

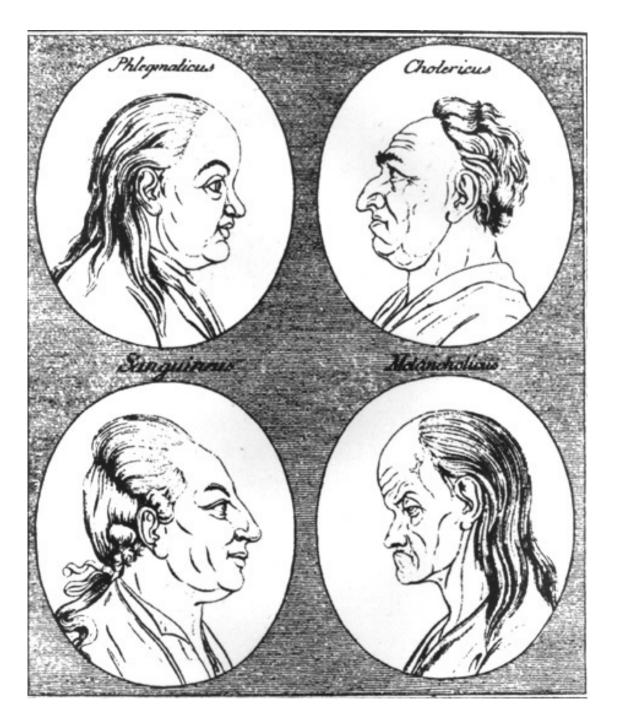
Biocritique, entre fausses routes et pas de côté

- 1/ Mensonges, gros mensonges et statistiques
- 2/ La biométrie, mesure de la réalité ou fabrication de fantasmes
- 3/ Vraies erreurs contre théories fausses
- 4/ « Ça ne marche pas! » Ethique des sciences?

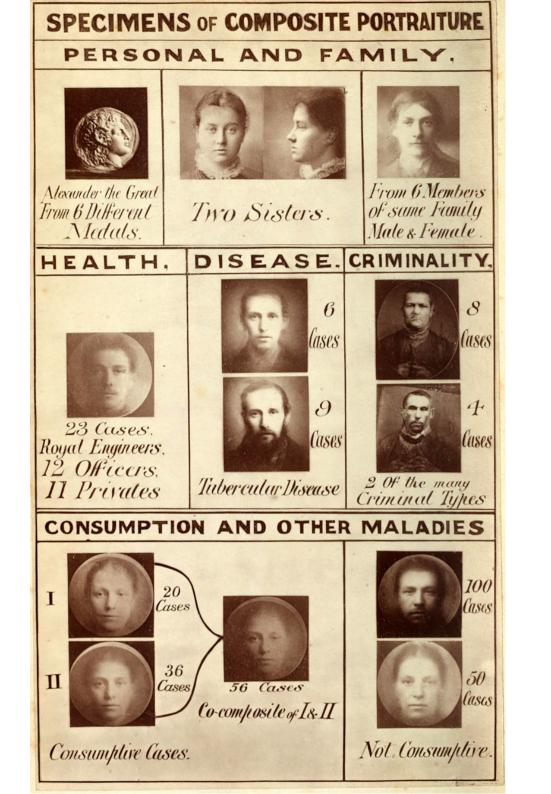
Composite heterosexual faces Composite gay faces Average facial landmarks gay straight







Lavater, 1775

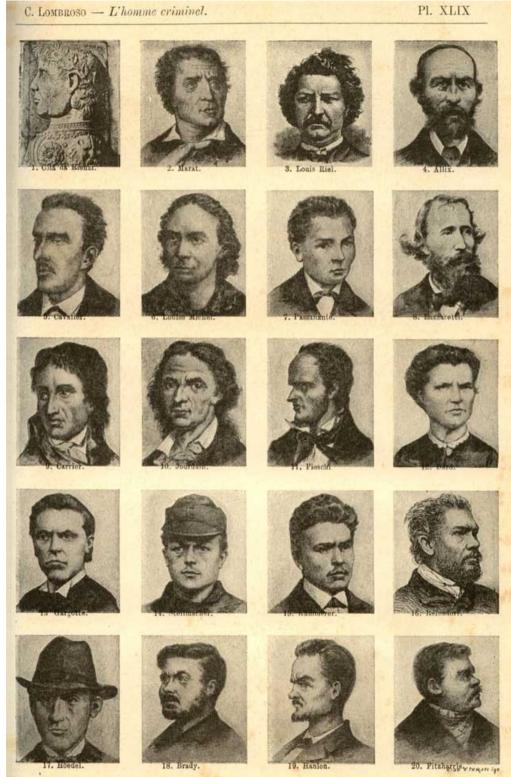


Galton, 1883



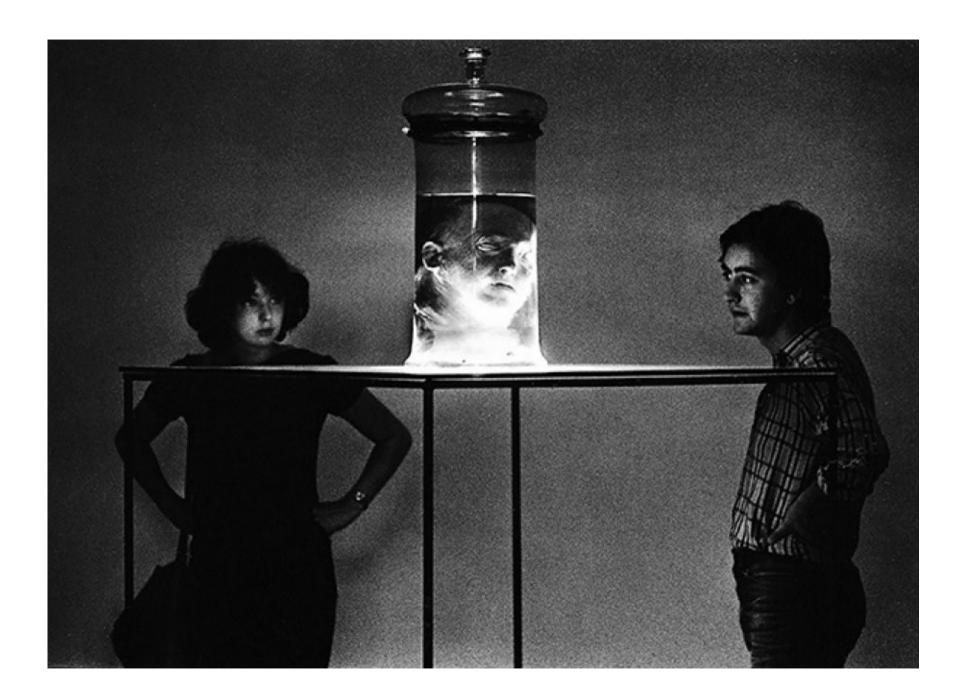


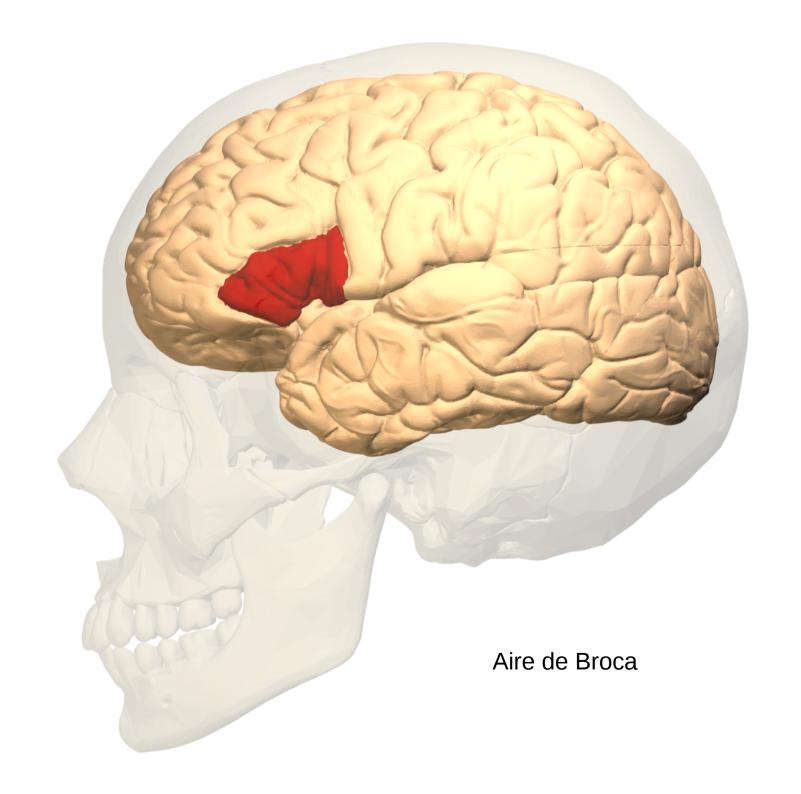
Oberlin, d'après Franz Gall, 1810



Lumbroso, 1876

RÉVOLUTIONNAIRES ET CRIMINELS POLITIQUES. - MATTOÏDES ET FOUS MORAUX.





## A Linkage Between DNA Markers on the X Chromosome and Male Sexual Orientation

Dean H. Hamer, Stella Hu, Victoria L. Magnuson, Nan Hu, Angela M. L. Pattatucci

The role of genetics in male sexual orientation was investigated by pedigree and linkage analyses on 114 families of homosexual men. Increased rates of same-sex orientation were found in the maternal uncles and male cousins of these subjects, but not in their fathers or paternal relatives, suggesting the possibility of sex-linked transmission in a portion of the population. DNA linkage analysis of a selected group of 40 families in which there were two gay brothers and no indication of nonmaternal transmission revealed a correlation between homosexual orientation and the inheritance of polymorphic markers on the X chromosome in approximately 64 percent of the sib-pairs tested. The linkage to markers on Xq28, the subtelomeric region of the long arm of the sex chromosome, had a multipoint lod score of  $4.0 \ (P = 10^{-5})$ , indicating a statistical confidence level of more than 99 percent that at least one subtype of male sexual orientation is genetically influenced.

Characteristics of study participants. The subjects studied were self-acknowledged homosexual men and their relatives over age 18. The initial sample for pedigree analysis consisted of 76 index subjects who were recruited through the outpatient HIV clinic at the National Institutes of Health Clinical Center, the Whitman-Walker Clinic in Washington, D.C., and local homophile organizations. One or more relatives from 26 of these families also participated in the project (total n = 122). The sample for the sib-pair pedigree study consisted of 38 pairs of homosexual brothers, together with their parents or other relatives when available, who were recruited through advertisements in local and national homophile publications. Two additional families who were originally in the random-or ly ascertained pool were added to this group for the DNA linkage study (total n = 114). Subjects signed an Informed Consent, approved by the NCI Clinical Review Sub-