

Patients affected by Hematologic Malignancies still have unmet needs.

By sharing Big Data we can improve patient outcomes.

By applying Big Data Analytics we can enable better and faster treatments for patients with Hematologic Malignancies.





Introducing the HARMONY Alliance

Healthcare Alliance for Resourceful Medicines Offensive against Neoplasms in HematologY

A pan-European project of the Innovative Medicines Initiative (IMI) uniting and aligning healthcare system stakeholders and key opinion leaders in the field of Hematologic Malignancies (blood cancers).





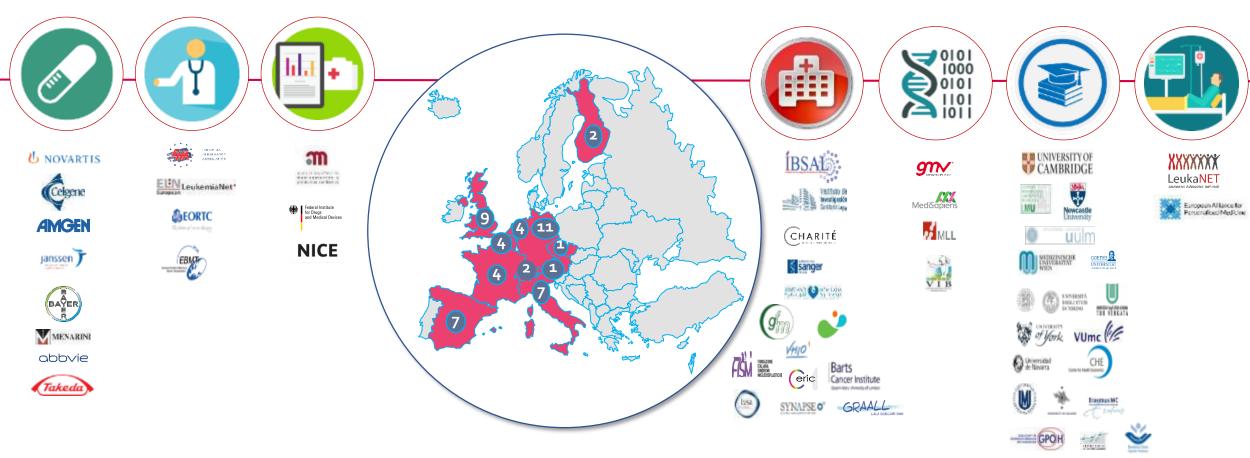








Involving every stakeholder group to meet patients' needs.



Focus on 7 HM diseases: AML Acute Myeloid Leukemia . ALL Acute Lymphoblastic Leukemia . CLL Chronic Lymphocytic Leukemia . MDS Myelodysplastic Syndrome . MM Multiple Myeloma . NHL Non-Hodgkin Lymphoma. Pediatric HMs.



A unique European Network of Excellence for Big Data in Hematology

















First IMI project on BD4BO for Hematologic Malignancies (HMs) Open project: EU Cooperative Groups and Hospitals welcome Stakeholders involvement: Academia, Industry, Payers, HTA, Regulators and Patients First and largest Public-Private partnership (PPP) in hematology High-quality
HARMONY Big Data
platform to include
and harmonize data
on Hematological
Malignancies

Increase the application of omics data in clinical practice

Speed up drug development, access pathways and bench-to-bedside process











European Network of Excellence for Big Data in Hematology, consisting of 53 partners from 11 countries.

First year achievements

Guillermo SanzHARMONY Co-Chair, HULAFE

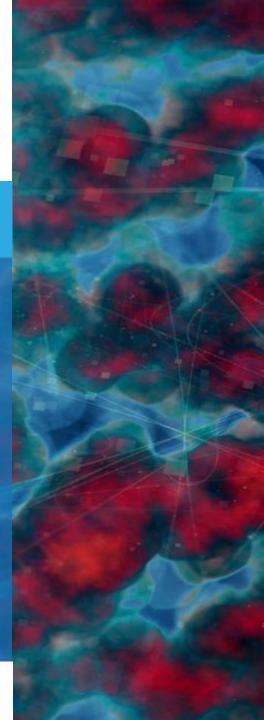
Pam Bacon
HARMONY Project Co-Leader, CELGENE

23rd Congress of EHA, Stockholm, 16th June 2018



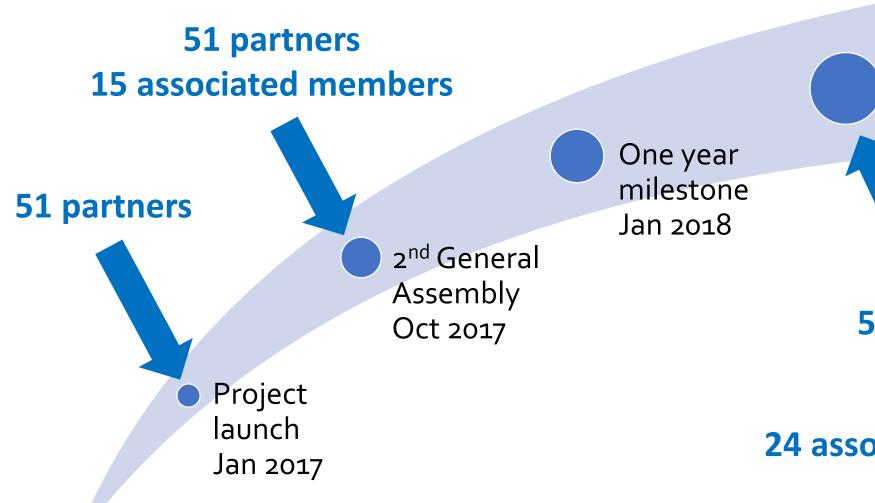






HARMONY – First 18 months

We have grown in number!



EHA congress Jun 2018 53 partners + 1 public + 1 private 24 associated members

HARMONY – First 18 months

We have achieved significant milestones

One year

Jan 2018

milestone









Engagement Framework and Data Sharing **Agreements**

2nd General Assembly Oct 2017



SOPs for the approval of bench-to-bedside research proposals

Project launch Jan 2017



Policy Health Stakeholder Feedback Forum



Communication & Dissemination activities



Core outcome set definition for HMs started & ongoing



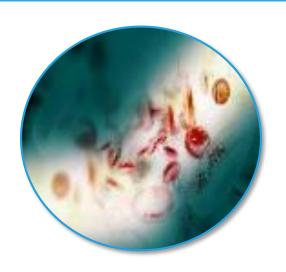


External Law Firm



HARMONY – First 18 months

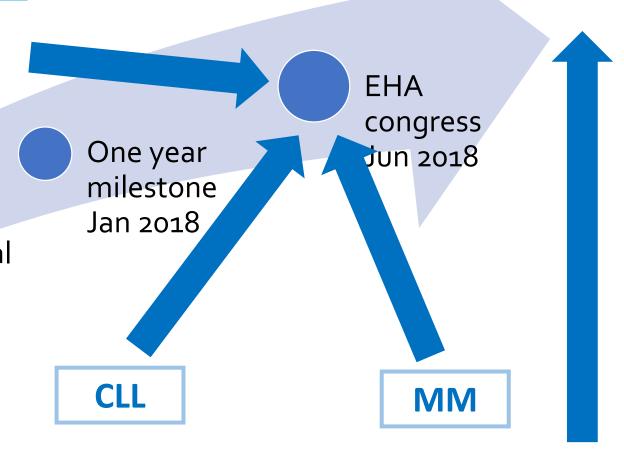
Bench-to-bedside projects ready to start!



"Bench-to-Bedside" Projects AML (and APL)

2nd General Assembly Oct 2017

Project launchJan 2017



First data transfer to database expected in coming weeks!







Data Management Data Analysis

Michel van Speybroeck
HARMONY WP3 Lead, Janssen

Ana HerediaHARMONY WP₃, GMV

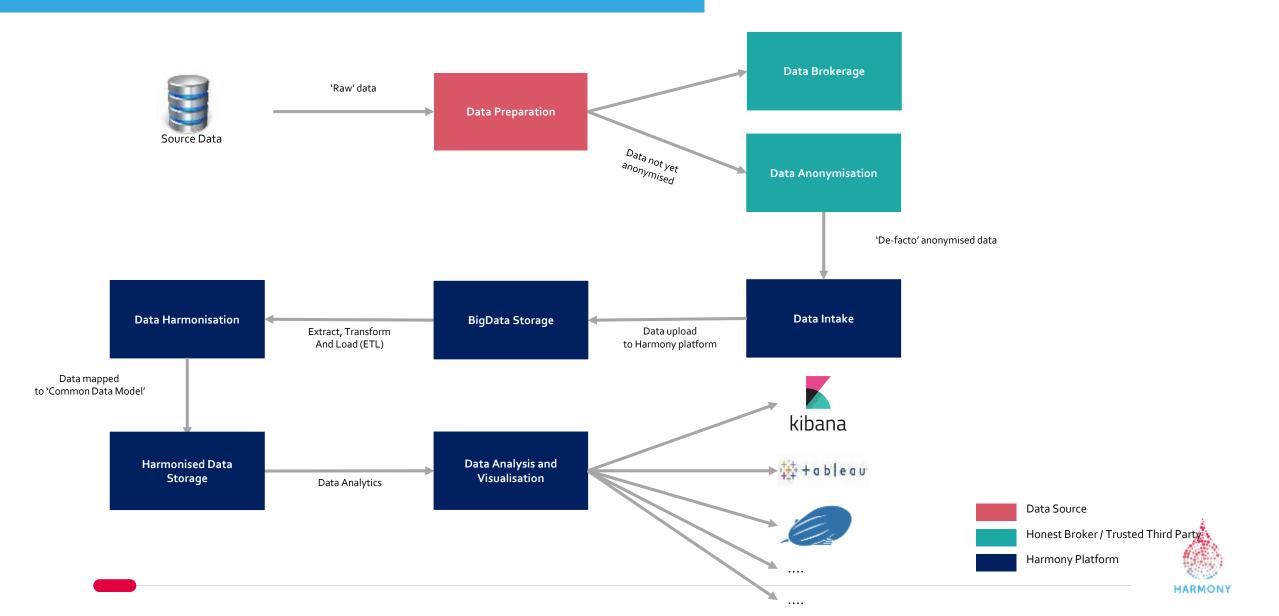
23rd Congress of EHA, Stockholm, 16th June 2018







Data pipeline



Anonymisation "De Facto"

Data for which attributing the individual data to the relevant individual concerned requires unreasonable effort in terms of time, cost and manpower!



Keeping the data safe



Technical

- Data anonymisation
- Data encryption in transit and at rest
- Data Access Restrictions
- Backup process



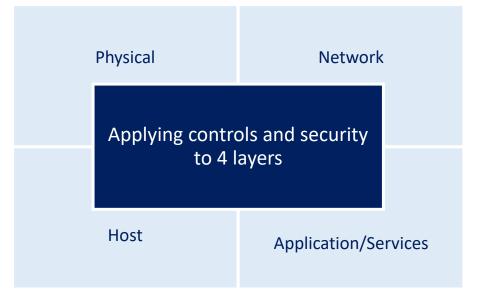
)rganisational

- Physical and logical data center security
- Audit trail
- Contracts and SOP's
- Training



Privacy and security

- VPN (Virtual Private Network)
- Firewall with two levels
- Audit: WHO, WHEN, WHERE, WHAT,HOW
- Risk analysis
- Named access
- Roles segregation
- Data governance: nobody has access to the data



The platform is hosted on CNAF Hosting with ISO 27001



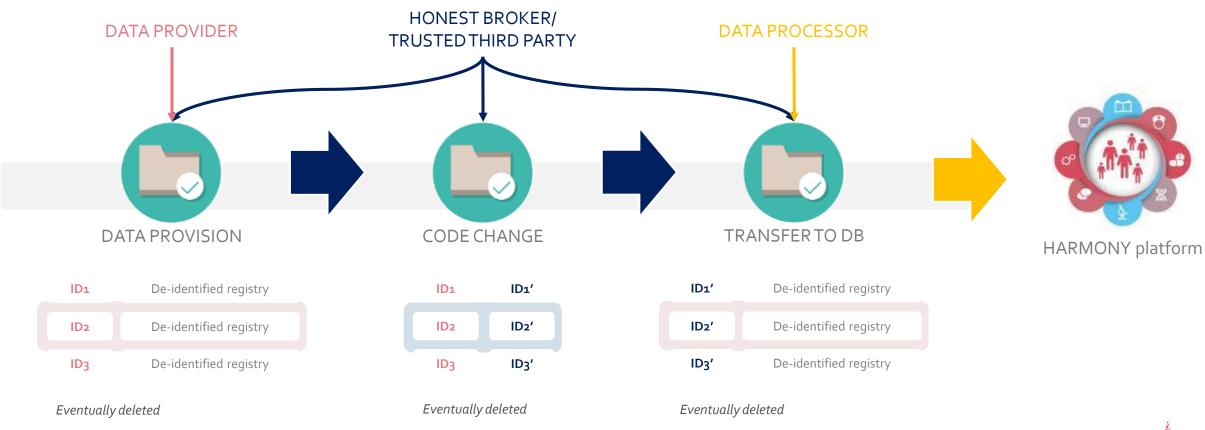




Data journey to HARMONY

* Communication channel: harmony-data@synapse-managers.com

Data transfer SharePoint*

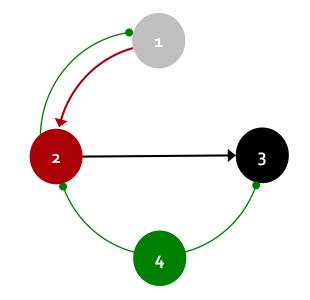




Data pipeline: summary

Data Provider reviews the contracts and prepares the data according to the AMDS and anonymisation SOP

Honest Broker / Trusted Third Party verifies
the data is anonymised and replaces IDs and
Data Provider's identity



HARMONY Platfrom performs an analysis and generates a Quality Report without knowing who the Data Provider is. Data enters the platform and gets harmonised.

DQSC evaluates the Reports and communicates the value to the HB, who shares this information with the Coordinaton Office



Quality Gate: Minimum fields a data source must contain in order to be used on the Platform.

- Minimum fields to be mapped in the CDM.
- Minimum fields are defined by the KOLs (per disease).

Quality Report: analysis performed on every data source to determine its quality according to the cost matrix defined by the DQSC and KOLs (per disease).



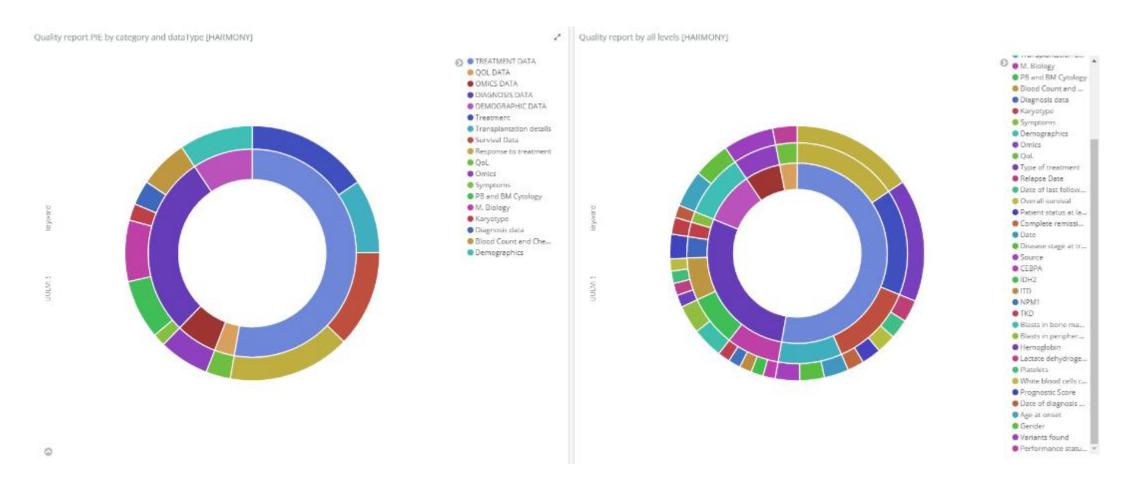




Quality report DATATABLE

CATEGORY \$	DATATYPE	NAME \$	WEIGHT 0	VALID \$	VALUE \$
DEMOGRAPHIC DATA	Demographics	Age at onset	1.5	35	105
DEMOGRAPHIC DATA	Demographics	Gender	1.5	35	105
DIAGNOSIS DATA	M. Biology	CEBPA	0.5	35	35
DIAGNOSIS DATA	M. Biology	IDH2	0.5	35	35
DIAGNOSIS DATA	M. Biology	ITD	0.5	35	35
DIAGNOSIS DATA	M. Biology	NPM1	0.5	35	35
DIAGNOSIS DATA	M. Biology	TKD	0.5	35	35
DIAGNOSIS DATA	PB and BM Cytology	Blasts In bone marrow	1.3	34	88.4
DIAGNOSIS DATA	PB and BM Cytology	Blasts in peripheral blood	1.3	31	80.6
DIAGNOSIS DATA	Blood Count and Chemistry	Hemoglobin	0.5	35	35
DIAGNOSIS DATA	Blood Count and Chemistry	Lactate dehydrogenase	0.5	35	35
DIAGNOSIS DATA	Blood Count and Chemistry	Platelets	0.5	35	35
DIAGNOSIS DATA	Blood Count and Chemistry	White blood cells count	0.5	35	35
DIAGNOSIS DATA	Diagnosis data	Prognostic Score	1	35	70
DIAGNOSIS DATA	Karyotype	Karyotype	3	8	48
DIAGNOSIS DATA	Symptoms	Date of diagnosis and Type AML	1	18	36
OMICS DATA	Omics	Variants found	9	8	144
QOL DATA	QoL	Performance status (ECOG/Karnofski)	1	35	70
TREATMENT DATA	Response to treatment	Response to treatment	5	35	350
TREATMENT DATA	Treatment	Type of treatment	5	35	350
TREATMENT DATA	Survival Data	Relapse Date	1	20	40
TREATMENT DATA	Survival Data	Date of last follow-up	0.5	35	35





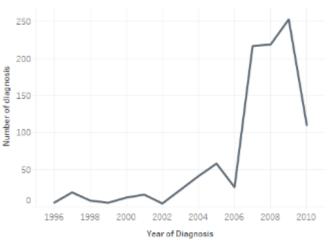


Outcomes demonstration

Gender distribution



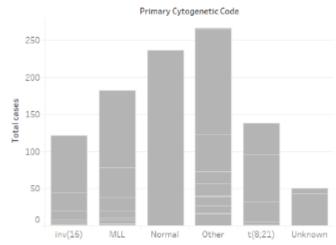
Cases diagnosed per year



FAB disease classification



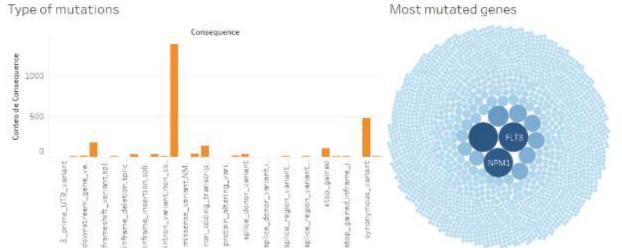
Primary cytogenetic anomalies





Outcomes demonstration











Legal aspects of Data Protection in HARMONY

Dr. John Butler (Bayer AG)HARMONY WP8 Lead, Bayer

23rd Congress of EHA, Stockholm, 16th June 2018





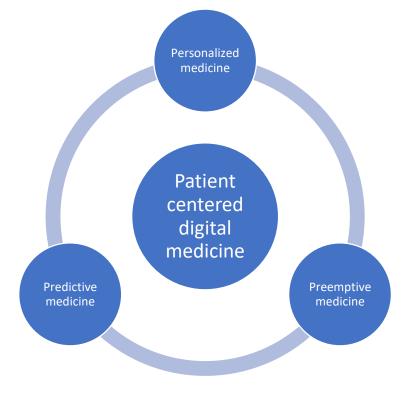


A Paradigm-shift in Health Care

Our health care payment and delivery systems are shifting from volume-based to value-based care

We get sick

We seek treatment "some one" pays

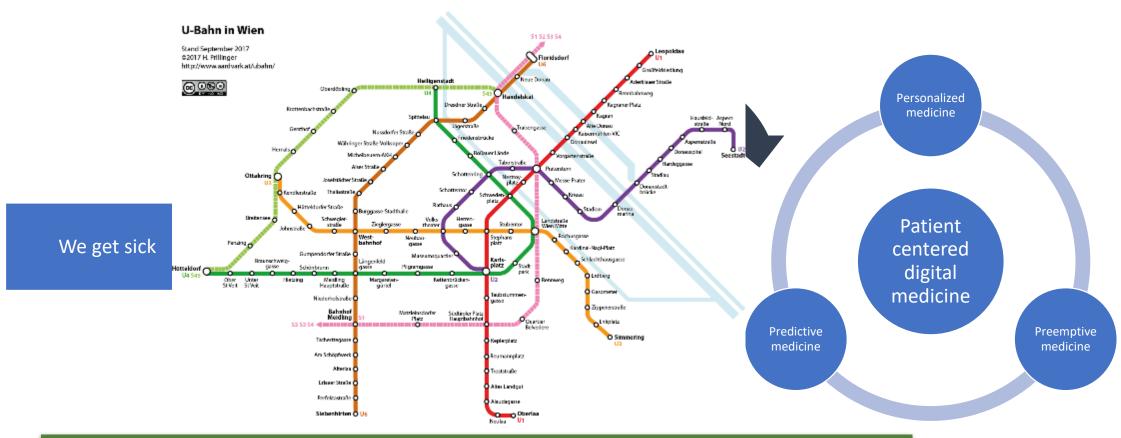






How do we get from here to there?

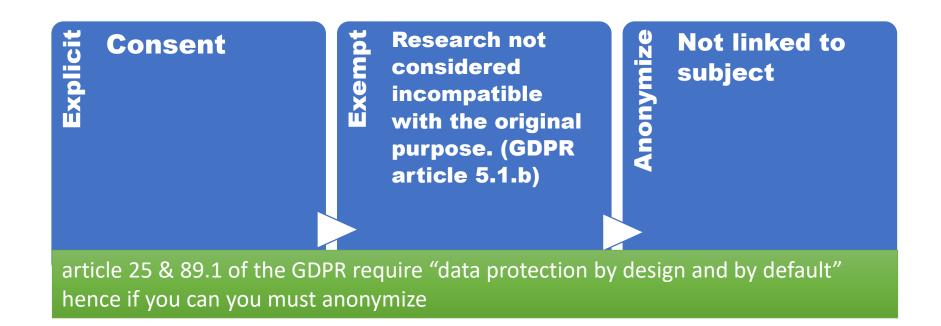
By building the health information backbone necessary to deliver on the promise of Digital Medicine



Without protocol and patient-specific outcomes data, predictive analytics is largely vendor smoke and mirrors in all but a very small number of use cases.*1



HARMONY CHOICES





The Fun Stuff: Using Big Data for Predictive -, Prescriptive Analytics, and Genomics

What is Big Data in Health Care?

- HC Providers have large amounts of patient's data on diagnosis, treatment choice and outcomes.
- Payers (Insurance) have large amounts of patients data on prescription costs and care measures.
- Some countries and regions have large data sources pertaining social consequences of disease.
 - Combining this data should:
 - 1. Improve diagnosis and patient stratification,
 - 2. Optimize therapeutic choices,
 - 3. Provide robust data on therapeutic value

But....

- Data Privacy is the biggest hurdle.
- Changing regulations and legal environment have generated two phenomena:
 - ➤ Naïve ignorance of the current legal framework
 - Paralysis by analysis: uncertainty leading to fear and inaction.



Two extreme positions lead to paralysis by analysis





- "the GDPR has only unified the fines"
- "you can be fined up to 5% of revenues!"
- "Media/NGO can get us introuble"
- "Anonymization (with genomics) is impossible"

- "this is for the advancement of medicine"
- "no one wants to identify patients"
- "there must be valid exceptions"
- "Anonymization renders data useless"



Absolute anonymization is impossible

The *infinite monkey theorem*

a monkey hitting keys at random on a typewriter keyboard for an infinite amount of time will almost surely type any given text, such as the complete works of Shakespeare.

If this holds true, high performance computing can eventually break any code and identify individuals based on unique data sets.





Absolute anonymization is impossible

The *infinite monkey theorem*

a monkey hitting keys at random on a typewriter keyboard for an infinite amount of time will almost surely type any given text, such as the complete works of Shakespeare.

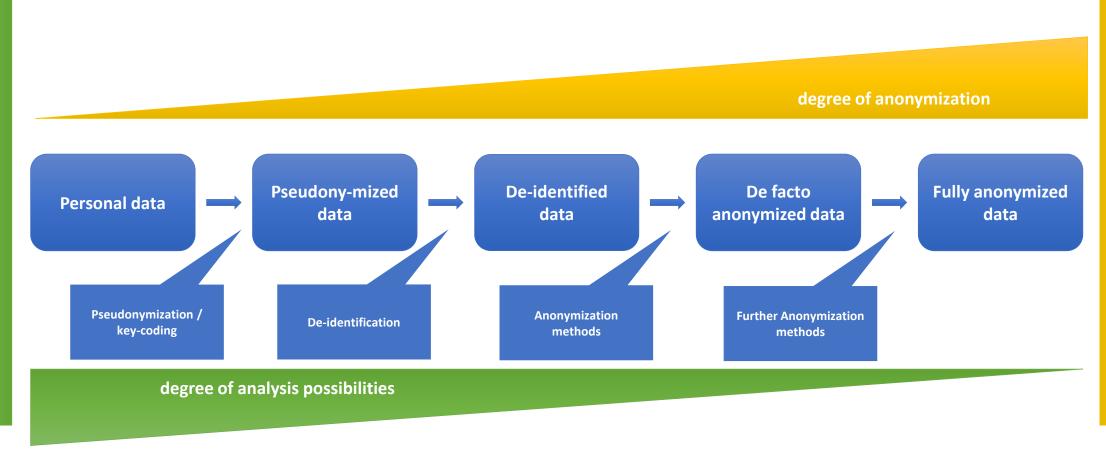
Does this sound exaggerated?

If this holds true, high performance computing can eventually break any code and identify individuals based on unique data sets.

DP-Purists argue like that!

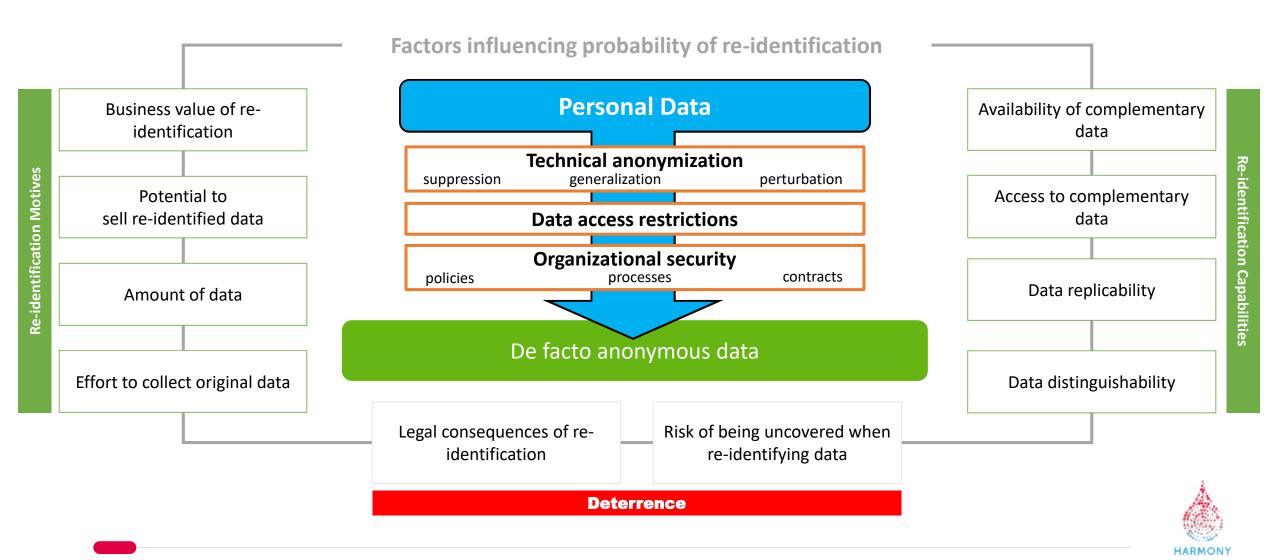


Anonymization is not black & white





De facto anonymization assessment



Keeping the Data Safe in HARMONY



Technical

- Data anonymization
- Data encryption in transit and at rest
- Data Access Restrictions
- Backup process



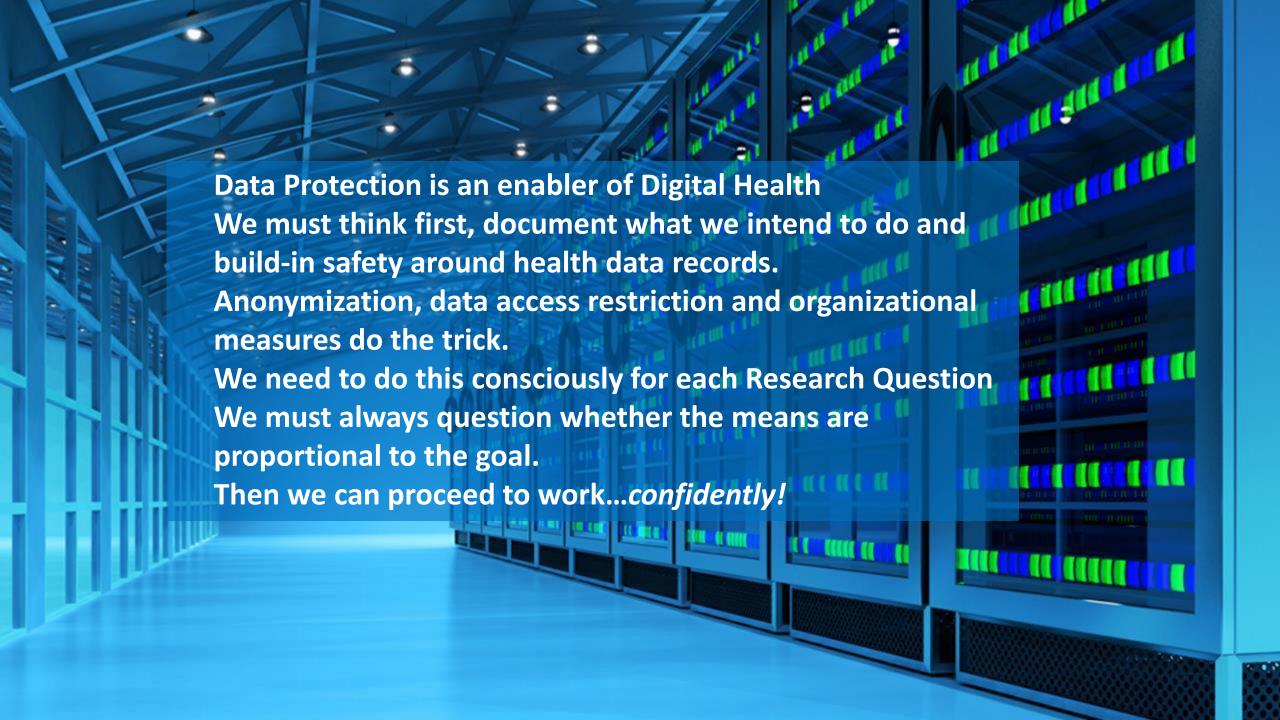
Physical and logical data center security

- Audit trail
- Contracts and SOP's
- Training



External Legal Assessment in a nutshell

- "the HARMONY Anonymization Concept can ensure that the intended import
 of data into the HARMONY Platform and their subsequent uses as envisaged
 within the HARMONY Project complies with applicable data protection laws
 on EU level including the General Data Protection Regulation (GDPR)"
- Osborne Clarke "Legal Assessment of the Anonymization Concept for the HARMONY Project" V 29.01.18
- HARMONY data sets qualify as anonymous and <u>not</u> personal data.
- a de-facto anonymization is sufficient to exclude qualification as "personal data"
- i.e. sufficient anonymity is reached if identification would require an unreasonable effort.
- "The HARMONY Anonymization Concept takes into account all necessary factors" to ensure that the "case-by-case assessments are complete and no means required by applicable data protection law is ignored".







Overview Bench-to-Bedside Pilot Projects

Lars Bullinger HARMONY WP2 Lead, Charité

Aliki Taylor HARMONY WP2 Co-Lead, Takeda

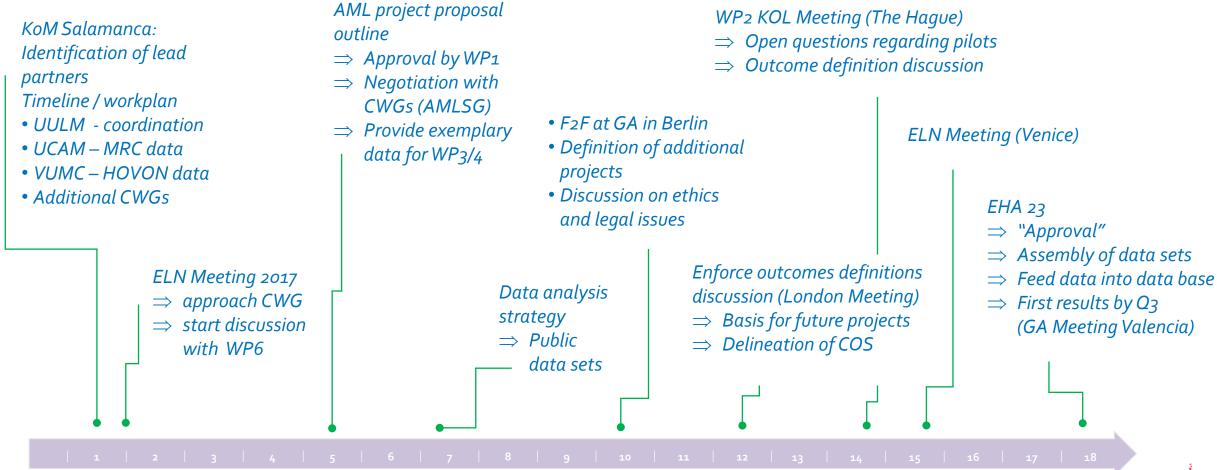
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AML pilot – time line





Additional pilots



The role of hypomethylating agents (HMAs) in high-risk MDS

15 + groups 2500 + patients



Large-scale mutation analysis - Novel prognostic/predictive scheme for improved risk stratification aimed at personalized medicine

ERIC: 24+ groups 5000 + patients



Revised International Staging System for Multiple Myeloma

15+ groups 6000 + patients



Definition of a common data set in childhood malignancies for cross entity analysis comparison of pediatric and adult data





Future projects

What are the next steps:

- Upload pilot data sets into HARMONY and run first analyses
- Continue project on definition of "core outcome sets" (Delphi)
- Joint WP2 and WP6 efforts:
 - follow-up projects?
 - additional data sets for HARMONY (including EFPIA data)?
 - how can we involve all stakeholder groups in the generation of meaningful new projects?





AML. Leading the way: the first results

Hartmut Döhner Ulm University

Estella MendelsonNovartis

23rd Congress of EHA, Stockholm, 16th June 2018





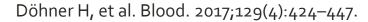


AML pilot – introduction

2017 ELN risk stratification by genetics

Risk Category	Genetic Lesion	
Favorable	t(8;21)(q22;q22.1); $RUNX1$ - $RUNX1T1$ inv(16)(p13.1q22) or t(16;16)(p13.1;q22); $CBFB$ - $MYH11$ Mutated $NPM1$ without $FLT3$ -ITD or with $FLT3$ -ITD low * Biallelic mutated $CEBPA$	
Intermediate	Mutated NPM1 and FLT3-ITD high Wild type NPM1 without FLT3-ITD or with FLT3-ITD low* (w/o adverse-risk gene mutations) t(9;11)(p21.3;q23.3); MLLT3-KMT2A Cytogenetic abnormalities not classified as favorable or adverse	
Adverse	t(6;9)(p23;q34.1); DEK-NUP214 t(v;11q23.3); KMT2A rearranged t(9;22)(q34.1;q11.2); BCR-ABL1 inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2); GATA2,MECOM(EVI1) -5 or del(5q); -7; -17/abn(17p) Complex karyotype, monosomal karyotype Wild type NPM1 and FLT3-ITD ^{high*} Mutated RUNX1 [†] Mutated ASXL1 [†] Mutated TP53	

^{*} Low, low allelic ratio (<0.5); high, high allelic ratio (≥0.5)

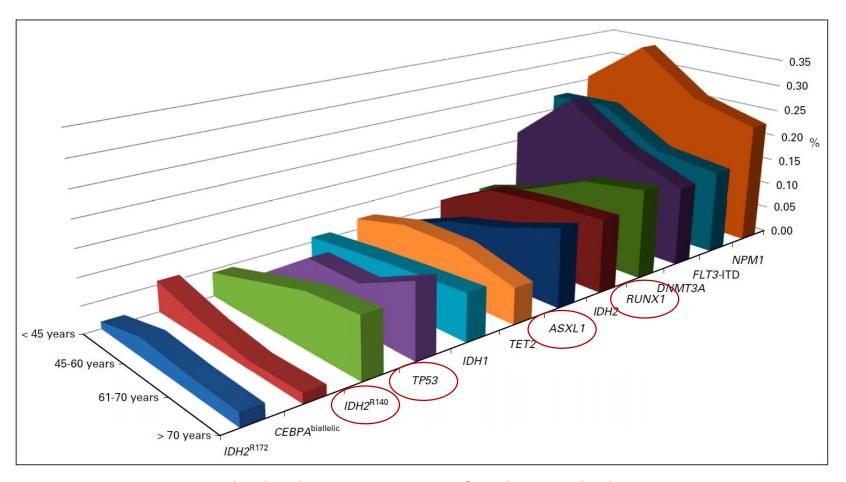




AML pilot – genetic landscape



Age-related frequency of selected gene mutations



Analysis based on 10,622 AML patients from the AMLSG data base Age distribution: <45 yrs, n=2,228; 45-60 yrs, n=3,392; 61-70 yrs, 2,517; >70 yrs, n=2,485



AML pilot – objectives

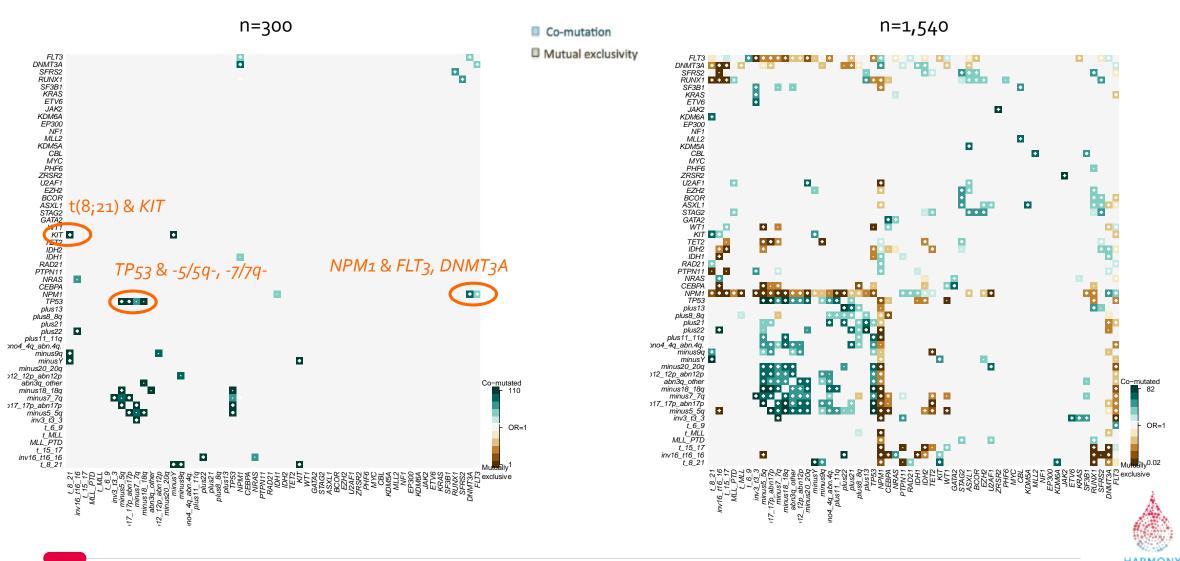
Compilation of comprehensive AML data sets

- Identification of gene-gene interactions
- Evaluation of the clinical impact of gene-gene interactions on outcome
- Validation and further refinement of novel genomic classification
- Evaluate the impact of intensive chemotherapy on "overlap cases", i.e., high-risk MDS cases (MDS-EB2), now commonly included in our AML protocols
- Identification of prognostic / predictive factors for novel (targeted) therapies



AML pilot – gene-gene interactions





AML pilot – achievements

Five most important achievements in 2017

- Establishment of HARMONY platform and work flows
- Identification of major AML data sets and mapping of data sources to pilot run
- Consent on data de-identification ("De-facto anonymization": double-brokerage pseudonymization)
- Description of the technical concept (pseudonymization and "hashing" approach)
- Associated Member Engagement Framework agreements



AML pilot – overview on data sets

AML data sets of Cooperative Working Groups (CWGs)

AMLSG: ~1,500 cases (incl. mol. genetics)

British MRC: ~1,500 cases (incl. mol. genetics)

HOVON: ~1,000 cases (incl. mol. genetics)

AMLCG: ~1,000 cases (incl. mol. genetics)

Additional CWGs: PETHEMA, ALFA, GIMEMA, ...

DSA under review

DSA pending

DSA under review

DSA under review

contacted

AML data sets of private partners

EFPIA data sets

Additional AML data sets from clinical centers

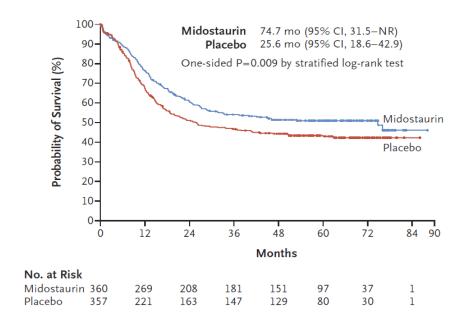
• Belfast, etc.

DSA pending

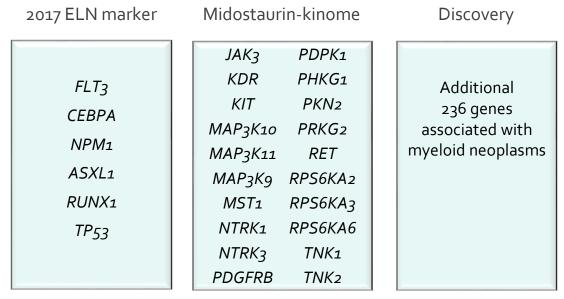


AML continued – therapy with targeted agents

Midostaurin plus chemotherapy for AML with FLT3 mutation – Targeted sequencing project



Stone R, et al. N Engl J Med. 2017;377(5):454-64.



n=496 patients; sequencing of coding region of 262 genes (1443 Mbp); target enrichment (SureSelectXT / Agilent)

N. Jahn, E. Panina, A. Dolnik, T. Blätte L. Bullinger, K. Döhner R. Stone, C. Thiede, F. Lo Coco, A. Ganser, E. Tiecke, C. Pallaud, R. Larson, C.D. Bloomfield

AML pilot – objectives

Aims 2018

- Include >5,000 AML data sets (first data set entry: June 2018)
- Identify additional EFPIA data sets to be included
- Continue discussion on outcomes definition Delphi survey
- Define novel projects
 - ⇒ E.g., horizontal projects linking different disease groups (e.g., high-risk MDS/low-blast AML, childhood/adult AML)
- Refine data entry, data analysis and data interpretation in collaboration with other WPs
- Communicate first results
 - ⇒ Publication of AML pilot results
 - ⇒ White paper on outcomes



Partnering for a better future for people with MH

Commitment to BD4BO





Commitment to sharing data







CLL. The second successful Pilot Study

Lesley Ann SuttonEuropean Research Initiative on CLL

23rd Congress of EHA, Stockholm, 16th June 2018







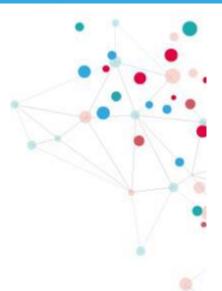
Recurrent gene mutations in CLL: An ERIC project in HARMONY

Rationale

- Many recurrent gene mutations exist in CLL
- Variable and low frequency (<10% each)</p>
- Correlate with distinct disease and clinical outcomes

Prognostic or predictive capacity of gene mutations?

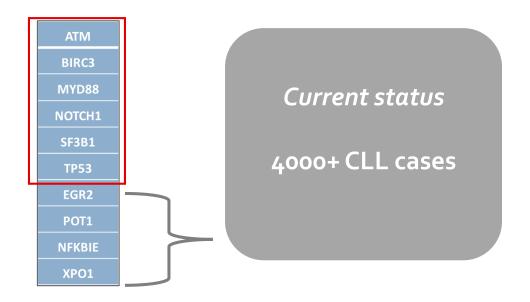
Could particular gene mutation(s) aid in clinical decisionmaking, including therapy selection and response prediction?

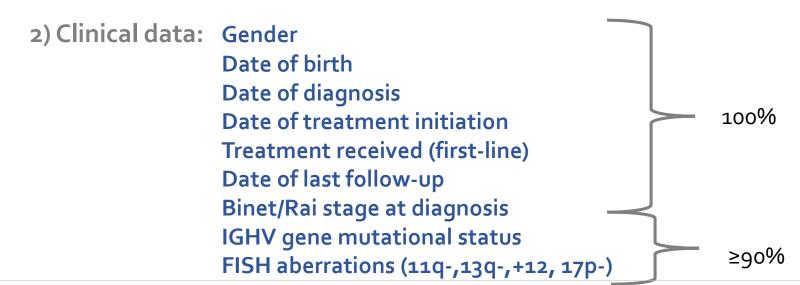




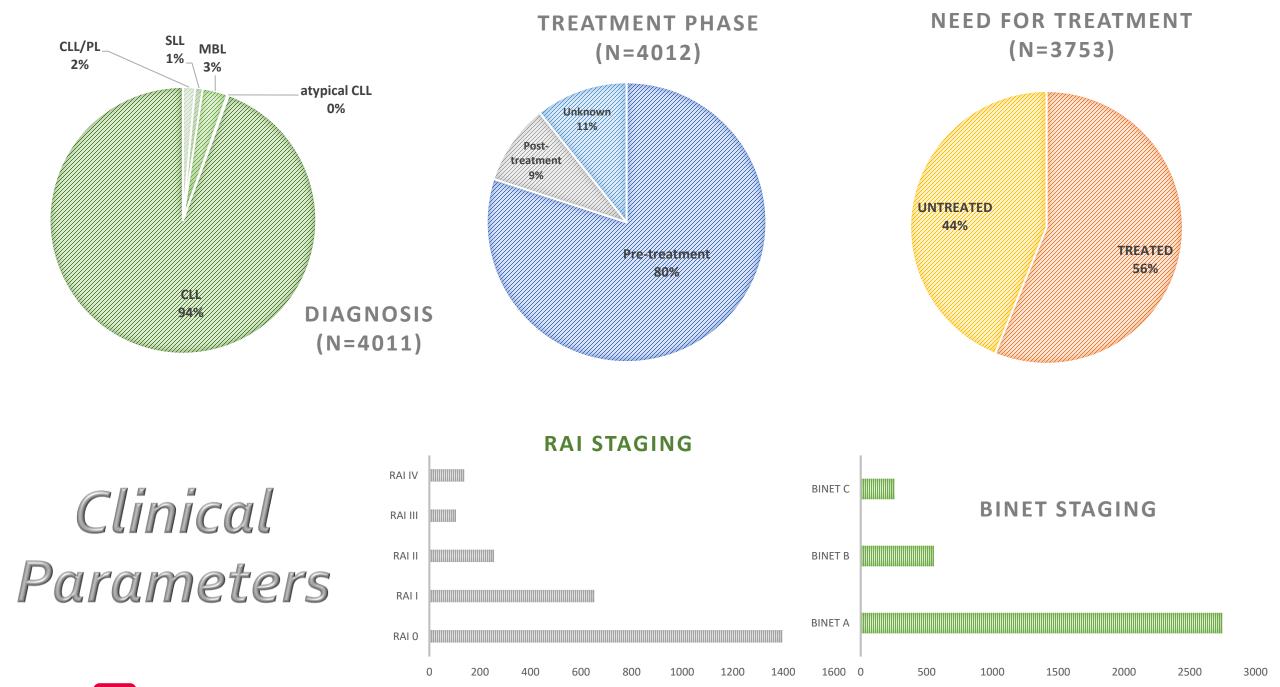
Recurrent gene mutations in CLL: An ERIC project in HARMONY

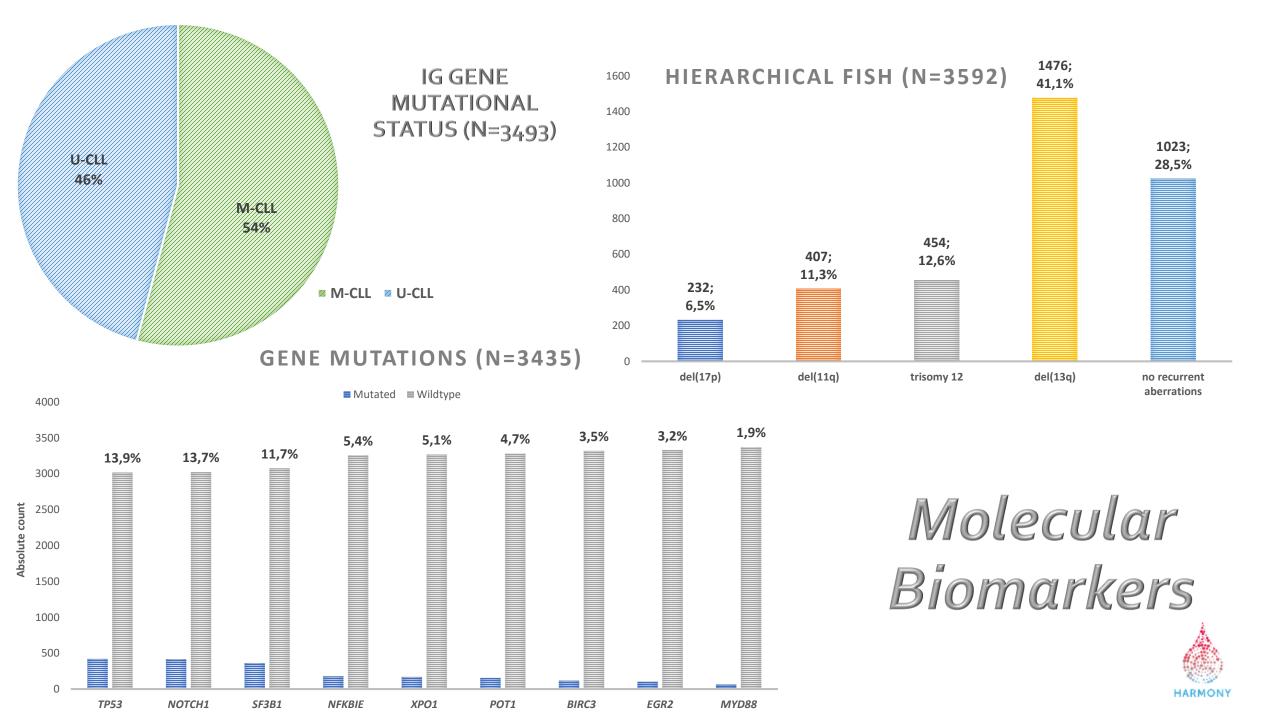
1) Gene mutations:











Recurrent gene mutations in CLL: An ERIC project in HARMONY

Specific project goals

- Evaluate the mutational status several recurrently mutated genes in a large and wellannotated (both molecular parameters and clinical characteristics) series of CLL cases.
- Assess the prognostic impact and clinical relevance of recurrent gene mutations.
- Identify distinct patterns of associations between recurrent mutations with other clinicobiological features in CLL
- Perform *robust validation* of recently proposed *prognostication models* that incorporate both cytogenetic and molecular lesions prognostic indices.







Update of the MM Project

Mario BoccadoroOspedale Molinette, Torino

Bruno CostaCELGENE



23rd Congress of EHA, Stockholm, 16th June 2018



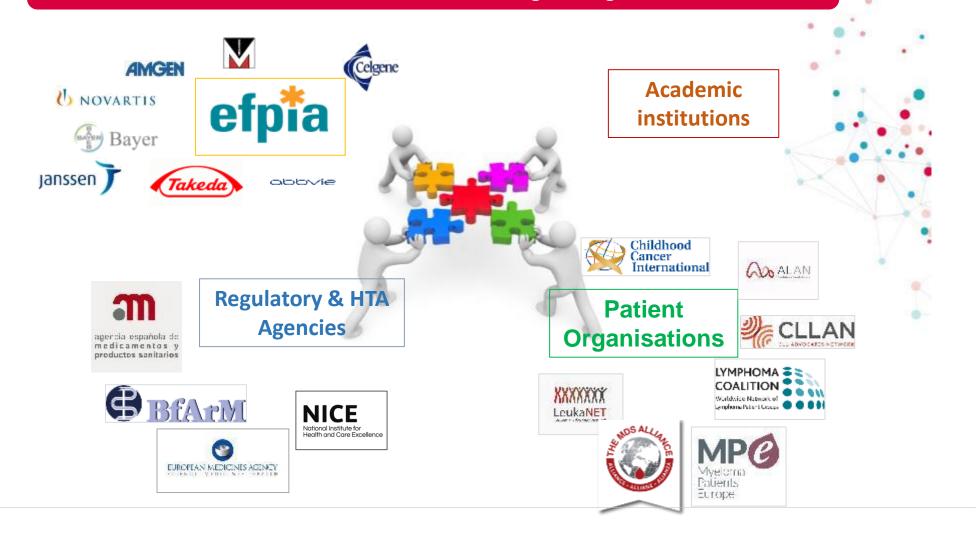




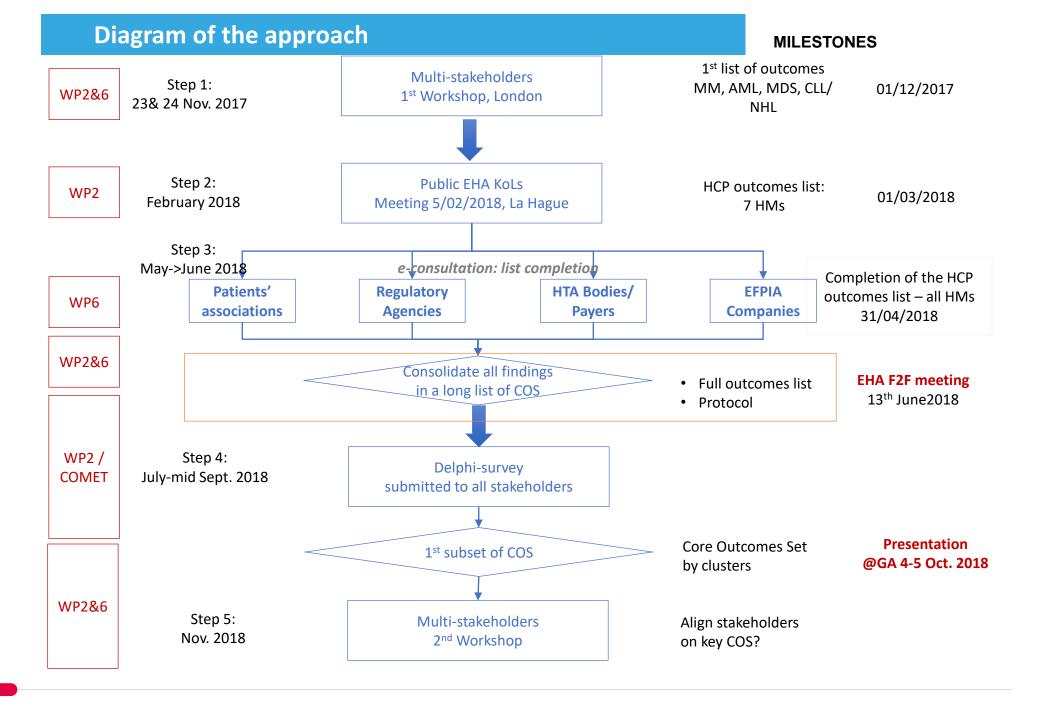
HARMONY WP6: The Stakeholders' Forum



A unique opportunity to involve all stakeholders in the definition of a core outcomes set across and within 7 hematologic malignancies









WP2 MM – progress update

1st Meeting of the MM WP2 in Berlin, during the general assembly (23/24 Oct 2017)

- Definition of MM-specific outcomes
- Identification of suitable data sets to be included in HARMONY
- Definition of the Work Plan/Principles and timelines

2nd Meeting during the MSH workshop, London (23/24 Nov 2017)

- Identification of existing COS applicable to MM
- Identification of additional, MM-specific COS
- Identification of additional global outcomes

3rd Meeting of public EHA KoLs (Den Haag, 05/02/2018)

4th Meeting of public MM KoLs (Torino, 19/04/2018)

Consensus on the design of the pilot study (R-ISS update)





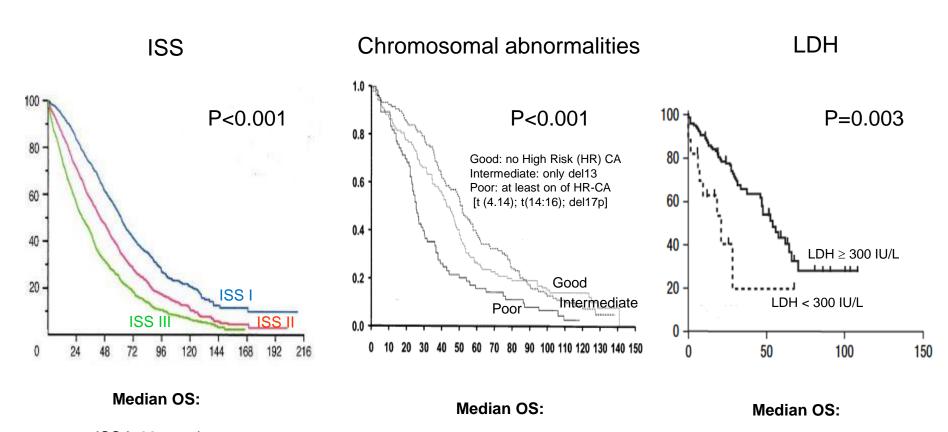
HARMONY MM pilot project

Revised International Staging System for Multiple Myeloma: extended follow-up in the European clinical trial population and evaluation of the efficacy of different novel agents and treatment approaches in subsets of patients with standard- and high-risk features.

Mario Boccadoro, Alessandra Larocca, Mattia D'Agostino, Jesus San Miguel, Marivi Mateos, Pieter Sonneveld, Philippe Moreau, Michele Cavo



Rationale: Standard risk factors for MM



ISS I: 62 monthsISS II: 44 months

• ISS III: 29 months

• Good: 50.5 months

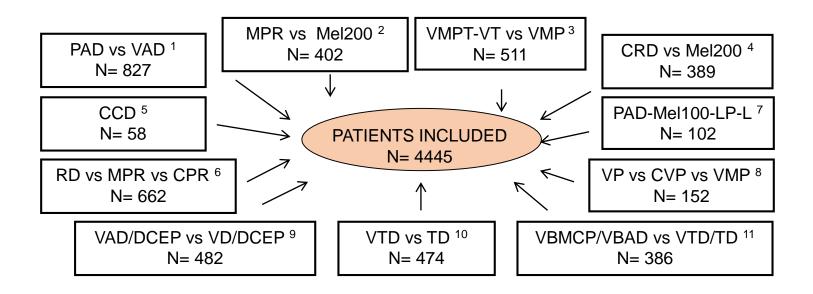
• Poor: 24.5 months

• LDH <300: 54 months

• LDH ≥300: 21 months

R-ISS database

11 phase II/III international trials



PAD: bortezomib, adriamycin, dexamethasone, VAD: vincristine,adriamycin ,dexamethasone; MPR: melphalan, prednisone, lenalidomide; Mel200: melphalan 200 mg/mq VMPT-VT: bortezomib, melphalan, prednisone, thalidomide + bortezomib-thalidomide maintenance, VMP: bortezomib, malphalan, prednisone, CRD: cyclophosfamide, lenalidomide, dexamethasone; CCD: carfilzomib, cyclophosfamide, dexamethasone, RD: lenalidomide, dexamethasone, CPR: cyclophosfamide, prednisone, dexamethasone, Mel100: melphalan 100 mg/mq, LP-L: lenalidomide prednisone + lenalidomide maintenance, VP: bortezomib, prednisone CVP: cyclophosfmaide, bortezomib, prednisone; DCEP: dexamethasone, cyclophosfamide, etoposide, cisplatin, VD: bortezomib, dexamethasone, VTD: bortezomib, thalidomide, dexamethasone; VBMCP: vincristine, BCNU, doxorubicin, dexamethasone



¹Sonneveld P et al J Clin Oncol 2012, ² Palumbo A et al. N Engl Journ Med 2014, ³ Palumbo A et al. J Clin Oncol 2010; ⁴ Gay F et al. EHA 2015 meeting abstract,

⁵ Bringhen S et al *Blood* 2014; ⁶ Palumbo A et al. *Blood* 2013 abstract 763; ⁷ Gay F et al *Blood* 2013; ⁸Larocca A et al *Blood* 2013 abstract 539, ⁹Harousseau JL et al *J Clin Oncol* 2010, ¹⁰Cavo M et al *Lancet* 2010, ¹¹ Rosinol L et al *Blood* 2012

Revised International Staging System for Multiple Myeloma: A Report From International Myeloma Working Group

Antonio Palumbo, Hervé Avet-Loiseau, Stefania Oliva, Henk M. Lokhorst, Hartmut Goldschmidt, Laura Rosinol, Paul Richardson, Simona Caltagirone, Juan José Lahuerta, Thierry Facon, Sara Bringhen, Francesca Gay, Michel Attal, Roberto Passera, Andrew Spencer, Massimo Offidani, Shaji Kumar, Pellegrino Musto, Sagar Lonial, Maria T. Petrucci, Robert Z. Orlowski, Elena Zamagni, Gareth Morgan, Meletios A. Dimopoulos, Brian G.M. Durie, Kenneth C. Anderson, Pieter Sonneveld, Jésus San Miguel, Michele Cavo, S. Vincent Rajkumar, and Philippe Moreau

A new risk stratification model in novel agents era

Includes simple and widely used prognostic markers

- Allows to define three MM entities with significant different outcome
- Future personalized treatments??



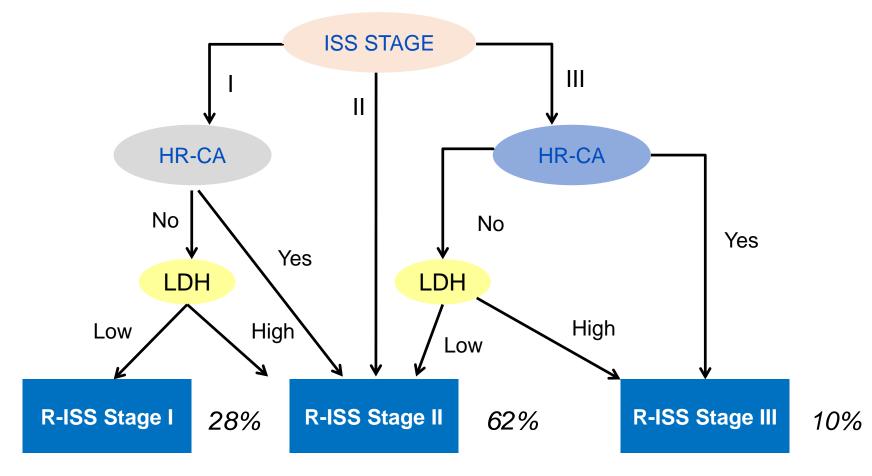
HARMONY MM pilot project

 Provide an extended follow-up of the original trials included in the R-ISS project adding other relevant datasets with mature data from clinical trials enrolling NDMM patients treated with novel agents.

 Evaluation of the efficacy of different novel agents and treatment approaches in subsets of patients with standard- and high-risk features.



A new model for risk stratification: k-adaptive partitioning for survival data



ISS: International Staging System, HR: high risk, CA: chromosomal abnormalities LDH: lactate dehydrogenase,

Endpoints

Primary endpoint

 Validation of R-ISS comparing it with ISS, CA and LDH levels alone after an extended follow-up.

Secondary endpoints

• Outcome of patients with low and high-risk features (defined according to R-ISS, ISS alone, CA alone, LDH alone, baseline creatinine clearance, best response < VGPR vs ≥VGPR) treated with different novel agents (i.e. thalidomide, bortezomib, lenalidomide) and different treatment approaches (i.e. ASCT vs no ASCT, FDT vs CT)

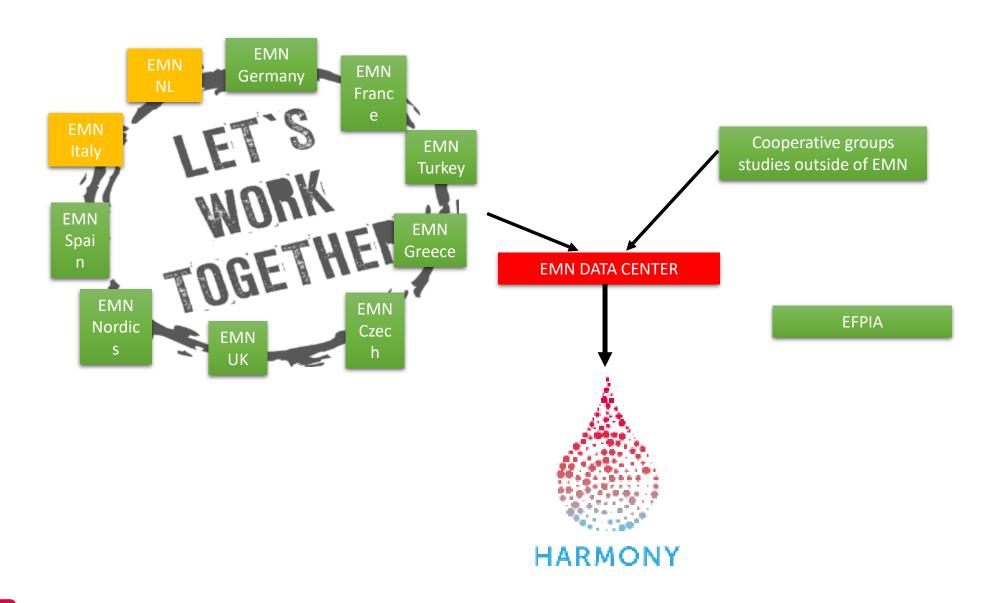


Suitable Data sets

- R-ISS database (11 clinical trials)
- Addition of other relevant data sets with mature data from clinical trials enrolling NDMM treated with novel agents (European Cooperative groups)
- Data from large completed Phase III studies from EFPIA partners will be extremely relevant (VISTA, FIRST trials....)



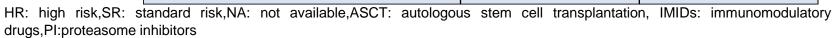
Data workflow: MM Pilot Study



Preliminary analysis

	Original R-ISS paper (N=3060)	Available updated data (N=1354)
Follow-up – median (months)	46	65
Age – median (months)	61	68
≤ 65 years	68 %	39%
> 65 years	32%	61%
Male sex	54%	50%
ISS Stage I II III NA	38% 38% 24% -	35% 39% 26% -
Chromosomal Abnormalities (CA) HR: Del17 or t(4:14) or t(14:16) SR: neither of HR-CA NA	24% 76% -	28% 72% -
LDH levels Low High NA	87% 13% -	89% 11% -
Treatments: ASCT IMIDs PI No new drugs	65% 66% 44% 6%	22% 81% 33% -





Next steps

- 1. HARMONY's full approval of the project (already approved by steering committee)
- 2. EMN as an intermediate depository between cooperative working groups and Harmony for data collection
- 3. EMN data centre as an associated member in Harmony project
- 4. As soon as Harmony data platform will be ready to receive data, EMN will transfer data to Harmony.
- 5. Reimbursement from Harmony to cooperative groups (amount per patient will be decided by Harmony according to data quality and completeness)
- 6. After the pilot project → big data, not only big database (Toxicity, real-life registry data, QoL, MRD, molecular data, omics)







Update of the APL Project

Francesco Lo Coco
University of Rome Tor Vergata
Laura Ciccone
University of Rome Tor Vergata

23rd Congress of EHA, Stockholm, 16th June 2018







Background

Completed trials in front-line therapy of APL:

French-Belgian-Swiss, PETHEMA (Spain), GIMEMA (Italy), SAL, AMLSG and AMLCG (Germany), HOVON (Netherlands), French-Belgian-Swiss, NCRI (UK) and others

Key achievements of these trials include:

- risk classification of APL
- adoption of risk-adapted strategies with improved survival
- demonstration that target therapy (ATO+ATRA) is superior to ATRA+Chemo, leading to ATO
 approval by EMA based on academic, non-sponsored studies (NCRI, Gimema-SAL-AMLSG)



European APL trials



- > 5000 APL patients enrolled
- Heterogeneous prevention and mangement of complications in homogeneous treatment context



Open issues in front-line APL therapy

- Differentiation Syndrome: role of steroid prophylaxis in prevention (heterogeneity of approaches, e.g. NCRI vs others)
- **t-APL**: Prognosis in chemo- and ATO-based studies
- **CNS disease**: management; role of IT prophylaxis
- Maintenance therapy: compare maintenance vs no maintenance strategies
- Early mortality: compare rates in different trials and analyze predictive factors.
 Role of ATO vs chemo in control of the coagulopathy
- Elderly patients



APL proposal- Timeline

- 28 March 2018 APL study proposal (P.I. F Lo-Coco)
- 9 April 2018 Proposal accepted by Harmony Coordination Office
- Next steps:
 - 1. Outline to be sent to APL cooperative group chairs to ask EOI to include pt data:

M Sanz (PETHEMA), P Fenaux (French-Belgian-Swiss), U Platzbecker (SAL), H Dohner (AMLSG), G Ossenkoppele (HOVON), Niederwiser, E Lengfelder (AMLCG), Others?

- 2. Establishment of a Steering committee
- 3. Elaboration of study protocol, CRF and definition of ethical requirements in collaboration with Harmony Central Office







European Network of Excellence for Big Data in Hematology, consisting of 53 partners from 11 countries.

Future Plans

Jesus Maria Hernandez
HARMONY Coordinator, IBSAL

Mirko Vukcevic
HARMONY Project Leader, NOVARTIS



23rd Congress of EHA, Stockholm, 16th June 2018







Roadmap to the 3rd General Assembly



Incorporating the first datasets to the platform











Starting the analysis phase of the **pilot studies**







Access to Industry structure & data







More achievements coming...



Data Analytics

Evidence and Value Framework

Continue defining a Standard Set of Outcomes

New project proposals

Modeling & Machine Learning



HARMONY Future Meetings





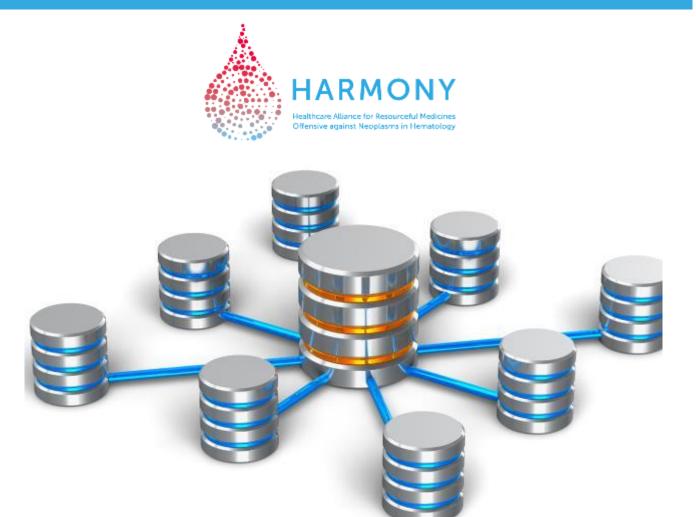
ELN SymposiumMannheim, 12th February







HARMONY is aimed at the entire haematological community!



We are an open project

- More than a 100 European organisations have shown their interest in HARMONY: co-operative Working Groups, Hospitals, Academic Institutions...
- 80 institutions are in the process of becoming HARMONY Associated Members
- Apart from our 53 partners, we already count with
 24 Associated Members.

Your data are crucial!

- All of you are invited to join the HARMONY Alliance as Associated Members!
- Help us meet the needs of patients with HMs.

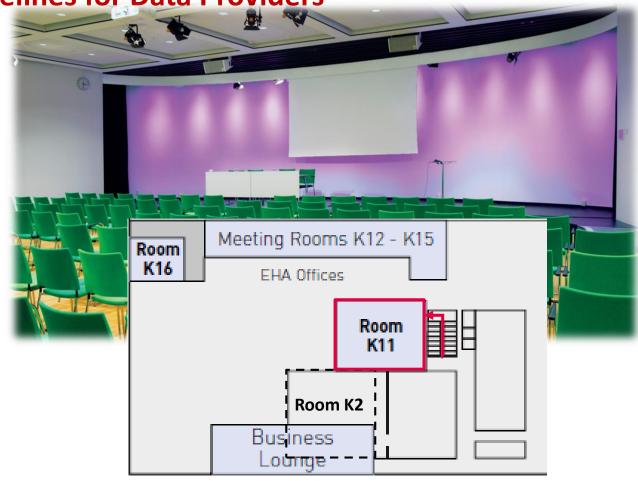




Join us in Room K11 for our Partnering Session

Feeding the HARMONY Platform: Guidelines for Data Providers

- Room K11, 16:15 17:15
- Q&A Roundtable Session
 - Steps in the data intake process
 - HARMONY Agreements
 - The HARMONY anonymisation concept
 - Submission of Research Proposals
 - What is the data going to be used for?
 - Data Quality Assessment
- Chairmen:
 - WP1: Jesús M Hernández, IBSAL, Spain;
 - WP2: Lars Bullinger, Charité, Germany;
 - WP3: Ana Heredia, GMV, Spain;
 - WP3&4: Michel van Speybroeck, Janssen, Belgium;
 - WP8: John Butler, Bayer, Germany.







Thank you!





Any questions?





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Acknowledgement

This project has received funding from the Innovative Medicines Initiative 2 Joint Undertaking under HARMONY Grant Agreement n°116026. This Joint Undertaking receives support from the European Union's Horizon 2020 Research and Innovation Programme and EFPIA.