

## CanRisk Tool

The CanRisk tool is a web interface to BOADICEA, the **B**reast and **O**varian **A**nalysis of **D**isease **I**ncidence and **C**arrier **E**stimation **A**lgorithm, risk prediction model used to calculate future breast and ovarian cancer risks in women. This is the first comprehensive model that allows for reliable breast cancer risk prediction in unaffected women on the basis of mutation screening information for rare (high risk and moderate risk) breast cancer genetic susceptibility variants, common cancer genetic susceptibility variants (using polygenic risk scores), explicit family history, personal lifestyle, hormonal and reproductive risk factors, and mammographic density. This model is described in [Lee et al. 2019](#).

The ovarian cancer risks are calculated using a separate prediction model that is based on the BOADICEA methodology, and extensions of the ovarian cancer risk model described by [Jervis et al.](#) The model includes the effects of rare pathogenic variants BRCA1, BRCA2, RAD51D, RAD51C and BRIP1. It also can use polygenic risk scores, explicit family history, personal lifestyle/hormonal/reproductive risk factors. For details see '[What information do the breast and ovarian cancer models use to determine risks?](#)'

This work is supported by grants through Cancer Research UK, the European Union's Horizon 2020 and Innovation programme, Genome Canada and a Wellcome Trust Collaborative Award.

Please see more details here on the Cancer Research-UK funded [CanRisk programme](#).

**The CanRisk Tool carries the CE marking and has been created and maintained by the University of Cambridge.**

## CanRisk Team

### Team Leaders

[Antonis Antoniou](#),  
Department of Public Health and Primary Care,  
University of Cambridge.

[Douglas Easton](#),  
Department of Public Health and Primary Care,  
University of Cambridge.

[Fiona Walter](#),  
Department of Public Health and Primary Care,  
University of Cambridge.

[Marc Tischkowitz](#),  
Department of Medical Genetics and National Institute for Health Research,  
University of Cambridge

### Development team at the Department of Public Health and Primary Care, University of Cambridge

Steph Archer,  
Research Associate

Andrew Lee,  
Research Associate

Alex Cunningham,  
Computer Programmer

Tim Carver,  
Computer Programmer

### Clinical Advisor

[Jonathan Roberts](#)

### Alumni

Chantal Babb de Villiers,  
Research Associate

Simon Hartley,  
Computer Programmer

## Publications

1. Parichoy Pal Choudhury et al. [Comparative validation of the BOADICEA and Tyrer-Cuzick breast cancer risk models incorporating classical risk factors and polygenic risk in a population-based prospective cohort](#) (submitted 2020).
2. Archer, S. et al. [Evaluating clinician acceptability of the prototype CanRisk tool for predicting risk of breast and ovarian cancer: A multi-methods study](#). PLoS ONE 15, e0229999 (2020)
3. Mavaddat, N. et al. [Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes](#). The American Journal of Human Genetics 104, 21–34 (2019).
4. Lee, A. et al. [BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors](#). Genet Med 21, 1708–1718 (2019).
5. Carver, T. et al. [pedigreejs: a web-based graphical pedigree editor](#). Bioinformatics 34, 1069–1071 (2018).
6. Lee, A. J. et al. [Incorporating truncating variants in PALB2, CHEK2, and ATM into the BOADICEA breast cancer risk model](#). Genet. Med. 18, 1190–1198 (2016).
7. Jervis, S. et al. [A risk prediction algorithm for ovarian cancer incorporating BRCA1, BRCA2, common alleles and other familial effects](#). Journal of Medical Genetics 52, 465–475 (2015).
8. Lee, A. J. et al. [BOADICEA breast cancer risk prediction model: updates to cancer incidences, tumour pathology and web interface](#). Br. J. Cancer 110, 535–545 (2014).
9. MacInnis, R. J. et al. [Prospective validation of the breast cancer risk prediction model BOADICEA and a batch-mode version BOADICEACentre](#). British Journal of Cancer 109, 1296–1301 (2013).
10. Mavaddat, N. et al. [Pathology of Breast and Ovarian Cancers among BRCA1 and BRCA2 Mutation Carriers: Results from the Consortium of Investigators of Modifiers of BRCA1/2 \(CIMBA\)](#). Cancer Epidemiol Biomarkers Prev 21, 134–147 (2012).
11. Cunningham, A. P., Antoniou, A. C. & Easton, D. F. [Clinical software development for the Web: lessons learned from the BOADICEA project](#). BMC Medical Informatics and Decision Making 12, 30 (2012).
12. Mavaddat, N., Rebbeck, T. R., Lakhani, S. R., Easton, D. F. & Antoniou, A. C. [Incorporating tumour pathology information into breast cancer risk prediction algorithms](#). Breast Cancer Research 12, R28 (2010).
13. Antoniou, A. C. et al. [Predicting the likelihood of carrying a BRCA1 or BRCA2 mutation: validation of BOADICEA, BRCAPRO, IBIS, Myriad and the Manchester scoring system using data from UK genetics clinics](#). Journal of Medical Genetics 45, 425–431 (2008).
14. Barcenas, C. H. et al. [Assessing BRCA Carrier Probabilities in Extended Families](#). JCO 24, 354–360 (2006).
15. Antoniou, A. C. & Easton, D. F. [Risk prediction models for familial breast cancer](#). Future Oncol 2, 257–274 (2006).
16. Antoniou, A. C. et al. [BRCA1 and BRCA2 mutation predictions using the BOADICEA and BRCAPRO models and penetrance estimation in high-risk French-Canadian families](#). Breast Cancer Research 8, R3 (2005).
17. Antoniou, A. C. et al. [The BOADICEA model of genetic susceptibility to breast and ovarian cancers: updates and extensions](#). British Journal of Cancer 98, 1457–1466 (2008).
18. Antoniou, A. C., Pharoah, P. P. D., Smith, P. & Easton, D. F. [The BOADICEA model of genetic susceptibility to breast and ovarian cancer](#). British Journal of Cancer 91, 1580–1590 (2004).