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Showcasing Sanger Science

- Celebrating 20 years of Sanger Institute
- DNA sequencing technologies
- Sanger Institute research:
 - Tracking hospital outbreak of MRSA
 - Mapping drug-resistant malaria parasites
 - Cancer genome sequencing
 - Sequencing 1000s of genomes in UK10K
 - Identifying genetic causes of developmental disorders
- Exploring the ethical issues of DNA sequencing





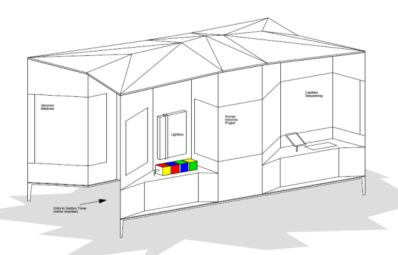
Scientific stakeholders

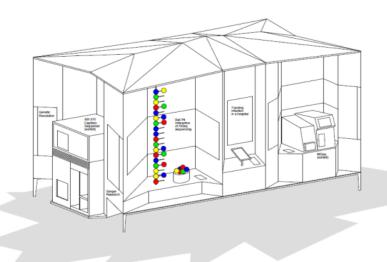
- Julia Willingale-Theune Public Engagement
- Steve Scott Public Engagement
- Don Powell Media and PR
- Cordelia Langford DNA sequencing
- Julian Parkhill / Matt Holden MRSA
- Julian Rayner Malaria
- Serena Nik-Zainal Cancer
- Dawn Muddyman UK10K
- Anna Middleton Ethics





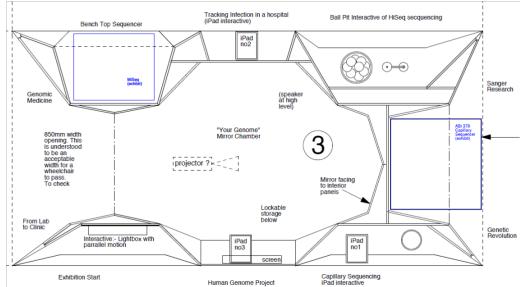
Our stand





Designed by Nick Bell Design and Nick Coombe Architecture







Our stand





Built by Van Rooij & Griffiths

Graphic production by Albermarle Graphics

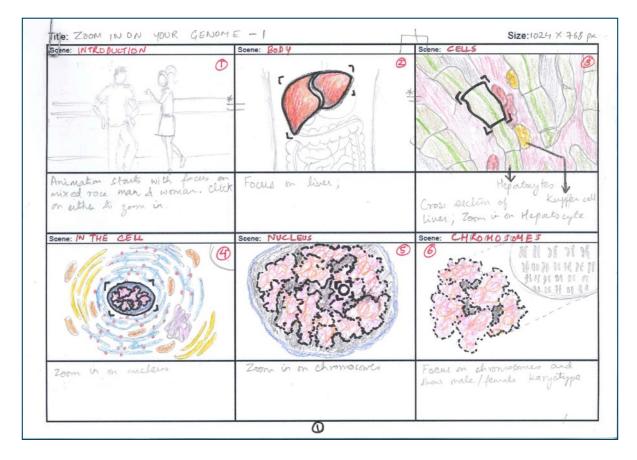








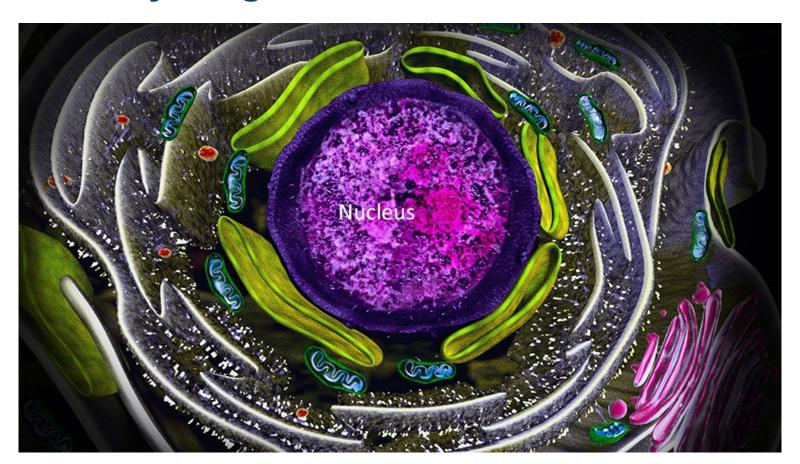
Zoom into your genome







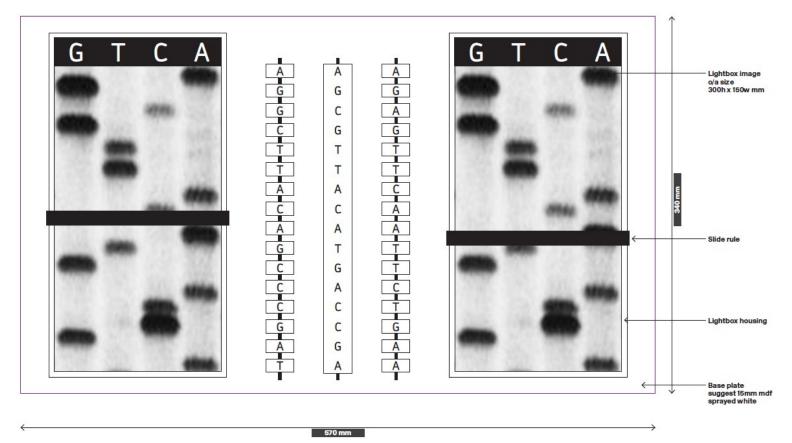
Zoom into your genome







Try your hand at sequencing







Try your hand at sequencing



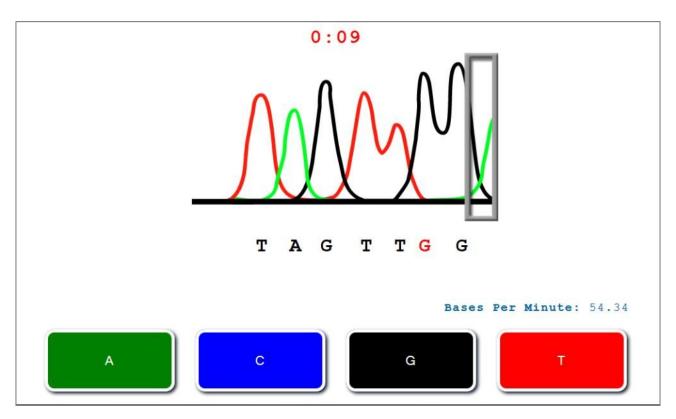


Built by Machineshop





You vs. machine

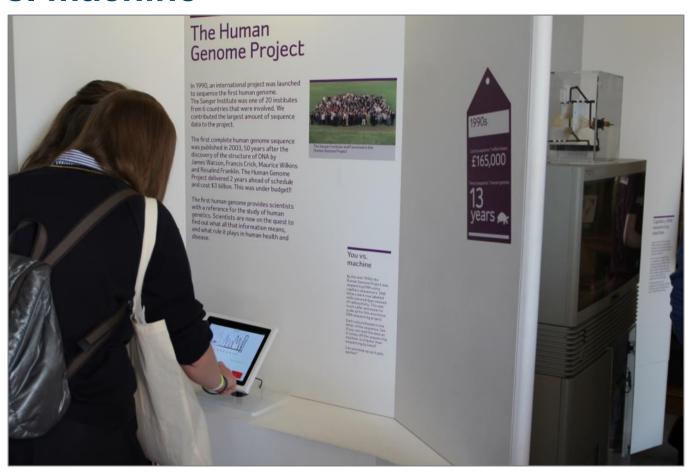


Created by Nicholas Tieman (freelancer via elance.com)





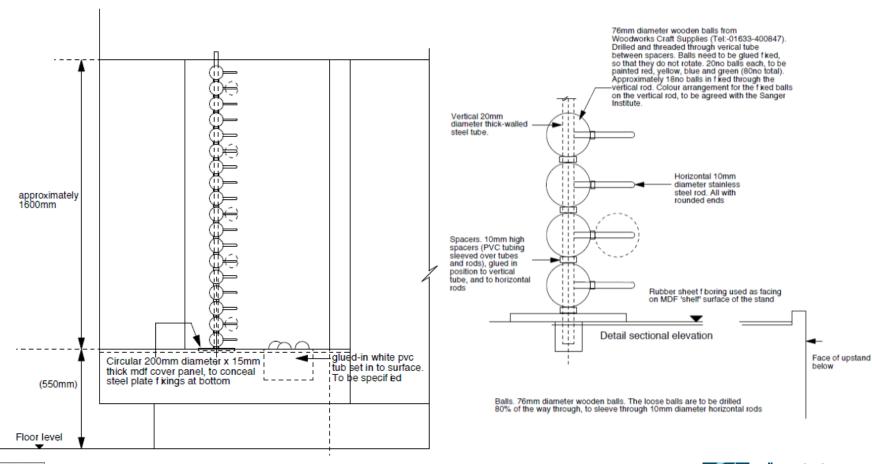
You vs. machine







Build DNA







Build DNA

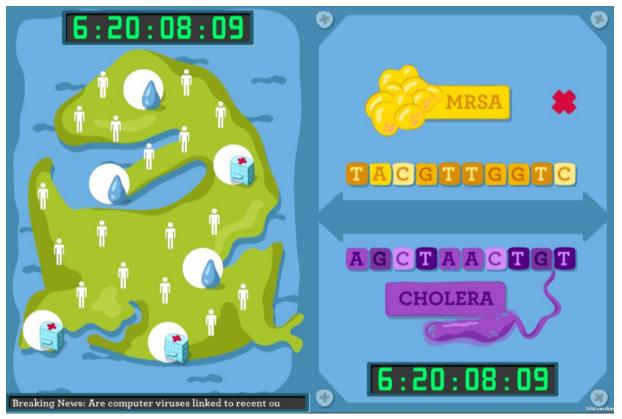








Game Jam – Bug outbreak

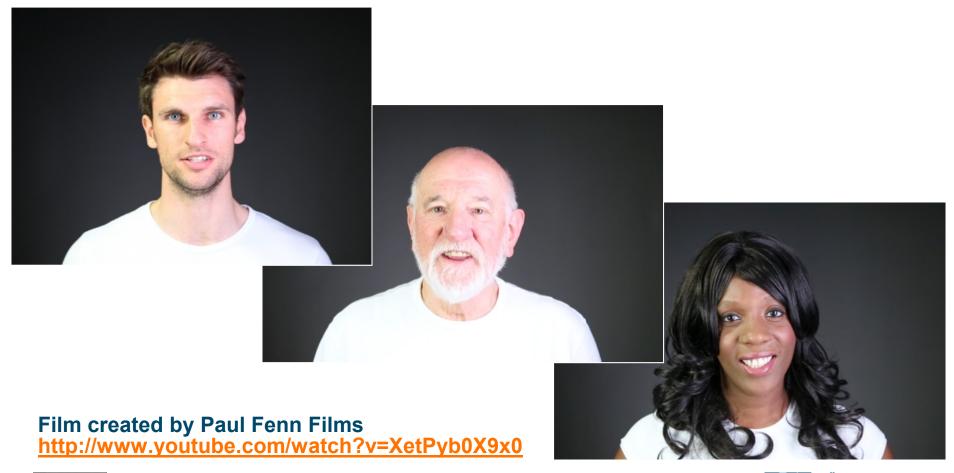


Created by Opposable Games via Royal Society





Your views







Transatlantic ethics poll







Online



Further reading

- Harris, S.R. et al. 2012 Using whole genome sequencing to dissect the cause and effect of a meticillin-resistant Staphylococcus aureus outbreak: a descriptive study?. Lancet Infectious Diseases 13, 2, 130-136.
- Manske, M. et al. 2012 Analysis of Plasmodium falciparum diversity in natural infections by deep sequencing. Nature 487, 375-37
- Garnett, M.J. et al. 2012 Systematic identification of genomic markers of drug sensitivity in cancer cells. Nature 483, 570-575

Genes influence a person's appearance, characteristics and their susceptibility to disease. They can even help archaeologists identify long lost kings. Rapid advances in DNA sequencing are providing scientists with the ability to explore the human genome, or genetic code, in more detail. This is leading to new discoveries about the genetic causes of human disease and new ways to improve our health.

How it works

This exhibit demonstrates how the combination of expertise from science, technology, engineering and maths, utilising powerful computing, can uncover the changes in DNA that lead to a variety of human diseases. For example, the Cancer Genome Project compares DNA from tumour



Presented by Wellcome Trust Sanger Institute



Anna Middleton

Wellcome Trust Sanger Institute



Karola Rehnstrom

Wellcome Trust Sanger Institute



Richard Durbin Wellcome Trust Sanger Institute



Serena Nik-Zainal Wellcome Trust Sanger Institute

Julian Rayner Wellcome Trust Sanger Institute



Images



Exhibit blog

Day 7 (last day!): Our volunteers

Blogging



aatatcaactgttttggaaaccttagacd aggtcat acttgcaai\agtagtgccataatta Caaacataaa baggatttattta ggggccactctc/figctttt cagaacagagto gccccttacgtgt tccatagcattte aacagctcttttatat

Home Archive



Would you have your genome sequenced?



Your genes can tell you about your past, present and future medical Your genes can tell you about your past, Present and tuture medical health. But what would you want to know from your genes? This is one of means. But, what, wome you want to know from your genes; 1mm is one or the questions we are asking this week on our stand Beyond the Genome at the proof for the Royal Society Summer Science Exhibition.

DNA sequencing is gradually becoming cheaper and cheaper and it won't be long before the cost of sequencing a human genome will be less than E1,000. Today, a CT scan carries a similar cost so it is not unrealistic for EXPLORATE VALUE OF A U.S. SCHOLLERS OF THE PROPERTY OF STREET, AND on where command or cover requestions and amountaine used transcribed eventually be used in our NHS hospitals. This is great when we consider the possibility of being able to accurately discover the DNA changes responding nor a cantage so endure the own daught as years of the control of the responsible for a cancer to ensure the best drug is given that are part of an MESA outbreak (the idea being to choke the bugs at that are part or an airxia outuress (the uses seing to chose use outp.)
source and prevent the MSSA spreading further), Or even for DNA. sequencing to become a standard part of a newborn child's medical sequencing to occurre a standart part of a measure came a me records, that can be referred to if they become ill later in life. But hold on for a moment! What does all this information mean and what

Let's step back from the wonders of science and technology to think about if we don't want to know all of it? this for a minute. When we sequence a human genome we are looking at this for a minute. When we sequence a numan generate we are seening at 3,000,000,000 letters of DNA, finding out about all 20,000+ genes in 3:00U,000,000 retters at UNA, timming out about an 20,000 * genes in one 80. Realistically, such person's genome contains an average of around one go, meansument, each person's grinome curitains an average or around 100 different things of interest. Some of these may take effect on a person and unnerest unity or interest bonne or there are a series and a series from an adult and some may be relevant to their future on uney grow into an aount and gome may be reservant to users mouse children, if they have them. It has been estimated that counselling charge, μ may have them, it has been estimated that counseling, someone through all of this information, would take around five hours. you want to know from your genome? Would you want to Introducing the 'father of genomics': Fred Sanger



nger Institute takes its name from the double Nobel Prize winner 'her of genomics', Frederick Sanger. The techniques Fred and his ies developed during the 1970s are still being used today in s. His pioneering work defined genomics and provided the on for the way we explore genomes today, both here at the stitute and worldwide.

er, who will celebrate his 95th birthday in August, was born hire. His interest in biology originally stemmed from his ', and Fred initially set out to study medicine at the f Cambridge. During his time there he specialised in 7, allowing him the opportunity to work alongside some ng biochemists at that time. It comes as no surprise the schemistry inspired him to leave the path of medicine at area. As a conscientious objector during the Secon

Beyond the Genome - the week so far



We're now over half way through the Royal Society Summer Science research over one may through the anyer owners summer science exhibition, 50, what's happened so far? Well, we've had an amazing exmonuos, 30, wast's suspensed to sar; view, we ve stad an amazing response to our stand Beyond the genome. Visitors have been clambering response to our stanu segonu one genome. Vastors have own transcering to play with our hands-on interactives, racing to sequence DNA as fast as to play with our name-on interactives, racing to sequence excess as east as they can. Our You're, Machine game has brought the competitive spirit they call. Our row co. anumone gettie has brought the temperature sparse out of visitors, our explainers and even other exhibitors! Our neighbours on the Zebrafish genetics stand are currently top of the table. Please someone come and knock them off the top spot!!!

We've had some great chats with visitors about how DNA sequencing has the venau some great chair which you want how have sequencing in changed and revolutionised what we understand about human health changed and revolutionised what we understain about trained intensity and disease. The rapid advancement of DNA sequencing technologies has and sureage. The Legou out anteneut of LAVA requesting secunologies has astounded many people; from the incredible reduction in the time it takes to sequence a human genome, to the sharp fall in the cost of DNA to sequence a numan genome, to the snary ran in the cost of poor sequencing. All of this technology is enabling us to do amazing research on the genetics of humans and also the genetics of organisms that cause ton the generate on minutess arm may the generate or organization than the disease such as viruses, bacteria and eukaryotes, like malaria and

We've also had interesting, and challenging, conversations about the we've also man interesting, and conducting, the resonance of the social and ethical issues of DNA sequencing. Our inner future chamber social and ethical issues of MAA sequencing. Our inner nature chainner beams DNA sequence on to visitors and encourages them to think about ocans need a sequence on to statute and careful upon what they would like to know about their genome. We're certainly what they would like to allow about their genome, we be certainly getting to hear plently of opinions, which is fantastic. A lot of visitors seem genomes - what they might be able to find our short

The Royal Society summer science exhibition



Volunteers

	Morning	Afternoon	Evening	Overnight	
Sunday				Group A	
Monday	Group A (10:00-14:00)	Group B (14:00-18:00)	Group A (18:00-22:00)	Group B	Group A
Tuesday	Group B (10:00-14:00)	Group C (14:00-17:30)	Group B (17:30-21:00)	Group C	Group B
Wednesday	Group C (10:00-13:30)	Group D (13:30-17:00)	Group C (19:00-22:00) *	Group D	Group C
Thursday	Group D (10:00-13:30)	Group E (13:30-17:00)	Group D (19:00-22:00) *	Group E	Group D
Friday	Group E (10:00-13:30)	Group F (13:30-17:30)	Group E (17:30-21:00)	Group F	Group E
Saturday	Group F (10:00-13:30)	Group G (13:30-17:30)	Group F (17:30-21:00)	Group G	Group F
Sunday	Group G (10:00-12:30)	Group H (12:30-15:30)	Group G (15:30-1800)	Group H	





Volunteers

MONDAY 1 JULY								Accomm							
Start 10.00				Finish 14.00	Start 14.00				Finish 18.00	Start 18.0				Finish 22.00	
			Steve Scott					Steve Scott					Steve Scott		Steve Scott
Group 1 -1	Confirmed	James Torrance	Genome Referencing Informatics Group		1					Group 1 -1	Confirmed	James Torrance	Genome Referencing Informatics Group		No accomm
Group 1 - 2	Confirmed	Sarah Smith	Pathogens			Serena Nik Zair	nal some time			Group 1 - 2	Confirmed	Sarah Smith	Pathogens		Sarah Smith
Group 1 -3	Confirmed	Lia Chappell	Malaria		1					Group 1 -3	Confirmed	Lia Chappell	Malaria		Lia Chappell
Group 1 -4	Confirmed	Anna Middleton	HumGen							Group 1 -4	Confirmed	Serena Nik Zainal	CGP		No accomm
Group 1 -5	Confirmed	Valerie Vancollie	Model organisms		1					Group 1 -5	Confirmed	Valerie Vancollie	Model organisms		Valerie Vancollie
Group 1 -6	Confirmed	Howard Lightfoot	CGP		1					Group 1 -6	Confirmed	Howard Lightfoot	CGP		No accomm
Group 1 -7	Confirmed	Wendy Jones	Barrett Faculty							Group 1 -7					Anna Middleton
					Group 2 -1	Confirmed	Tomislav Illicic	Teichmann							Tomislav Illicic
					Group 2 -2										Group 2 -2
					Group 2 -3	Confirmed	Karen Kennedy	Admin							Karen Kennedy
					Group 2 -4	Confirmed	Lucy Yates	CGP							No accomm
					Group 2 -5	Confirmed	Sandra Reuter	Pathogens							Sandra Reuter
					Group 2 -6	Confirmed	Chris Illingworth	Genome Referencing Informatics Group							Chris Illingworth
					Group 2 -7	Confirmed	Amy Cain	Pathogens							Amy Cain

TUESDAY 2 JULY													
Start 10.00		Fini	ish 14.00 Star	rt 14.00			Finish 17.30	Start 17.30			Finish 21.0	0	1
		Steve Scott				Steve Scott					Steve Scott		Steve S
Group 2 -1	Confirmed Tomislav Illicic	Teichmann						Group 2 -1	Confirmed	Tomislav Illicic	Teichmann		Tomisla
Group 2 -2								Group 2 -2					Group 2
Group 2 -3	Confirmed Karen Kennedy	Admin						Group 2 -3	Confirmed	Karen Kennedy	Admin		Karen K
Group 2 -4	Confirmed Lucy Yates	CGP						Group 2 -4	Confirmed	Lucy Yates	CGP		No acco
Group 2 -5	Confirmed Sandra Reuter	Pathogens						Group 2 -5	Confirmed	Sandra Reuter	Pathogens		Sandra I
Group 2 -6	Confirmed Chris Illingworth	Genome Referencing Informatics Group						Group 2 -6	Confirmed	Chris Illingworth	Genome Referencing Informatics Group		Chris Illi
Group 2 -7	Confirmed Amy Cain	Pathogens						Group 2 -7	Confirmed	Amy Cain	Pathogens		Amy Cai
			Group	3-1 Confirmed	Klaudia Walter	HumGen							Klaudia \
			Group	3 - 2 Confirmed	Lucy Crooks	HumGen							Lucy Cro
			Group	3 - 3 Confirmed	Magdalena Zarowiecki	PathGen							No accor
			Group	3 - 4 Confirmed	Christine Boinett	Pathogens							No accor
			Group	3 - 5 Confirmed	Anna Middleton	HumGen							Anna Mi
			Group	3 - 6 Confirmed	Hayley Bennett	Pathogens							Hayley B
			Group	3 - 7 Confirmed	Katja Kivinen	Malaria							No accor

	WEDNESDAY 3 JULY]							
Start 10.00)			Finish 13.30	Start 13.30					Finish 17.00		Start 19.00		SOIREE - DRESS CODI		Finish 22.00	
			Steve Scott						Steve Scott				Ste	ve Scott			Steve Scott
Group 3-1	Confirmed	Klaudia Walter	HumGen									Group 3-1	Confirmed	Klaudia Walter	HumGen		Klaudia Walter
Group 3 - 2	Confirmed	Lucy Crooks	HumGen									Group 3 - 2	Confirmed	Lucy Crooks	HumGen		Lucy Crooks
Group 3 - 3	Confirmed	Magdalena Zarowiecki	PathGen									Group 3 - 3	Confirmed	Magdalena Zarowiecki	PathGen		No accom
Group 3 - 4	Confirmed	Christine Boinett	Pathogens									Group 3 - 4	Confirmed	Christine Boinett	Pathogens	No due to Soiree	No accom
Group 3 - 5	Confirmed	Anna Middleton	HumGen									Group 3 - 5	Confirmed	Anna Middleton	HumGen		Anna Middleton
Group 3 - 6	Confirmed	Hayley Bennett	Pathogens									Group 3 - 6	Confirmed	Hayley Bennett	Pathogens		Hayley Bennett
Group 3 - 7	Confirmed	Richard Durbin	HumGen									Group 3 - 7	Confirmed	Richard Durbin	HumGen	Fellow	Richard Durbin
					Group 4 - 1	Confirmed	Yasin Memari	Humgen					Steve Scott				Yasin Memari
					Group 4 - 2	Confirmed	Stuart McLaren	CGP									Stuart McLaren
					Group 4 - 3	Confirmed	Frank Schwach	Malaria									Frank Schwach
					Group 4 - 4	Confirmed	Will Proto	Malaria									WillProto
1					Group 4 - 5	Confirmed	Kevin Dawson	CGP									No accom
					Group 4 - 6												Group 4 - 6
					Group 4 - 7	Confirmed	Elizabeth Wynn										No accom

78 staff expressed interest and 55 attended





Budget

Work Package	Cost
Stand Design and Build	£55,780.34
AV hire	£2,231.76
Digital content	£2,842.94 (Game Jam = £2,000.00)
Accommodation for 55 explainers (Queen Mary, University of London)	£4,982.00
Travel for 55 explainers (Cambridge>London & around London)	£3,551.66
T-shirts (80) and wrist bands (2,500)	£2,215.20





Sponsors







Deciphering Developmental Disorders



MRC | Centre for Genomics and Global Health





Tips

- Plan with Royal Society early
- Plan stand build early
- Delegate responsibility
- Provide training for volunteers
- Be prepared to compromise
- Have lots of explainers
- Have giveaways with website on for more information
- Make it a memorable experience!





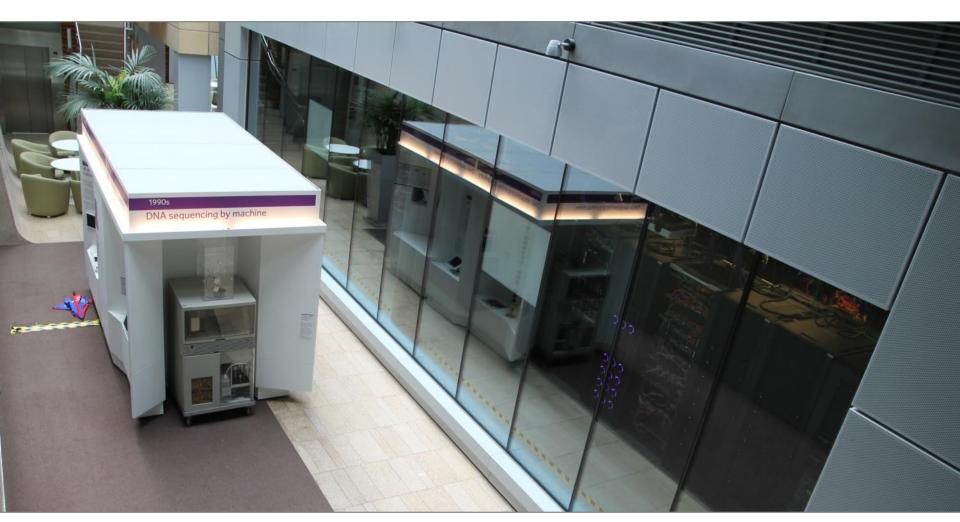
Legacy

- Physical exhibit on campus
- Reinvigorated staff
- Enthusiasm for public engagement
- New perspectives
- Community of researchers
- Increased interest in our research





Life after the RSSE







Life after the RSSE







Credits

- Exhibit designed by Nick Bell Design with Nick Coombe Architecture
- Built by Van Rooij & Griffiths
- Graphic production by Albermarle Graphics
- Films and falling letters by Paul Fenn Films
- AV equipment from Creative Staging
- Sequencing interactive by Machineshop
- You vs. machine app by Nicholas Tieman (freelancer via Elance.com)
- Bug outbreak by Opposable Games (via RS)



