



ANTOINE LUCAS

Computer scientist

CONTACT

 +33 7 69 24 38 00
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 1 rue Corisande
 64160 Morlaàs France.

DIPLOMA

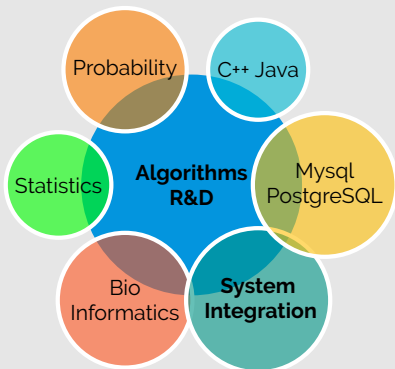
2017 CAP Électricien, Auch
2014 Ingénieur INSA, Toulouse
2000 Magistère d'économiste statisticien
2000 DEA in Mathematics, Toulouse
1999 Maîtrise d'économétrie, Toulouse

SKILLS

Languages

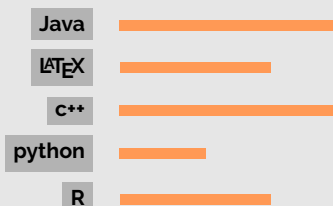
French | mother tongue
English | ● ● ● ●

Interests



OS:  

IT & programming



REFERENCES

Total Pau | Pierre Thore
Thales Brest | Jean-Yves Gindre
Inra Toulouse | David Allouche

PROFESSIONAL EXPERIENCE

2014 – now | **Total**, Pau
 R&D and java software industrialisation
 Publication and Patents

2007 – 2014 | **Thales**, Brest
 Software and System integration of mine warefare ships
 Software development
 Integration and **sea tests** in Danemark, Singapore and India.

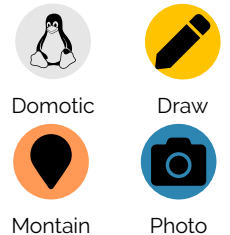
2006 | **EADS** Val de Rueil – software development

2001 – 2006 | **INRA INRIA CNRS** Bioinformatics
 Publications, courses, and softwaree development

EMPLOYERS

2023 Freelance – Morlaàs
2017-2022 Tech Advantage – Pau
2008-2017 Thales Service – Brest, Toulouse
2006-2008 Alten / Gist – Paris, Brest
2004-2006 CNRS – Gif sur Yvette
2002-2003 INRIA – Auzeville
2001-2002 INRA – Auzeville

HOBBIES



PATENTS

2022 Method and system for analyzing a reservoir geological formation by skeleton computation on a large reservoir grid

2022 Method and system for determining streamlines in a reservoir geological formation by a dual front propagation.

PUBLICATIONS

2023 Box Airbnb, domotique avec des SMS, *Hackable*

2023 Extracting connectivity paths in 3D reservoir property: A pseudo skeletonization approach, *Computers and Geosciences*.

2009 Novel long non-protein coding RNAs Involved in Arabidopsis differentiation and stress response, *Genome Res*.

2006 Using Amap and ctc package for huge clustering *R News*.

2006 Characterization of 43 non-protein coding m-RNA genes in Arabidopsis, including the MIR162a-derived transcript *Plant Physiol*.

2004 Nitrogen regulation in Sinorhizobium meliloti probed with whole genome arrays, *FEMS Microbiol*.