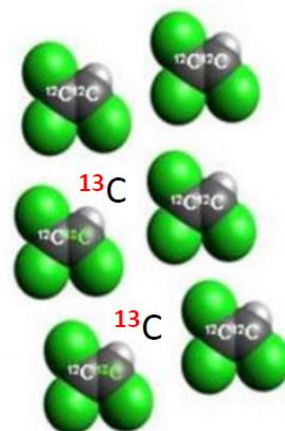
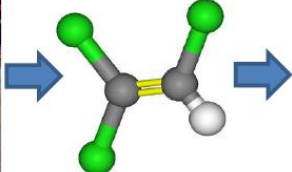
Politecnico di Milano has a research line dedicated to CSIA. Research development as analytical methods and field tests are developed in collaboration with **ENI** and **IT²E** laboratories and analysis for $^{13}/^{12}\text{C}$, $^{37}/^{35}\text{Cl}$, $^2/^1\text{H}$ are performed through GC-IRMS.

An isotope is an atom of a same chemical element (e.g. C) having the same atomic number but a different atomic mass: this because they have a different number of neutrons (e.g. ^{12}C and ^{13}C)



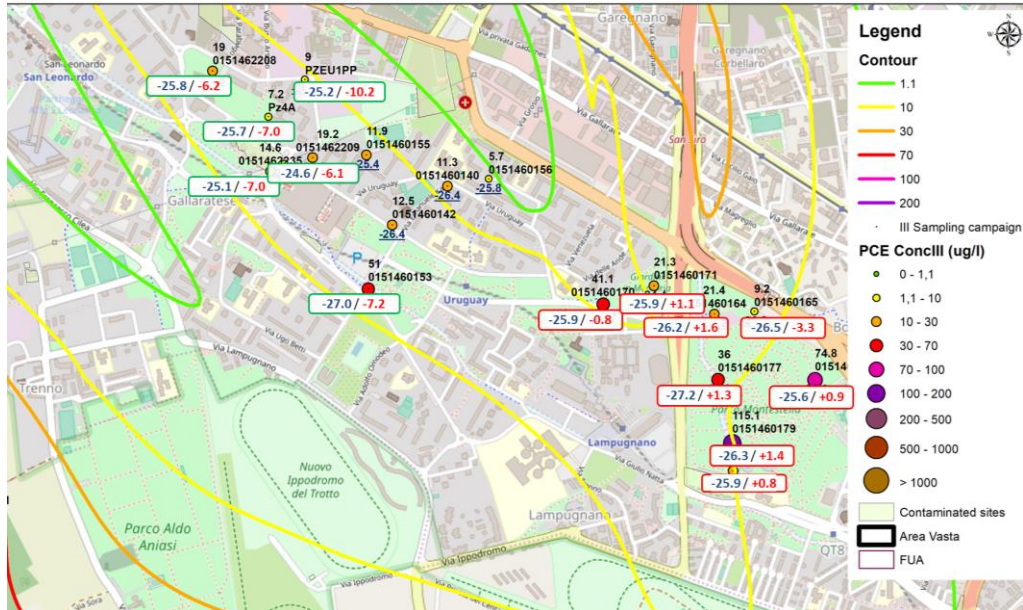
TCE

Trichloroethylene (TCE)



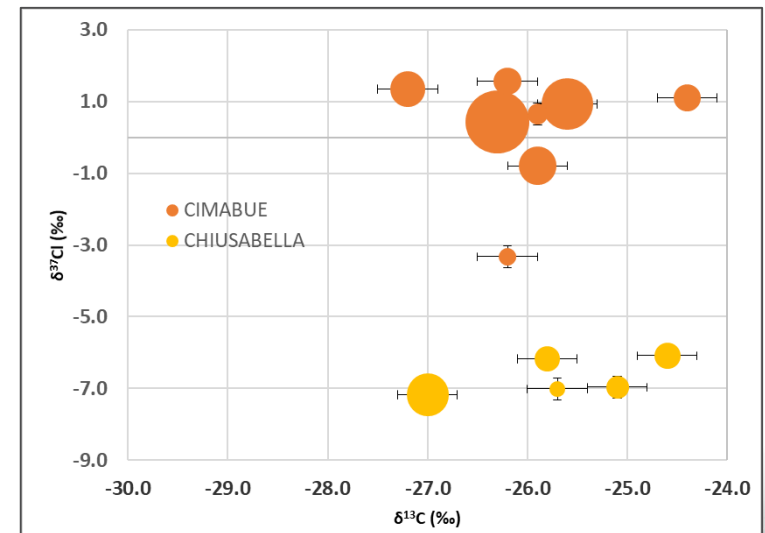
— TAKING COOPERATION FORWARD

ISOTOPE FINGERPRINTING



Analysis of $^{13}/^{12}\text{C}$, $^{37}/^{35}\text{Cl}$ (dual isotope) allowed to confirm that the Chiusabella e Cimabue pumping stations are reached by 2 different plumes

In the AMIIGA project Compound Specific Isotope Analysis have been applied in Italy, Germany, Poland and Czech Rep. In Milano have been applied in order to verify the results of the groundwater and transport modeling and than confirm the developed conceptual model.



ISOTOPE FINGERPRINTING



Deliverable D.T1.2.3

Freeware software for CSIA data analysis for remediation assessment

groundwater pollutants with BIOCHLOR-ISO. *Journal of Contaminant Hydrology*, 2016

P. Hühner

patrick.huhner@univ-smu.fr

Version 4.2V with Cretnik-Correction

Aix-Marseille Université-CNRS, Laboratoire Chimie Environnement UMR 7376, Marseille

Run on Excel 2010 or later

1D Case, no sorption, constant source PCE

With decreasing rate constant

White cells

115

Enter value directly... or if you want to calculate:

Blue cells

0,02

Use blue cells for calculating the white cell; formula is given under the arrow

Orange or

grey cells

Do not change anything in grey or orange cells

TYPE OF CHLORINATED SOLVENT: **Ethenes**

1. ADVECTION

Seepage Velocity	V_z	310,1	(m/yr)
Hydraulic Conductivity	K	5,9E-04	(m/sec)
Hydraulic Gradient	i	0,005	(m/m)
Effective Porosity	n	0,3	(-)

2. DISPERSION

Alpha _{xx}	20	(m)
Alpha _{yy}	2	(m)
Alpha _{zz}	0,20	(m)

3. ADSORPTION

Retardation Factor*	R_f	
Soil Bulk Density, rho _b	1,7	(kg/L)
Fraction Organic Carbon, f _{oc}	0,0010	(-)
Partition Coefficient	K _{oc}	
PCE	426	(L/kg)
TCE	130	(L/kg)
DCE	125	(L/kg)
VC	30	(L/kg)
Common R _f (used in model)*	2,01	(-)

4. BIOTRANSFORMATION First Order Decay Coefficients

	k (1/yr)	half-life (yr)
PCE	0,69	1,00
TCE	0,69	1,00
DCE	0,69	1,00
VC	0,69	1,00

5. ISOTOPES

	δ C bulk	Initial $\delta^{13}C$	δ C bulk	δ offset Cl	Initial $\delta^{37}Cl$
PCE	-1,00	-26,5	-2,0	na	0,0
TCE	-10,0	-30,0	-3,0	na	0,0
DCE	-10,0	-30,0	-2,0	-1,0	0,0
VC	-10,0	-30,0	-2,0	na	0,0

Switch for TCE-DCE

1

0: Cretnik correction; 1: Standard approach

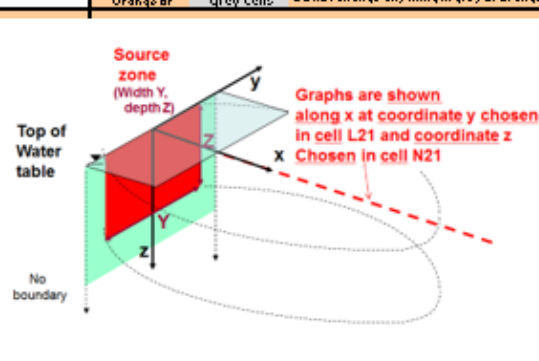
6. GENERAL

Simulation Time	50,0	(yr)	Used time	58,00
Modeled Area Width	na	(m)	Integ. Step	
Modeled Area Length	1200	(m)		1,08875

7. SOURCE DATA

Source Thickness in Sat.:	Z	25	(m)
Width* (m)	50	Y	

Compound Conc. (mg/L)	Conc. (mM)	Threshold (mM)
PCE	4,0	0,024
TCE	0,1	0,001
DCE	0,1	0,001
VC	0,0	0,000
ETH	na	0



4a. FIELD DATA FOR COMPARISON (in mg/L)		y Coordinate		z Coordinate		Date:		na	
Dist. x from Source		0	125	176	200	224	231	1163	
PCE	mg/L	4,00	0,15	0,03	0,03	0,01	0,00	0,00	
TCE	mg/L	0,00	0,00	0,00	0,00	0,00	0,00	0,00	
DCE	mg/L	0,00	0,02	0,01	0,01	0,00	0,00	0,00	
VC	mg/L								
ETH	mg/L								
Chloride	mg/L								
Carbon isotopes									
PCE	$\delta^{13}C$	-26,5	-26,5	-23,1	-24,1	-25,0	-24,3	-24,0	
TCE	$\delta^{13}C$								
DCE	$\delta^{13}C$								
VC	$\delta^{13}C$								
ETH	$\delta^{13}C$								
Chlorine isotope									
PCE	$\delta^{37}Cl$								
TCE	$\delta^{37}Cl$								
DCE	$\delta^{37}Cl$								
VC	$\delta^{37}Cl$								
Cl	$\delta^{37}Cl$								



ACTIVITIES



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BIOMOLECULAR TOOLS



Deliverable D.T1.3.1

BMTs technical protocol for remedial implementation and performance evaluation (draft)

University of Liberec is driving the Activity 1.3 and they prepared a protocol explaining how Biomolecular Tools can be used in assessing Natural Attenuation processes in order to design remediation actions based on Enhanced bioremediation

■ BMT = bio-molecular tools

- ☐ Assessing contaminant's biodegradation on polluted sites
- ☐ Evidence of remediation rate

■ Type of material

- ☐ Groundwater, soil, nanofiber carrier samples, ...

■ Methods

- ☐ Real-time PCR - specific bacteria or functional genes detection
- ☐ Next-generation sequencing (NGS) - microbial composition

Biological molecular tools (BMT): a brief guideline about why and how to use BMT for characterization and remediation of contaminated sites in Europe



BIOMOLECOLAR TOOLS



Deliverable
D.T1.3.2

Report on BMTs analysis from studies
and remediation pilot actions

Delivery date:
05.2018 concluding

Biomolecular analysis were performed in Parma, Stuttgart, Novy Bidzov and Jaworzno

Groundwater						
Primer	MR-1	MR-2	MR-5	MR-6	ZMS-4	ZMS-5
U16SRT						
bvcA						
vcrA						
DHC-RT						
Dsb						
Dre						
dsrA2						
nirK						

Nanofiber carriers					
Primer	B 72	B 373	FB 4neu	KE 3-4	KE 3-6
U16SRT					
bvcA					
vcrA					
DHC-RT					
Dsb					
Dre					
dsrA2					
nirK					
AlkB1					
etnE					
linA					

Groundwater						
Primer	PM3	PM5	PZ3	PZ4	PZ5	PZ8
U16SRT						
bvcA						
vcrA						
DHC-RT						
Dsb						
Dre						
dsrA2						
nirK						
linA						
DEF/G						
bssA						




BIOMOLECOLAR TOOLS



Deliverable D.T1.3.3

Freeware software for BMT's data analysis for remediation assessment

An excel spreadsheet was created by Liberec University in order to give an overview of the contamination detected at the site and to assess the presence of a microflora suitable for CHC degradation




BMT Freeware Software

Deliverable D.T1.3.3: Freeware software for BMT's data analysis for remediation assessment

Thank you for using our BMT software.

THIS SOFTWARE IS DESIGNED FOR:

GROUNDWATER SAMPLES
ONE SAMPLING ROUND
CHLORINATED ETHENES CONTAMINATION
MICROSOFT OFFICE EXCEL 2016



HOW TO USE THIS SOFTWARE

WITH VBA MACROS

- Click on symbol above, this will get you to next part
- In Basic Parameters, fill what analysis you have done, how many samples you have etc.
- Click on CONFIRM PARAMETERS button.
- Click on NEXT button.
- In respective columns, insert your analysis results as values
- Click on NUMBER CHECK button to check if the cells contain numbers.
- Click on START button.
- Now, you have got an interpretation of analysis results.
- To get figure interpretations, click on FIGURES button.
- To modify intervals for parameters, click on SETTINGS button.

WITHOUT VBA MACROS

- Under these instructions, there are Basic Parameters, where you will fill what analysis you have done, how many samples you have etc. Then click on the next sheet INPUT.
- In respective columns, insert your analysis results as values, NOT with formatting.
- After data insertion, check if all data cells (not sample names) contain numbers. If they do not and the mistake is not corrected, there will be a mistake in the Results.
- Click on the next sheet Results.
- Now, you have got an interpretation of analysis results.
- To get figure interpretations, click on the next sheet Figures.
- To modify intervals for parameters, click on sheet Settings

NOTES:

- This software is designed for the latest versions of Microsoft Excel, from Microsoft Excel 2010. It is possible to use older versions but there will occur errors connected to functions enabled only in the latest versions, e.g. custom data labels in a chart.
- Ci values mean normalized average Ci value.
- CRP - there is a possibility of CRP conversion from Ag/Ag electrode to hydrogen electrode.
- The concentration of dichloroethene (DCE) given in this software was of 1,2-DCE and 1,1-DCE.
- This software is intended for groundwater samples. In case of not groundwater samples, the interpretation of results is not reliable.

INPUT														
Microbiological analysis										Physicochemical analysis				
Sample name	UNIT	NO.	NO.	NO.	NO.	NO.	NO.	NO.	NO.	Conductivity (µS/cm)	ORP (mV)	ORP (mV)	ORP (mV)	ORP (mV)
MB-1-10-01		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-02		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-03		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-04		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-05		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-06		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-07		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-08		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-09		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-10		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-11		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-12		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-13		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-14		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-15		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-16		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-17		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-18		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-19		100	100	100	100	100	100	100	100	100	100	100	100	100
MB-1-10-20		100	100	100	100	100	100	100	100	100	100	100	100	100

RESULTS

MB-1-10-01: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-02: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-03: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-04: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-05: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-06: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-07: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-08: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-09: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-10: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-11: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-12: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

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MB-1-10-14: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-15: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-16: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-17: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-18: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-19: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-20: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

FIGURES

MB-1-10-01: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-02: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-03: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-04: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-05: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-06: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-07: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-08: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-09: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-10: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-11: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-12: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-13: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-14: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-15: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-16: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-17: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-18: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-19: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

MB-1-10-20: 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100, 100

CONCLUSIONS



The tools settled in the AMIIGA project are improving the capacity to face the groundwater contamination at FUA scale:

Web-GIS, statistics, isotope fingerprinting and inverse modeling can be applied to evaluate the **diffuse contamination level**

Web-GIS, inverse modeling and isotope fingerprinting can be applied in order to find the most probable **position of Punctual Sources**

Isotope fingerprinting and biomolecular tools can be applied at contaminated site scale in order to **evaluate Natural Attenuation** processes and the possibility to implement **Enhanced Bioremediation** actions

