Data-driven methods generating synthetic data in genomics: the HLA “avatars” are shifting paradigms in data sharing.

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Introduction – Problem

- **GDRP is both a constraint and an opportunity**
  - Reassess how we manage biomedical data from patients
- **Genetic data is both pioneer and large scale**
  - Quantitative leap forward since the late 90's
  - 1.5 millions genotype (A/T/C/G, A/T/C/G)
  - ~ 80 euros /patient

Genetic data is not anonymous

- **Pseudonymous data** (ARTICLE 29 DATA PROTECTION WORKING PARTY)

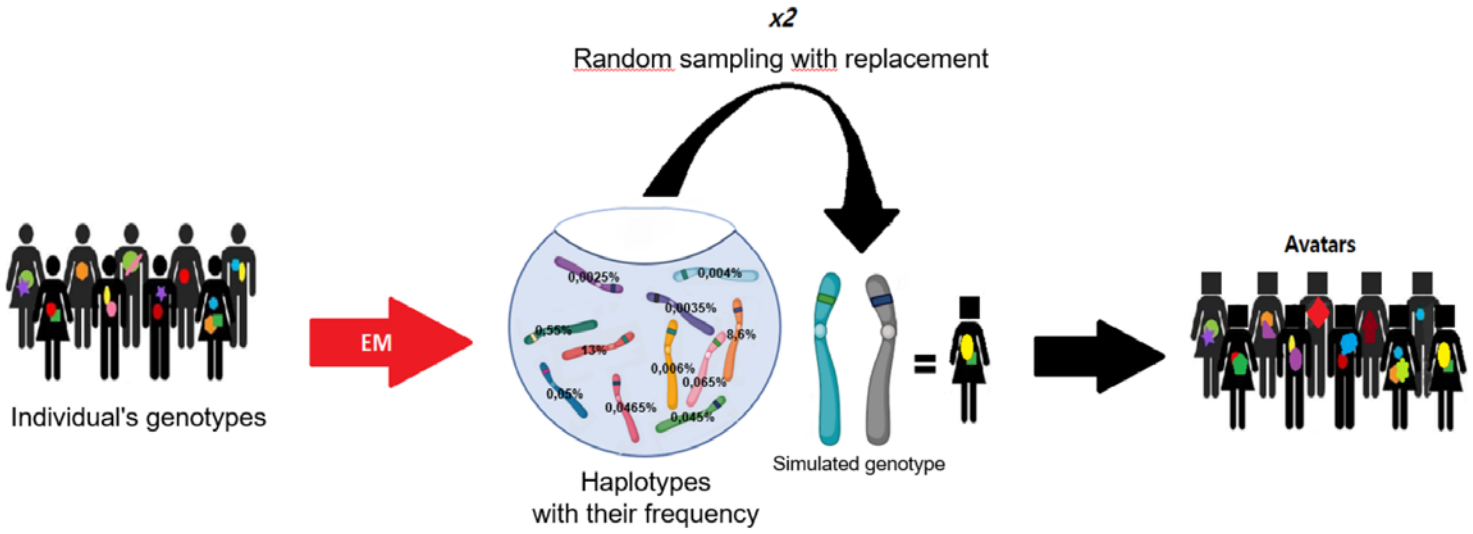
  (i) is it still possible to single out an individual ? Yes…

  (ii) is it still possible to link records relating to an individual ? Yes…

  (iii) can information be inferred concerning an individual ? Yes…

Solution : *Synthetic genetic data : Avatars*

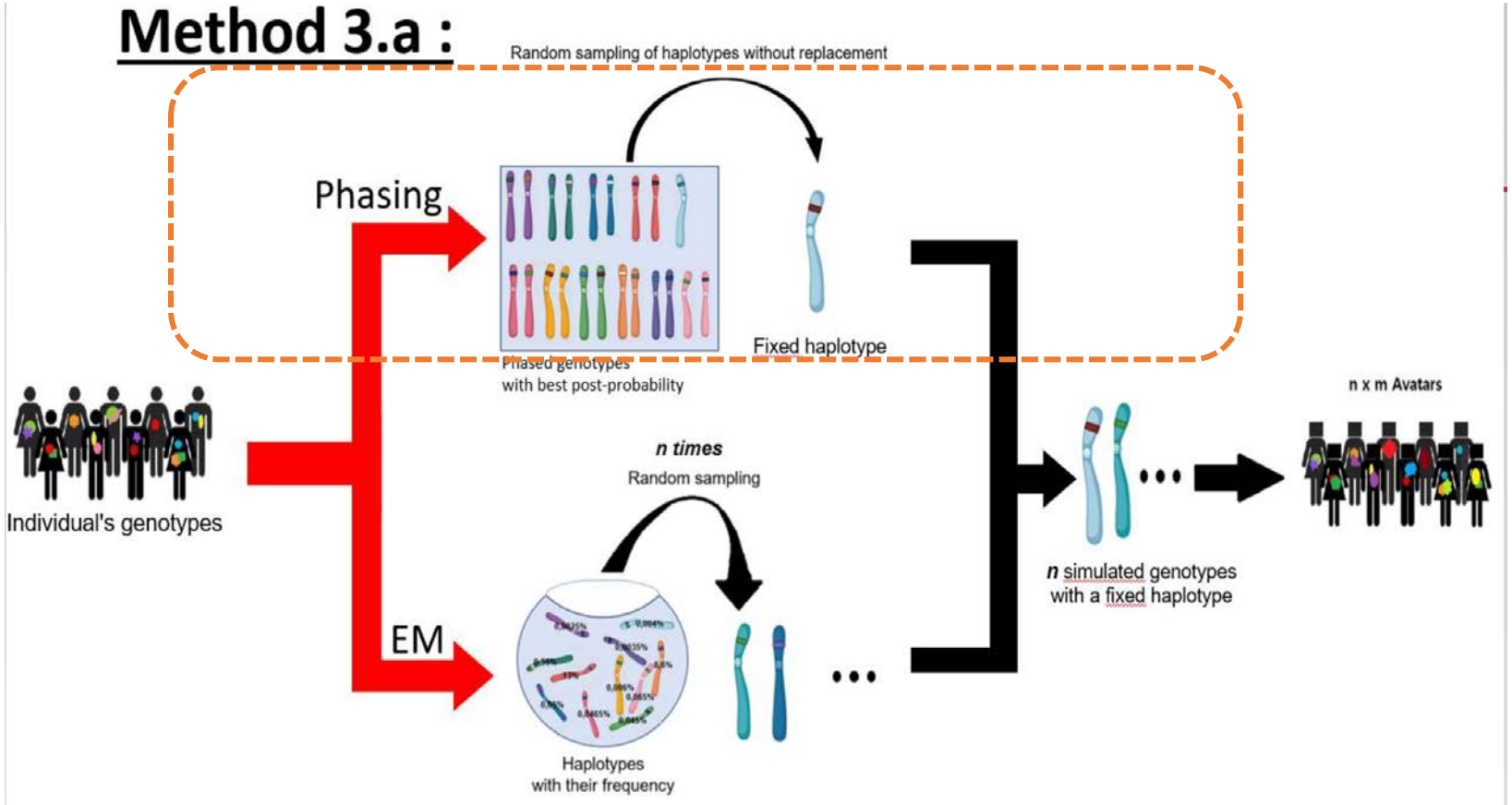
- "In silico Fertilization" vs. IVF : Computationally-assisted procreation
- **Application:** individual HLA genotype, Bone Marrow donor registries (26 millions worldwide)
- Method "1"



Methods :

- **Method 3a** : “Stochastic Filiation method”
- **Objective :** Keep link between **sensitive individual** and his.her **Avatar**

Filiation is achieved through the stochastic conservation of a single haplotype



Results 1: Re-identification #1

- Re-identification statistics :

Pourcentage d'avatars ayant exactement le même génotype qu'un individu de la population réelle initiale

- 4232 génotypes simulés :

	Method 1a	Method 1b	Method 2	Method 3a	Method 3b
Individus ré-identifiables (%)	0.071	0.047	0.047	0.071	0.118
Génotypes à MO* retrouvés dans la table d'avatars(%)	0	0	0	0	0

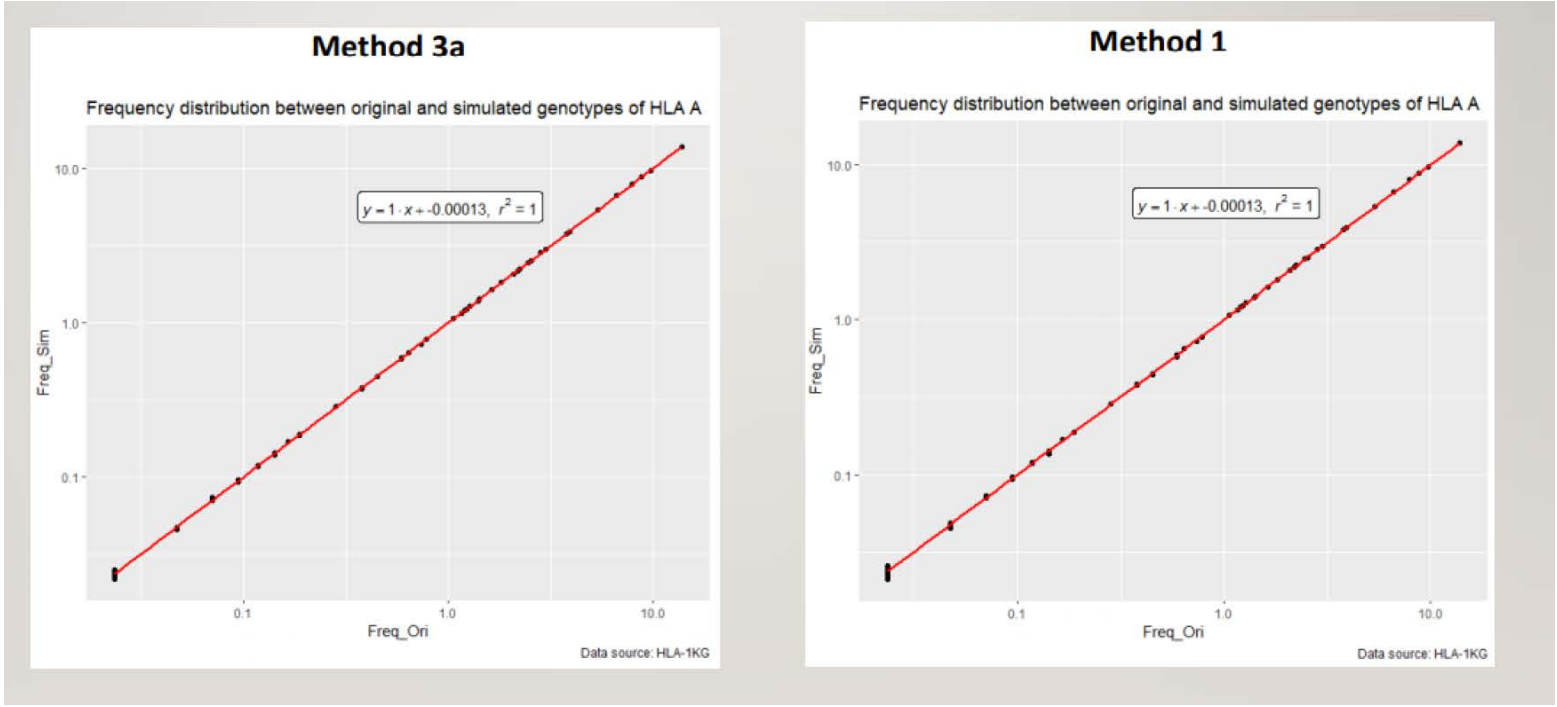
*MO = multiples occurrences

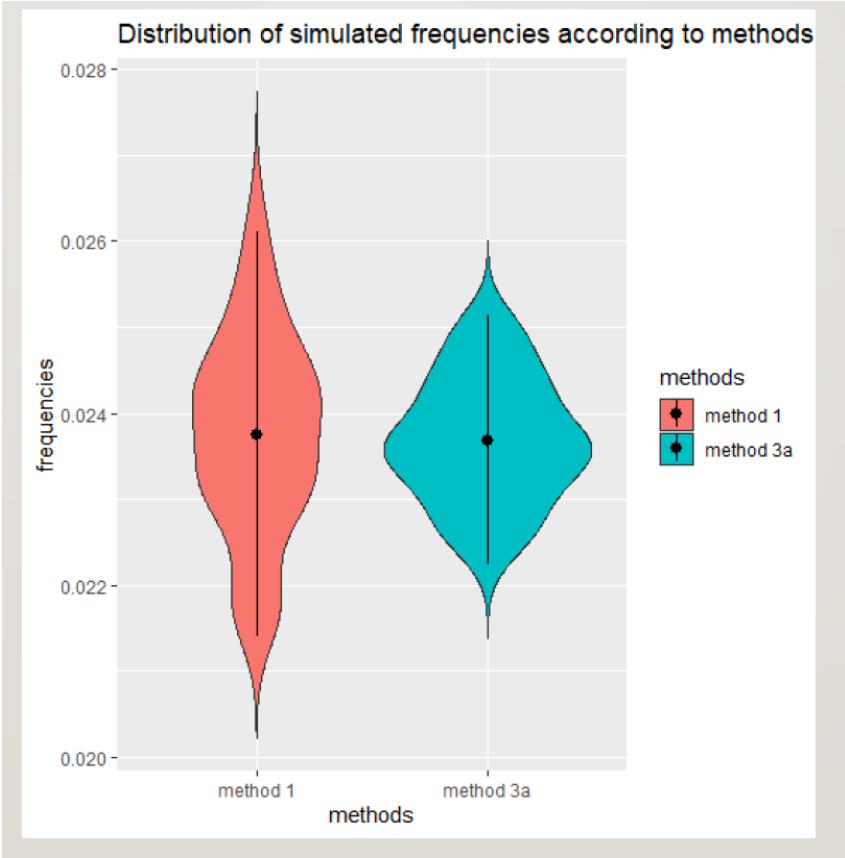
- 1058000, 2116000 et 4232000 génotypes simulés :

	Method 1a	Method 3a	Method 1	Method 3a	Method 1	Method 3a
Individus ré-identifiables (%)	$6*10^{-3}$	$5*10^{-3}$	$3,4*10^{-3}$	$3,6*10^{-3}$	$1,7*10^{-3}$	$1,7*10^{-3}$
Génotypes à MO* retrouvés dans la table d'avatars(%)	$2*10^{-4}$	$2*10^{-4}$	$9,5*10^{-5}$	$9*10^{-5}$	$4.7*10^{-5}$	$4.7*10^{-5}$

Results 2 : statistical relevance #2

- **Haplotype frequencies are well-conserved**





Discussion

- **Directed re-sampling**
  - Based on random re-identification statistics

	Method 1a	Method 1b	Method 2	Method 3a	Method 3b
Individus ré-identifiables (%)	0.071	0.047	0.047	0.071	0.118
Individus ré-identifiables après un premier remix (%)	0	0	0	0	0

  - A false-good idea – if multiple avatarisation can be achieved ..
    - " holes" are identifying

Conclusion

1. It is unethical to use potentially identify biomedical data for reseach…
   - Even high-dimension ones like genetic data
   - When computational techniques can deliver synthetic data of

   1- (virtually) no risk of re-identification

   2- good (enough) statistical relevance

2. Synthetic (genetic) data are out of the GDPR perimerter

1. There use of synthetic data that can be unethical

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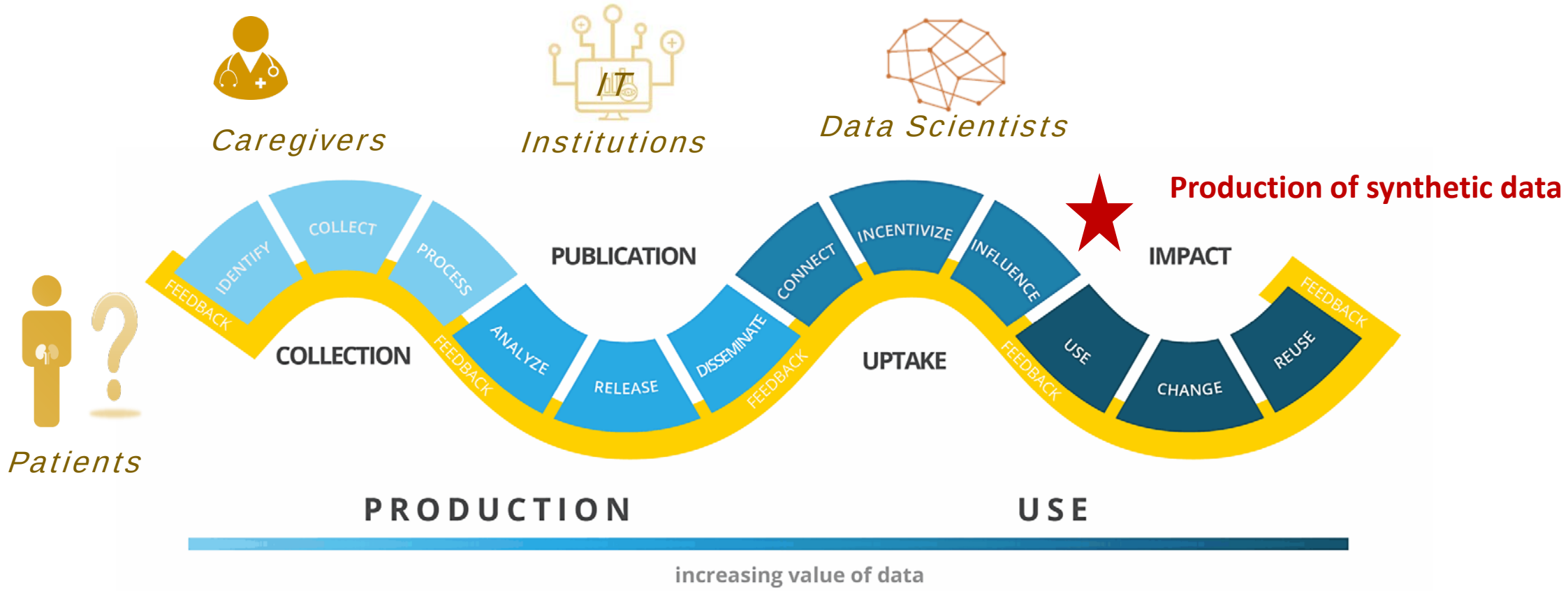
Multiples stakeholders and contributions to the data chain value.



(Adapted From https://opendatawatch.com)